

Active optical clock based on four-level quantum system

Active optical clock, a new conception of atomic clock, has been proposed recently. In this work, we propose a scheme of active optical clock based on four-level quantum system. The final accuracy and stability of two-level quantum system are limited by second-order Doppler shift of thermal atomic beam. To three-level quantum system, they are mainly limited by light shift of pumping laser field. These limitations can be avoided effectively by applying the scheme proposed here. Rubidium atom four-level quantum system, as a typical example, is discussed. The population inversion between $6S_{1/2}$ and $5P_{3/2}$ states can be built up at a time scale of 10^{-6} s. With the mechanism of active optical clock, in which the cavity mode linewidth is much wider than that of the laser gain profile, it can output a laser with quantum-limited linewidth narrower than 1 Hz in theory. An experimental configuration is designed to realize this active optical clock.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Frontier Photonics, Peking University, State Key Laboratory of Advanced Optical Communication Systems and Networks

Contributors: Zhang, T. G., Wang, Y. F., Zang, X. R., Zhuang, W., Chen, J. B.

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Peer-reviewed: Yes

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ASJC Scopus subject areas: General

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Research output: Contribution to journal > Article > Scientific > peer-review

Combining deep learning with token selection for patient phenotyping from electronic health records

Artificial intelligence provides the opportunity to reveal important information buried in large amounts of complex data. Electronic health records (eHRs) are a source of such big data that provide a multitude of health related clinical information about patients. However, text data from eHRs, e.g., discharge summary notes, are challenging in their analysis because these notes are free-form texts and the writing formats and styles vary considerably between different records. For this reason, in this paper we study deep learning neural networks in combination with natural language processing to analyze text data from clinical discharge summaries. We provide a detail analysis of patient phenotyping, i.e., the automatic prediction of ten patient disorders, by investigating the influence of network architectures, sample sizes and information content of tokens. Importantly, for patients suffering from Chronic Pain, the disorder that is the most difficult one to classify, we find the largest performance gain for a combined word- and sentence-level input convolutional neural network (ws-CNN). As a general result, we find that the combination of data quality and data quantity of the text data is playing a crucial role for using more complex network architectures that improve significantly beyond a word-level input CNN model. From our investigations of learning curves and token selection mechanisms, we conclude that for such a transition one requires larger sample sizes because the amount of information per sample is quite small and only carried by few tokens and token categories. Interestingly, we found that the token frequency in the eHRs follow a Zipf law and we utilized this behavior to investigate the information content of tokens by defining a token selection mechanism. The latter addresses also issues of explainable AI.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Computing Sciences, BioMediTech, Research group: Predictive Society and Data Analytics (PSDA), Research group: Computational Medicine and Statistical Learning Laboratory (CMSL), University of Applied Sciences Upper Austria, School of Management, Nankai University, UMIT-The Health and Life Sciences University, Institute for Systems Biology, Seattle, Washington, USA

Contributors: Yang, Z., Dehmer, M., Yli-Harja, O., Emmert-Streib, F.

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Research output: Contribution to journal › Article › Scientific › peer-review

Mechanism of homodimeric cytokine receptor activation and dysregulation by oncogenic mutations

Homodimeric class I cytokine receptors are assumed to exist as preformed dimers that are activated by ligand-induced conformational changes. We quantified the dimerization of three prototypic class I cytokine receptors in the plasma membrane of living cells by single-molecule fluorescence microscopy. Spatial and spatiotemporal correlation of individual receptor subunits showed ligand-induced dimerization and revealed that the associated Janus kinase 2 (JAK2) dimerizes through its pseudokinase domain. Oncogenic receptor and hyperactive JAK2 mutants promoted ligand-independent dimerization, highlighting the formation of receptor dimers as the switch responsible for signal activation. Atomistic modeling and molecular dynamics simulations based on a detailed energetic analysis of the interactions involved in dimerization yielded a mechanistic blueprint for homodimeric class I cytokine receptor activation and its dysregulation by individual mutations.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Biological Physics and Soft Matter, Physics, University of Osnabrück, University of Dundee, University of York, University of Helsinki, NYU School of Medicine, University of Helsinki, Stanford University School of Medicine

Contributors: Wilmes, S., Hafer, M., Vuorio, J., Tucker, J. A., Winkelmann, H., Löchte, S., Stanly, T. A., Pulgar Prieto, K. D., Poojari, C., Sharma, V., Richter, C. P., Kurre, R., Hubbard, S. R., Christopher Garcia, K., Moraga, I., Vattulainen, I., Hitchcock, I. S., Piehler, J.

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Publication information

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Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1126/science.aaw3242

Bibliographical note

EXT="Poojari, Chetan"

EXT="Sharma, Vivek"

Source: Scopus

Source ID: 85079082079

Research output: Contribution to journal › Article › Scientific › peer-review

Insulin resistance is associated with altered amino acid metabolism and adipose tissue dysfunction in normoglycemic women

Insulin resistance is associated with adiposity, but the mechanisms are not fully understood. In this study, we aimed to identify early metabolic alterations associated with insulin resistance in normoglycemic women with varying degree of adiposity. One-hundred and ten young and middle-aged women were divided into low and high IR groups based on their median HOMA-IR (0.9 ± 0.4 vs. 2.8 ± 1.2). Body composition was assessed using DXA, skeletal muscle and liver fat by proton magnetic resonance spectroscopy, serum metabolites by nuclear magnetic resonance spectroscopy and adipose tissue and skeletal muscle gene expression by microarrays. High HOMA-IR subjects had higher serum branched-chain amino acid concentrations (BCAA) ($p < 0.05$ for both). Gene expression analysis of subcutaneous adipose tissue revealed significant down-regulation of genes related to BCAA catabolism and mitochondrial energy metabolism and up-regulation of several inflammation-related pathways in high HOMA-IR subjects ($p < 0.05$ for all), but no differentially expressed genes in skeletal muscle were found. In conclusion, in normoglycemic women insulin resistance was associated with increased serum BCAA concentrations, down-regulation of mitochondrial energy metabolism and increased expression of inflammation-related genes in the adipose tissue.

General information

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MoE publication type: A1 Journal article-refereed

Organisations: Department of Signal Processing, University of Jyväskylä, Shanghai Jiaotong University, Pirkanmaa Hospital District and School of Health Sciences, University of Oulu, Oulu University Hospital

Contributors: Wiklund, P., Zhang, X., Pekkala, S., Autio, R., Kong, L., Yang, Y., Keinänen-Kiukaanniemi, S., Alen, M., Cheng, S.

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Publication information

Journal: Scientific Reports

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Ratings:

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Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Insulin resistance is associated with altered amino acid metabolism and adipose tissue dysfunction in normoglycemic women

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Bibliographical note

EXT="Autio, Reija"

Source: Scopus

Source ID: 84964253523

Research output: Contribution to journal > Article > Scientific > peer-review

Redox-coupled quinone dynamics in the respiratory complex I

Complex I couples the free energy released from quinone (Q) reduction to pump protons across the biological membrane in the respiratory chains of mitochondria and many bacteria. The Q reduction site is separated by a large distance from the proton-pumping membrane domain. To address the molecular mechanism of this long-range proton-electron coupling, we perform here full atomistic molecular dynamics simulations, free energy calculations, and continuum electrostatics calculations on complex I from *Thermus thermophilus*. We show that the dynamics of Q is redox-state-dependent, and that quinol, QH₂, moves out of its reduction site and into a site in the Q tunnel that is occupied by a Q analog in a crystal structure of *Yarrowia lipolytica*. We also identify a second Q-binding site near the opening of the Q tunnel in the membrane domain, where the Q headgroup forms strong interactions with a cluster of aromatic and charged residues, while the Q tail resides in the lipid membrane. We estimate the effective diffusion coefficient of Q in the tunnel, and in turn the characteristic time for Q to reach the active site and for QH₂ to escape to the membrane. Our simulations show that Q moves along the Q tunnel in a redox-state-dependent manner, with distinct binding sites formed by conserved residue clusters. The motion of Q to these binding sites is proposed to be coupled to the proton-pumping machinery in complex I.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Technische Universität München, Max Planck Institute of Biophysics, University of Helsinki, University of Helsinki Institute of Biotechnology, Laboratory of Physics, MEMPHYS – Center for Biomembrane Physics, University of Southern Denmark, Goethe-University Frankfurt

Contributors: Warnau, J., Sharma, V., Gamiz-Hernandez, A. P., Luca, A. D., Haapanen, O., Vattulainen, I., Wikström, M., Hummer, G., Kaila, V. R.
Pages: E8413-E8420
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Original language: English

ASJC Scopus subject areas: General

Keywords: Cell respiration, Diffusion model, Electron transfer, Molecular simulations, NADH:ubiquinone oxidoreductase
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10.1073/pnas.1805468115

Bibliographical note

EXT="Sharma, Vivek"

Source: Scopus

Source ID: 85052742187

Research output: Contribution to journal > Article > Scientific > peer-review

Rapid growth of new atmospheric particles by nitric acid and ammonia condensation

A list of authors and their affiliations appears at the end of the paper. New-particle formation is a major contributor to urban smog^{1,2}, but how it occurs in cities is often puzzling³. If the growth rates of urban particles are similar to those found in cleaner environments (1–10 nanometres per hour), then existing understanding suggests that new urban particles should be rapidly scavenged by the high concentration of pre-existing particles. Here we show, through experiments performed under atmospheric conditions in the CLOUD chamber at CERN, that below about +5 degrees Celsius, nitric acid and ammonia vapours can condense onto freshly nucleated particles as small as a few nanometres in diameter. Moreover, when it is cold enough (below –15 degrees Celsius), nitric acid and ammonia can nucleate directly through an acid–base stabilization mechanism to form ammonium nitrate particles. Given that these vapours are often one thousand times more abundant than sulfuric acid, the resulting particle growth rates can be extremely high, reaching well above 100 nanometres per hour. However, these high growth rates require the gas-particle ammonium nitrate system to be out of equilibrium in order to sustain gas-phase supersaturations. In view of the strong temperature dependence that we measure for the gas-phase supersaturations, we expect such transient conditions to occur in inhomogeneous urban settings, especially in wintertime, driven by vertical mixing and by strong local sources such as traffic. Even though rapid growth from nitric acid and ammonia condensation may last for only a few minutes, it is nonetheless fast enough to shepherd freshly nucleated particles through the smallest size range where they are most vulnerable to scavenging loss, thus greatly increasing their survival probability. We also expect nitric acid and ammonia nucleation and rapid growth to be important in the relatively clean and cold upper free troposphere, where ammonia can be convected from the continental boundary layer and nitric acid is abundant from electrical storms^{4,5}.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Carnegie Mellon University, California Institute of Technology, Paul Scherrer Institut, University of Helsinki, European Organization for Nuclear Research, Ita-Suomen yliopisto, Goethe-University Frankfurt, CENTRA and Faculdade de Ciências da Universidade de Lisboa, Karlsruhe Institute of Technology, Institute for Technical Physics, Germany, Tofwerk AG, Der Technischen Universität Wien Fakultät für Elektrotechnik und Informationstechnik, University of Colorado at Boulder, University of Innsbruck, Ionicon GesmbH, Aerodyne Research Inc., Finnish Meteorological Institute, Institute for Atmospheric and Earth System Research/Physics, Lebedev Physical Institute, University of Leeds, Grimm Aerosol Technik Ainring, IDL, Stockholm University, Nanjing University, Beijing University of Chemical Technology

Contributors: Wang, M., Kong, W., Marten, R., He, X. C., Chen, D., Pfeifer, J., Heitto, A., Kontkanen, J., Dada, L., Kürten, A., Yli-Juuti, T., Manninen, H. E., Amanatidis, S., Amorim, A., Baalbaki, R., Baccarini, A., Bell, D. M., Bertozzi, B., Bräkling, S., Brilke, S., Murillo, L. C., Chiu, R., Chu, B., De Menezes, L. P., Duplissy, J., Finkenzeller, H., Carracedo, L. G., Granzin, M., Guida, R., Hansel, A., Hofbauer, V., Krechmer, J., Lehtipalo, K., Lamkaddam, H., Lampimäki, M., Lee, C. P., Makhmutov, V., Marie, G., Mathot, S., Mauldin, R. L., Mentler, B., Müller, T., Onnela, A., Partoll, E., Petäjä, T., Philippov, M., Pospisilova, V., Ranjithkumar, A., Rissanen, M., Rörup, B., Scholz, W., Shen, J., Simon, M., Sipilä, M., Steiner, G., Stolzenburg, D., Tham, Y. J., Tomé, A., Wagner, A. C., Wang, D. S., Wang, Y., Weber, S. K., Winkler, P. M., Wlasits, P. J., Wu, Y., Xiao, M., Ye, Q., Zauner-Wieczorek, M., Zhou, X., Volkamer, R., Riipinen, I., Dommen, J., Curtius, J., Baltensperger, U., Kulmala, M., Worsnop, D. R., Kirkby, J., Seinfeld, J. H., El-Haddad, I., Flagan, R. C., Donahue, N. M.

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URLs:
<http://urn.fi/URN:NBN:fi:tuni-202007076344>
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Source ID: 85084625341
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X-ray microtomography is a novel method for accurate evaluation of small-bowel mucosal morphology and surface area

The often poorly orientated small-bowel mucosal biopsies taken for the diagnostics of celiac disease and other intestinal disorders are prone to misinterpretation. Furthermore, conventional histopathology has suboptimal sensitivity for early histopathological changes observed in short-term challenge studies. X-ray microtomography (micro-CT) is a promising new method for accurate imaging of human-derived biological samples. Here, we report that micro-CT could be utilized to create virtual reconstructions of endoscopically obtained intestinal biopsies. The formed digital 3D images enabled selection of always optimal cutting angles for accurate measurement of the mucosal damage and revealed diagnostic lesions in cases interpreted as normal with conventional histomorphometry. We also demonstrate that computer-assisted point cloud analysis can be used to calculate biologically meaningful surface areas of the biopsies in different stages of mucosal damage with excellent replicability and correlation with other disease parameters. We expect the improved diagnostic accuracy and capability to measure the surface areas to provide a powerful tool for the diagnostics of intestinal diseases and for future clinical and pharmaceutical trials.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Research group: Computational Biophysics and Imaging Group, BioMediTech, Tampere University Hospital, Carol Davila University of Medicine and Pharmacy, Central Finland Central Hospital, University of Helsinki, The University Consortium of Seinäjoki, Tampere University
Contributors: Virta, J., Hannula, M., Tamminen, I., Lindfors, K., Kaukinen, K., Popp, A., Taavela, J., Saavalainen, P., Hiltunen, P., Hyttinen, J., Kurppa, K.
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X-ray microtomography is a novel method 2020
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URLs:
<http://urn.fi/URN:NBN:fi:tuni-202008256633>
Source: Scopus
Source ID: 85089006682
Research output: Contribution to journal › Article › Scientific › peer-review

Comparison of electron injection and recombination on TiO₂ nanoparticles and ZnO nanorods photosensitized by phthalocyanine

Titanium dioxide (TiO₂) and zinc oxide (ZnO) semiconductors have similar band gap positions but TiO₂ performs better as an anode material in dye-sensitized solar cell applications. We compared two electrodes made of TiO₂ nanoparticles and ZnO nanorods sensitized by an aggregation-protected phthalocyanine derivative using ultrafast transient absorption spectroscopy. In agreement with previous studies, the primary electron injection is two times faster on TiO₂, but contrary to the previous results the charge recombination is slower on ZnO. The latter could be due to morphology differences and the ability of the injected electrons to travel much further from the sensitizer cation in ZnO nanorods.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Chemistry and Bioengineering, Universidad Autónoma de Madrid, Mersin University, Instituto Madrileño de Estudios Avanzados (IMDEA)-Nanociencia

Contributors: Virkki, K., Tervola, E., Ince, M., Torres, T., Tkachenko, N. V.

Publication date: 11 Jul 2018

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Keywords: Photo-induced electron transfer, Phthalocyanine, Semiconductor–organic interface, TiO nanoparticles, ZnO nanorods

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Source ID: 85050034317

Research output: Contribution to journal › Article › Scientific › peer-review

Three-Dimensional Printing of the Nasal Cavities for Clinical Experiments

3D printing has produced many beneficial applications for surgery. The technique's applicability in replicating nasal cavity anatomy for clinical use has not been studied. Our aim was to determine whether 3D printing could realistically replicate the nasal cavities and the airflow passing through them from a clinical point of view. We included Cone Beam Computed Tomography (CBCT) scans of five patients with symptoms of chronic nasal congestion. These CBCT scans were used to print plastic 3D prints of the nasal cavities, which were also CBCT scanned and the measurements were compared. The results in vivo were higher than the results in vitro in maxillary sinus volumes with a ratio of 1.05 ± 0.01 (mean \pm SD) and in the nasal cavities with a ratio of 1.20 ± 0.1 (mean \pm SD). Linear measurements in vitro were very close to those in vivo. Rhinomanometric results showed some differences, but rhinomanometric graphs in vitro were close to the graphs in vivo. 3D printing proved to be a suitable and fast method for replicating nasal cavity structures and for the experimental testing of nasal function. It can be used as a complementary examination tool for rhinomanometry.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Sensor Technology and Biomeasurements (STB), BioMediTech, Tampere University Hospital, Texas Tech University Health Sciences Center at Lubbock, Ear & Sinus Institute, Tampere University, Boston Children's Hospital

Contributors: Valtonen, O., Ormiskangas, J., Kivekäs, I., Rantanen, V., Dean, M., Poe, D., Järnstedt, J., Lekkala, J., Saarenrinne, P., Rautiainen, M.

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Electronic versions:

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Bibliographical note

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INT=atme,"Saarenrinne, Pentti"

Source: Scopus

Source ID: 85077941852

Research output: Contribution to journal › Article › Scientific › peer-review

Analysis of spatial heterogeneity in normal epithelium and preneoplastic alterations in mouse prostate tumor models

Cancer involves histological changes in tissue, which is of primary importance in pathological diagnosis and research. Automated histological analysis requires ability to computationally separate pathological alterations from normal tissue with all its variables. On the other hand, understanding connections between genetic alterations and histological attributes requires development of enhanced analysis methods suitable also for small sample sizes. Here, we set out to develop computational methods for early detection and distinction of prostate cancer-related pathological alterations. We use analysis of features from HE stained histological images of normal mouse prostate epithelium, distinguishing the descriptors for variability between ventral, lateral, and dorsal lobes. In addition, we use two common prostate cancer models, Hi-Myc and Pten+/" mice, to build a feature-based machine learning model separating the early pathological lesions provoked by these genetic alterations. This work offers a set of computational methods for separation of early neoplastic lesions in the prostates of model mice, and provides proof-of-principle for linking specific tumor genotypes to quantitative histological characteristics. The results obtained show that separation between different spatial locations within the organ, as well as classification between histologies linked to different genetic backgrounds, can be performed with very high specificity and sensitivity.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Prostate cancer research center (PCRC), Signal Processing, Faculty of Biomedical Sciences and Engineering, BioMediTech, BioMediTech Institute and Faculty of Biomedical Sciences and Engineering, Tampere University Hospital

Contributors: Valkonen, M., Ruusuvoori, P., Kartasalo, K., Nykter, M., Visakorpi, T., Latonen, L.

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Source: Scopus

Source ID: 85016015946

Research output: Contribution to journal › Article › Scientific › peer-review

Behaviour of one-step spray-coated carbon nanotube supercapacitor in ambient light harvester circuit with printed organic solar cell and electrochromic display

A printed energy harvesting and storage circuit powered by ambient office lighting and its use to power a printed display is reported. The autonomous device is composed of three printed electronic components: an organic photovoltaic module, a carbon-nanotubes-only supercapacitor and an electrochromic display element. Components are fabricated from safe and environmentally friendly materials, and have been fabricated using solution processing methods, which translate into low-cost and high-throughput manufacturing. A supercapacitor made of spray-coated carbon nanotube based ink and aqueous NaCl electrolyte was charged using a printed organic photovoltaic module exposed to office lighting conditions. The supercapacitor charging rate, self-discharge rate and display operation were studied in detail. The supercapacitor self-discharge rate was found to depend on the charging rate. The fully charged supercapacitor was used as a power source to run the electrochromic display over 50 times.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Automation Science and Engineering, Research area: Microsystems, Research area: Measurement Technology and Process Control, Department of Electronics and Communications Engineering, Research group: Laboratory for Future Electronics, VTT Technical Research Centre of Finland

Contributors: Tuukkanen, S., Välimäki, M., Lehtimäki, S., Vuorinen, T., Lupo, D.

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Electronic versions:

Behaviour of one-step spray-coated carbon nanotube supercapacitor in ambient light harvester circuit with printed organic solar cell and electrochromic display

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Source ID: 84960540095

Research output: Contribution to journal › Article › Scientific › peer-review

Genomically amplified Akt3 activates DNA repair pathway and promotes glioma progression

Akt is a robust oncogene that plays key roles in the development and progression of many cancers, including glioma. We evaluated the differential propensities of the Akt isoforms toward progression in the well-characterized RCAS/Ntv-a mouse model of PDGFB-driven low grade glioma. A constitutively active myristoylated form of Akt1 did not induce high-grade glioma (HGG). In stark contrast, Akt2 and Akt3 showed strong progression potential with 78% and 97% of tumors diagnosed as HGG, respectively. We further revealed that significant variations in polarity and hydrophathy values among the Akt isoforms in both the pleckstrin homology domain (P domain) and regulatory domain (R domain) were critical in mediating glioma progression. Gene expression profiles from representative Akt-derived tumors indicated dominant and distinct roles for Akt3, consisting primarily of DNA repair pathways. TCGA data from human GBM closely reflected the DNA repair function, as Akt3 was significantly correlated with a 76-gene signature DNA repair panel. Consistently, compared with Akt1 and Akt2 overexpression models, Akt3-expressing human GBM cells had enhanced activation of DNA repair proteins, leading to increased DNA repair and subsequent resistance to radiation and temozolomide. Given the wide range of Akt3-amplified cancers, Akt3 may represent a key resistance factor.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Signal Processing, Research group: Computational Systems Biology, BioMediTech, Multi-scaled biodata analysis and modelling (MultiBAM), Prostate cancer research center (PCRC), University of Texas, M. D. Anderson Cancer Center, Cancer Genomics Laboratory, Houston, TX, USA, Department of Pathology and Neuro-Oncology, Department of Neuro-Oncology, Duke University, Department of Computer Science and Center for Systems Biology, Durham, NC, USA, Institute for Systems Biology

Contributors: Turner, K. M., Sun, Y., Ji, P., Granberg, K. J., Bernard, B., Hu, L., Cogdell, D. E., Zhou, X., Yli-Harja, O., Nykter, M., Shmulevich, I., Yung, W. K. A., Fuller, G. N., Zhang, W.
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Keywords: Akt, DNA repair, Glioma, RCAS/tv-a mouse model
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Bibliographical note

EXT="Zhang, Wei"
Source: Scopus
Source ID: 84925242229
Research output: Contribution to journal > Article > Scientific > peer-review

Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes

Long interspersed nuclear element-1 (L1) retrotransposons are mobile repetitive elements that are abundant in the human genome. L1 elements propagate through RNA intermediates. In the germ line, neighboring, nonrepetitive sequences are occasionally mobilized by the L1 machinery, a process called 3' transduction. Because 3' transductions are potentially mutagenic, we explored the extent to which they occur somatically during tumorigenesis. Studying cancer genomes from 244 patients, we found that tumors from 53% of the patients had somatic retrotranspositions, of which 24% were 3' transductions. Fingerprinting of donor L1s revealed that a handful of source L1 elements in a tumor can spawn from tens to hundreds of 3' transductions, which can themselves seed further retrotranspositions. The activity of individual L1 elements fluctuated during tumor evolution and correlated with L1 promoter hypomethylation. The 3' transductions disseminated genes, exons, and regulatory elements to new locations, most often to heterochromatic regions of the genome.

General information

Publication status: Published
MoE publication type: A2 Review article in a scientific journal
Organisations: Prostate cancer research center (PCRC), Wellcome Trust Sanger Institute, University of Santiago de Compostela (USC), Department of Applied Health Research, Haukeland University Hospital, KU Leuven, Royal Marsden National Health Service (NHS) Foundation Trust, University of Cambridge, University of Liverpool, University of East Anglia, Institute of Cancer Research London, School of Management (JKK), Johns Hopkins University, Netherlands Cancer Institute, Université Libre de Bruxelles, Breast Cancer Translational Research Laboratory J-C Heuson, Institut Jules Bordet, Bld de Waterloo, British Columbia Cancer Agency, Erasmus University Medical Center, University of Iceland, University of Queensland, Claude Bernard-University, Oslo University Hospital, Radboud University Medical Center, Dana-Farber Cancer Institute, Academic Medical Center, Institut Curie, Universiteit Antwerpen, University of Texas, M. D. Anderson Cancer Center, Cancer Genomics Laboratory, Houston, TX, USA
Contributors: Tubio, J. M., Li, Y., Ju, Y. S., Martincorena, I., Cooke, S. L., Tojo, M., Gundem, G., Pipinikas, C. P., Zamora, J., Raine, K., Menzies, A., Roman-Garcia, P., Fullam, A., Gerstung, M., Shlien, A., Tarpey, P. S., Papaemmanuil, E., Knappskog, S., Van Loo, P., Ramakrishna, M., Davies, H. R., Marshall, J., Wedge, D. C., Teague, J. W., Butler, A. P., Nik-Zainal, S., Alexandrov, L., Behjati, S., Yates, L. R., Bolli, N., Mudie, L., Hardy, C., Martin, S., McLaren, S., O'Meara, S., Anderson, E., Maddison, M., Gamble, S., Foster, C., Warren, A. Y., Whitaker, H., Brewer, D., Eeles, R., Cooper, C., Neal, D., Lynch, A. G., Visakorpi, T., Isaacs, W. B., Van't Veer, L., Caldas, C., Desmedt, C., Sotiriou, C., Aparicio, S., Foekens, J. A., Eyfjörd, J. E., Lakhani, S. R., Thomas, G., Myklebost, O., Span, P. N., Børresen-Dale, A. L., Richardson, A. L., Van De Vijver, M., Vincent-Salomon, A., Van Den Eynden, G. G., Flanagan, A. M., Futreal, P. A., Janes, S. M., Bova, G. S., Stratton, M. R., McDermott, U., Campbell, P. J.
Publication date: 1 Aug 2014
Peer-reviewed: Yes

Publication information

Journal: Science
Volume: 345

Issue number: 6196
Article number: 1251343
ISSN (Print): 0036-8075
Ratings:

Scopus rating (2014): CiteScore 46 SJR 12.052 SNIP 8.05

Original language: English

ASJC Scopus subject areas: Medicine(all), General

DOIs:

10.1126/science.1251343

URLs:

<http://www.scopus.com/inward/record.url?scp=84905900534&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84905900534

Research output: Contribution to journal › Review Article › Scientific › peer-review

Sub-parts-per-trillion level sensitivity in trace gas detection by cantilever-enhanced photo-acoustic spectroscopy

An exceptional property of photo-acoustic spectroscopy is the zero-background in wavelength modulation configuration while the signal varies linearly as a function of absorbed laser power. Here, we make use of this property by combining a highly sensitive cantilever-enhanced photo-acoustic detector, a particularly stable high-power narrow-linewidth mid-infrared continuous-wave optical parametric oscillator, and a strong absorption cross-section of hydrogen fluoride to demonstrate the ability of cantilever-enhanced photo-acoustic spectroscopy to reach sub-parts-per-trillion level sensitivity in trace gas detection. The high stability of the experimental setup allows long averaging times. A noise equivalent concentration of 650 parts-per-quadrillion is reached in 32 minutes.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Photonics, Research group: Infrared Light Sources, University of Helsinki, Gasera Ltd.

Contributors: Tomberg, T., Vainio, M., Hieta, T., Halonen, L.

Publication date: 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 1848

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-018-20087-9

DOIs:

10.1038/s41598-018-20087-9

URLs:

<http://urn.fi/URN:NBN:fi:tty-201802201295>

Source: Scopus

Source ID: 85041227218

Research output: Contribution to journal › Article › Scientific › peer-review

Emergent rogue wave structures and statistics in spontaneous modulation instability

The nonlinear Schrödinger equation (NLSE) is a seminal equation of nonlinear physics describing wave packet evolution in weakly-nonlinear dispersive media. The NLSE is especially important in understanding how high amplitude "rogue waves" emerge from noise through the process of modulation instability (MI) whereby a perturbation on an initial plane wave can evolve into strongly-localised "breather" or "soliton on finite background (SFB)" structures. Although there has been much study of such structures excited under controlled conditions, there remains the open question of how closely the analytic solutions of the NLSE actually model localised structures emerging in noise-seeded MI. We address this question here using numerical simulations to compare the properties of a large ensemble of emergent peaks in noise-seeded MI with the known analytic solutions of the NLSE. Our results show that both elementary breather and higher-order SFB structures are observed in chaotic MI, with the characteristics of the noise-induced peaks clustering closely around analytic NLSE predictions. A significant conclusion of our work is to suggest that the widely-held view that the Peregrine soliton forms a rogue wave prototype must be revisited. Rather, we confirm earlier suggestions that NLSE rogue

waves are most appropriately identified as collisions between elementary SFB solutions.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research group: Nonlinear Fiber Optics, Frontier Photonics, The University of Auckland, School of Mathematical Sciences, University College Dublin, Institut FEMTO-ST, Université de Franche-Comté

Contributors: Toenger, S., Godin, T., Billet, C., Dias, F., Erkintalo, M., Genty, G., Dudley, J. M.

Publication date: 20 May 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 10380

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep10380

URLs:

<http://www.scopus.com/inward/record.url?scp=84930225624&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

EXT="Erkintalo, Miro"

Source: Scopus

Source ID: 84930225624

Research output: Contribution to journal > Article > Scientific > peer-review

Automatic knee osteoarthritis diagnosis from plain radiographs: A deep learning-based approach

Knee osteoarthritis (OA) is the most common musculoskeletal disorder. OA diagnosis is currently conducted by assessing symptoms and evaluating plain radiographs, but this process suffers from subjectivity. In this study, we present a new transparent computer-Aided diagnosis method based on the Deep Siamese Convolutional Neural Network to automatically score knee OA severity according to the Kellgren-Lawrence grading scale. We trained our method using the data solely from the Multicenter Osteoarthritis Study and validated it on randomly selected 3,000 subjects (5,960 knees) from Osteoarthritis Initiative dataset. Our method yielded a quadratic Kappa coefficient of 0.83 and average multiclass accuracy of 66.71% compared to the annotations given by a committee of clinical experts. Here, we also report a radiological OA diagnosis area under the ROC curve of 0.93. Besides this, we present attention maps highlighting the radiological features affecting the network decision. Such information makes the decision process transparent for the practitioner, which builds better trust toward automatic methods. We believe that our model is useful for clinical decision making and for OA research; therefore, we openly release our training codes and the data set created in this study.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Signal Processing, Research group: Artificial Intelligence and Vision - AIV, Univ of Oulu, Oulu University Hospital

Contributors: Tiulpin, A., Thevenot, J., Rahtu, E., Lehenkari, P., Saarakkala, S.

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 1727

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

10.1038/s41598-018-20132-7

URLs:

<http://urn.fi/URN:NBN:fi:tty-201802201294>

Source: Scopus

Source ID: 85041225492

Research output: [Contribution to journal](#) › [Article](#) › [Scientific](#) › [peer-review](#)

Multimodal Machine Learning-based Knee Osteoarthritis Progression Prediction from Plain Radiographs and Clinical Data

Knee osteoarthritis (OA) is the most common musculoskeletal disease without a cure, and current treatment options are limited to symptomatic relief. Prediction of OA progression is a very challenging and timely issue, and it could, if resolved, accelerate the disease modifying drug development and ultimately help to prevent millions of total joint replacement surgeries performed annually. Here, we present a multi-modal machine learning-based OA progression prediction model that utilises raw radiographic data, clinical examination results and previous medical history of the patient. We validated this approach on an independent test set of 3,918 knee images from 2,129 subjects. Our method yielded area under the ROC curve (AUC) of 0.79 (0.78–0.81) and Average Precision (AP) of 0.68 (0.66–0.70). In contrast, a reference approach, based on logistic regression, yielded AUC of 0.75 (0.74–0.77) and AP of 0.62 (0.60–0.64). The proposed method could significantly improve the subject selection process for OA drug-development trials and help the development of personalised therapeutic plans.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Computing Sciences, Research group: Artificial Intelligence and Vision - AIV, Univ of Oulu, Oulu University Hospital, Erasmus University Medical Center

Contributors: Tiulpin, A., Klein, S., Bierma-Zeinstra, S. M., Thevenot, J., Rahtu, E., Meurs, J. V., Oei, E. H., Saarakkala, S.

Publication date: 1 Dec 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 20038

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-56527-3

DOIs:

10.1038/s41598-019-56527-3

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202001201402>

Source: Scopus

Source ID: 85077338521

Research output: [Contribution to journal](#) › [Article](#) › [Scientific](#) › [peer-review](#)

An Optical Method for the In-Vivo Characterization of the Biomechanical Response of the Right Ventricle

The intraoperative in-vivo mechanical function of the left ventricle has been studied thoroughly using echocardiography in the past. However, due to technical and anatomical issues, the ultrasound technology cannot easily be focused on the right side of the heart during open-heart surgery, and the function of the right ventricle during the intervention remains largely unexplored. We used optical imaging and digital image correlation for the characterization of the right ventricle motion and deformation during open-heart surgery. This work is a pilot study focusing on one patient only with the aim of establishing the framework for long term research. These experiments show that optical imaging and the analysis of the images can be used to obtain similar parameters, and partly at higher accuracy, for describing the mechanical functioning of the heart as the ultrasound technology. This work describes the optical imaging based method to characterize the mechanical response of the heart in-vivo, and offers new insight into the mechanical function of the right ventricle.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science, Tampere University Hospital
Contributors: Soltani, A., Lahti, J., Järvelä, K., Curtze, S., Laurikka, J., Hokka, M., Kuokkala, V. T.
Publication date: 1 Dec 2018
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 6831

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-018-25223-z

DOIs:

10.1038/s41598-018-25223-z

URLs:

<http://urn.fi/URN:NBN:fi:tty-201805221685>

Source: Scopus

Source ID: 85046338835

Research output: Contribution to journal > Article > Scientific > peer-review

Proton-coupled electron transfer and the role of water molecules in proton pumping by cytochrome c oxidase

Molecular oxygen acts as the terminal electron sink in the respiratory chains of aerobic organisms. Cytochrome c oxidase in the inner membrane of mitochondria and the plasma membrane of bacteria catalyzes the reduction of oxygen to water, and couples the free energy of the reaction to proton pumping across the membrane. The proton-pumping activity contributes to the proton electrochemical gradient, which drives the synthesis of ATP. Based on kinetic experiments on the O-O bond splitting transition of the catalytic cycle ($A \rightarrow PR$), it has been proposed that the electron transfer to the binuclear iron-copper center of O₂ reduction initiates the proton pump mechanism. This key electron transfer event is coupled to an internal proton transfer from a conserved glutamic acid to the proton-loading site of the pump. However, the proton may instead be transferred to the binuclear center to complete the oxygen reduction chemistry, which would constitute a short-circuit. Based on atomistic molecular dynamics simulations of cytochrome c oxidase in an explicit membrane-solvent environment, complemented by related free-energy calculations, we propose that this short-circuit is effectively prevented by a redoxstate-dependent organization of water molecules within the protein structure that gates the proton transfer pathway. cell respiration , atomistic molecular dynamics simulations , functional water molecules ,free-energy calculations

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research group: Biological Physics and Soft Matter, Computational Science X (CompX), University of Southern Denmark, Programme for Structural Biology and Biophysics, University of Helsinki Institute of Biotechnology

Contributors: Sharma, V., Enkavi, G., Vattulainen, I., Róg, T., Wikström, M.

Number of pages: 6

Pages: 2040-2045

Publication date: 17 Feb 2015

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 112

Issue number: 7

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2015): CiteScore 17.8 SJR 6.814 SNIP 2.664

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1073/pnas.1409543112

URLs:

<http://www.scopus.com/inward/record.url?scp=84923209928&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84923209928

Research output: Contribution to journal › Article › Scientific › peer-review

Redox-induced activation of the proton pump in the respiratory complex I

Complex I functions as a redox-linked proton pump in the respiratory chains of mitochondria and bacteria, driven by the reduction of quinone (Q) by NADH. Remarkably, the distance between the Q reduction site and the most distant proton channels extends nearly 200 Å. To elucidate the molecular origin of this long-range coupling, we apply a combination of large-scale molecular simulations and a site-directed mutagenesis experiment of a key residue. In hybrid quantum mechanics/molecular mechanics simulations, we observe that reduction of Q is coupled to its local protonation by the His-38/Asp-139 ion pair and Tyr-87 of subunit Nqo4. Atomistic classical molecular dynamics simulations further suggest that formation of quinol (QH₂) triggers rapid dissociation of the anionic Asp-139 toward the membrane domain that couples to conformational changes in a network of conserved charged residues. Site-directed mutagenesis data confirm the importance of Asp-139; upon mutation to asparagine the Q reductase activity is inhibited by 75%. The current results, together with earlier biochemical data, suggest that the proton pumping in complex I is activated by a unique combination of electrostatic and conformational transitions.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research group: Biological Physics and Soft Matter, Computational Science X (CompX), Institute of Molecular Biotechnology, Jena, Germany, Technische Universität München, Institut für Informatik, Department of Theoretical Biophysics, Helsinki Bioenergetics Group Programme for Structural Biology and Biophysics, University of Helsinki Institute of Biotechnology, Max Planck Institute of Biophysics

Contributors: Sharma, V., Belevich, G., Gamiz-Hernandez, A. P., Róg, T., Vattulainen, I., Verkhovskaya, M. L., Wikström, M., Hummer, G., Kaila, V. R. I.

Number of pages: 6

Pages: 11571-11576

Publication date: 15 Sep 2015

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 112

Issue number: 37

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2015): CiteScore 17.8 SJR 6.814 SNIP 2.664

Original language: English

ASJC Scopus subject areas: General

Keywords: Cell respiration, Electron transfer, Molecular dynamics simulations, NADH-quinone oxidoreductase, QM/MM simulations

DOIs:

10.1073/pnas.1503761112

URLs:

<http://www.scopus.com/inward/record.url?scp=84941671298&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84941671298

Research output: Contribution to journal › Article › Scientific › peer-review

Bioinspired underwater locomotion of light-driven liquid crystal gels

Soft-bodied aquatic invertebrates, such as sea slugs and snails, are capable of diverse locomotion modes under water. Recapitulation of such multimodal aquatic locomotion in small-scale soft robots is challenging, due to difficulties in precise spatiotemporal control of deformations and inefficient underwater actuation of existing stimuli-responsive materials. Solving this challenge and devising efficient untethered manipulation of soft stimuli-responsive materials in the aquatic environment would significantly broaden their application potential in biomedical devices. We mimic locomotion modes common to sea invertebrates using monolithic liquid crystal gels (LCGs) with inherent light responsiveness and molecular anisotropy. We elicit diverse underwater locomotion modes, such as crawling, walking, jumping, and swimming, by local deformations induced by selective spatiotemporal light illumination. Our results underpin the pivotal role of the physicochemical properties of LCGs in the realization of diverse modes of light-driven robotic underwater locomotion. We envisage that our results will introduce a toolbox for designing efficient untethered soft robots for fluidic environments.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, Max Planck Institute for Intelligent Systems, Smart Photonic Materials, Next-Generation Wireless Communications Laboratory (NWCL)

Contributors: Shahsavan, H., Aghakhani, A., Zeng, H., Guo, Y., Davidson, Z. S., Priimägi, A., Sitti, M.

Number of pages: 9

Pages: 5125-5133

Publication date: 10 Mar 2020

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 117

Issue number: 10

ISSN (Print): 0027-8424

Original language: English

ASJC Scopus subject areas: General

Keywords: Azobenzene, Biomimetics, Liquid crystal gels, Soft robotics, Underwater locomotion

Electronic versions:

5125.full

DOIs:

10.1073/pnas.1917952117

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202004083142>

Source: Scopus

Source ID: 85081897274

Research output: Contribution to journal > Article > Scientific > peer-review

Mechanistic principles underlying regulation of the actin cytoskeleton by phosphoinositides

The actin cytoskeleton powers membrane deformation during many cellular processes, such as migration, morphogenesis, and endocytosis. Membrane phosphoinositides, especially phosphatidylinositol 4,5-bisphosphate [PI(4,5)P₂], regulate the activities of many actin-binding proteins (ABPs), including profilin, cofilin, Dia2, N-WASP, ezrin, and moesin, but the underlying molecular mechanisms have remained elusive. Moreover, because of a lack of available methodology, the dynamics of membrane interactions have not been experimentally determined for any ABP. Here, we applied a combination of biochemical assays, photobleaching/activation approaches, and atomistic molecular dynamics simulations to uncover the molecular principles by which ABPs interact with phosphoinositide-rich membranes. We show that, despite using different domains for lipid binding, these proteins associate with membranes through similar multivalent electrostatic interactions, without specific binding pockets or penetration into the lipid bilayer. Strikingly, our experiments reveal that these proteins display enormous differences in the dynamics of membrane interactions and in the ranges of phosphoinositide densities that they sense. Profilin and cofilin display transient, low-affinity interactions with phosphoinositide-rich membranes, whereas F-actin assembly factors Dia2 and N-WASP reside on phosphoinositide-rich membranes for longer periods to perform their functions. Ezrin and moesin, which link the actin cytoskeleton to the plasma membrane, bind membranes with very high affinity and slow dissociation dynamics. Unlike profilin, cofilin, Dia2, and N-WASP, they do not require high "stimulus-responsive" phosphoinositide density for membrane binding. Moreover, ezrin can limit the lateral diffusion of PI(4,5)P₂ along the lipid bilayer. Together, these findings demonstrate that membrane-interaction mechanisms of ABPs evolved to precisely fulfill their specific functions in cytoskeletal dynamics.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: Biological Physics and Soft Matter, University of Helsinki Institute of Biotechnology, Aalto University, FIN-00014 University of Helsinki, University of Helsinki

Contributors: Senju, Y., Kalimeri, M., Koskela, E. V., Somerharju, P., Zhao, H., Vattulainen, I., Lappalainen, P.

Pages: E8977-E8986

Publication date: 24 Oct 2017

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 114

Issue number: 43

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2017): CiteScore 17.1 SJR 6.092 SNIP 2.655

Original language: English

ASJC Scopus subject areas: General

Keywords: Actin cytoskeleton, Molecular dynamics simulations, Phosphoinositides, Protein-lipid interaction, Signal transduction

DOIs:

10.1073/pnas.1705032114

Source: Scopus

Source ID: 85032030690

Research output: Contribution to journal > Article > Scientific > peer-review

Porous poly-L-lactide-co-1-caprolactone scaffold: A novel biomaterial for vaginal tissue engineering

The surgical reconstruction of functional neovagina is challenging and susceptible to complications. Therefore, developing tissue engineering-based treatment methods for vaginal defects is important. Our aim was to develop and test a novel supercritical carbon dioxide foamed poly-L-lactide-co-1-caprolactone (scPLCL) scaffold for vaginal reconstruction. The scaffolds were manufactured and characterized for porosity (65 + 4%), pore size (350 + 150 nm) and elastic modulus (2.8 + 0.4 MPa). Vaginal epithelial (EC) and stromal cells (SC) were isolated, expanded and characterized with flow cytometry. Finally, cells were cultured with scPLCL scaffolds in separate and/or co-cultures. Their attachment, viability, proliferation and phenotype were analysed. Both cell types strongly expressed cell surface markers CD44, CD73 and CD166. Strong expression of CD326 was detected with ECs and CD90 and CD105 with SCs. Both ECs and SCs attached and maintained viability on scPLCL. Further, scPLCL supported the proliferation of especially ECs, which also maintained epithelial phenotype (cytokeratin expression) during 14-day assessment period. Interestingly, ECs expressed uroplakin (UP) Ia, UP Ib and UP III markers; further, UP Ia and UP III expression was significantly higher on ECs cultured on scPLCL than on cell culture plastic.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Biomaterials and Tissue Engineering Group, Research group: Computational Biophysics and Imaging Group, Tampere University Hospital

Contributors: Sartoneva, R., Kuismanen, K., Juntunen, M., Karjalainen, S., Hannula, M., Kyllönen, L., Hyttinen, J., Huhtala, H., Paakinaho, K., Miettinen, S.

Publication date: 1 Aug 2018

Peer-reviewed: Yes

Publication information

Journal: Royal Society Open Science

Volume: 5

Issue number: 8

Article number: 180811

ISSN (Print): 2054-5703

Ratings:

Scopus rating (2018): CiteScore 3 SJR 1.131 SNIP 1.095

Original language: English

ASJC Scopus subject areas: General

Keywords: Cell characterization, Neovagina, Poly-L-lactide-co-1-caprolactone, Vaginal epithelial cell, Vaginal stromal cell, Vaginal tissue engineering

Electronic versions:

180811.full

DOIs:

10.1098/rsos.180811

URLs:

<http://urn.fi/URN:NBN:fi:tty-201810162401>

Source: Scopus

Source ID: 85053196533

Research output: Contribution to journal > Article > Scientific > peer-review

Segmented molecular design of self-healing proteinaceous materials

Hierarchical assembly of self-healing adhesive proteins creates strong and robust structural and interfacial materials, but understanding of the molecular design and structure-property relationships of structural proteins remains unclear.

Elucidating this relationship would allow rational design of next generation genetically engineered self-healing structural proteins. Here we report a general self-healing and -assembly strategy based on a multiphase recombinant protein based material. Segmented structure of the protein shows soft glycine- and tyrosine-rich segments with self-healing capability and hard beta-sheet segments. The soft segments are strongly plasticized by water, lowering the self-healing temperature close to body temperature. The hard segments self-assemble into nanoconfined domains to reinforce the material. The healing strength scales sublinearly with contact time, which associates with diffusion and wetting of autohesion. The

finding suggests that recombinant structural proteins from heterologous expression have potential as strong and repairable engineering materials.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Carnegie Mellon University, Department of Electrical Engineering and Automation, Aalto University, Pennsylvania State University, BASF SE, Max Planck Institute for Intelligent Systems

Contributors: Sariola, V., Pena-Francesch, A., Jung, H., Çetinkaya, M., Pacheco, C., Sitti, M., Demirel, M. C.

Publication date: 1 Sep 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 13482

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

[10.1038/srep13482](https://doi.org/10.1038/srep13482)

URLs:

<http://www.scopus.com/inward/record.url?scp=84940883408&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84940883408

Research output: Contribution to journal > Article > Scientific > peer-review

Optical detection of radon decay in air

An optical radon detection method is presented. Radon decay is directly measured by observing the secondary radioluminescence light that alpha particles excite in air, and the selectivity of coincident photon detection is further enhanced with online pulse-shape analysis. The sensitivity of a demonstration device was 6.5 cps/Bq/l and the minimum detectable concentration was 12 Bq/m³ with a 1 h integration time. The presented technique paves the way for optical approaches in rapid radon detection, and it can be applied beyond radon to the analysis of any alpha-active sample which can be placed in the measurement chamber.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Optics, Research group: Applied Optics, STUK - Radiation and Nuclear Safety Authority, University of Oxford, HT Nuclear Ltd

Contributors: Sand, J., Ihanola, S., Peräjärvi, K., Toivonen, H., Toivonen, J.

Publication date: 12 Feb 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 21532

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Optical detection of radon decay in air

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[10.1038/srep21532](https://doi.org/10.1038/srep21532)

URLs:

<http://urn.fi/URN:NBN:fi:tty-201604123803>

Source: Scopus

Source ID: 84958093603

Machine learning analysis of rogue solitons in supercontinuum generation

Supercontinuum generation is a highly nonlinear process that exhibits unstable and chaotic characteristics when developing from long pump pulses injected into the anomalous dispersion regime of an optical fiber. A particular feature associated with this regime is the long-tailed “rogue wave”-like statistics of the spectral intensity on the long-wavelength edge of the supercontinuum, linked to the generation of a small number of “rogue solitons” with extreme red-shifts. Whilst the statistical properties of rogue solitons can be conveniently measured in the spectral domain using the real-time dispersive Fourier transform technique, we cannot use this technique to determine any corresponding temporal properties since it only records the spectral intensity and one loses information about the spectral phase. And direct temporal characterization using methods such as the time-lens has resolution of typically 100's of fs, precluding the measurement of solitons which possess typically much shorter durations. Here, we solve this problem by using machine learning. Specifically, we show how supervised learning can train a neural network to predict the peak power, duration, and temporal walk-off with respect to the pump pulse position of solitons at the edge of a supercontinuum spectrum from only the supercontinuum spectral intensity without phase information. Remarkably, the network accurately predicts soliton characteristics for a wide range of scenarios, from the onset of spectral broadening dominated by pure modulation instability to near octave-spanning supercontinuum with distinct rogue solitons.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, UMR 6174

Contributors: Salmela, L., Lapre, C., Dudley, J. M., Genty, G.

Publication date: 2020

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 10

Article number: 9596

ISSN (Print): 2045-2322

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

10.1038/s41598-020-66308-y

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202007066333>

Source: Scopus

Source ID: 85086336287

Research output: Contribution to journal › Article › Scientific › peer-review

Molecular mechanisms of Charcot-Marie-Tooth neuropathy linked to mutations in human myelin protein P2

Charcot-Marie-Tooth (CMT) disease is one of the most common inherited neuropathies. Recently, three CMT1-associated point mutations (I43N, T51P, and I52T) were discovered in the abundant peripheral myelin protein P2. These mutations trigger abnormal myelin structure, leading to reduced nerve conduction velocity, muscle weakness, and distal limb atrophy. P2 is a myelin-specific protein expressed by Schwann cells that binds to fatty acids and membranes, contributing to peripheral myelin lipid homeostasis. We studied the molecular basis of the P2 patient mutations. None of the CMT1-associated mutations alter the overall folding of P2 in the crystal state. P2 disease variants show increased aggregation tendency and remarkably reduced stability, T51P being most severe. In addition, P2 disease mutations affect protein dynamics. Both fatty acid binding by P2 and the kinetics of its membrane interactions are affected by the mutations. Experiments and simulations suggest opening of the β barrel in T51P, possibly representing a general mechanism in fatty acid-binding proteins. Our findings demonstrate that altered biophysical properties and functional dynamics of P2 may cause myelin defects in CMT1 patients. At the molecular level, a few malformed hydrogen bonds lead to structural instability and misregulation of conformational changes related to ligand exchange and membrane binding.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research area: Computational Physics, Research group: Biological Physics and Soft Matter, Univ of Oulu, University of Bergen, Haukeland University Hospital, University of Helsinki

Contributors: Ruskamo, S., Nieminen, T., Kristiansen, C. K., Vatne, G. H., Baumann, A., Hallin, E. I., Raasakka, A., Joensuu, P., Bergmann, U., Vattulainen, I., Kursula, P.

Publication date: 1 Dec 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 6510

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

10.1038/s41598-017-06781-0

URLs:

<http://urn.fi/URN:NBN:fi:tty-201708211690>

Source: Scopus

Source ID: 85026324686

Research output: Contribution to journal > Article > Scientific > peer-review

Trends for isolated amino acids and dipeptides: Conformation, divalent ion binding, and remarkable similarity of binding to calcium and lead

We derive structural and binding energy trends for twenty amino acids, their dipeptides, and their interactions with the divalent cations Ca^{2+} , Ba^{2+} , Sr^{2+} , Cd^{2+} , Pb^{2+} , and Hg^{2+} . The underlying data set consists of more than 45,000 first-principles predicted conformers with relative energies up to ~ 4 eV (~ 400 kJ/mol). We show that only very few distinct backbone structures of isolated amino acids and their dipeptides emerge as lowest-energy conformers. The isolated amino acids predominantly adopt structures that involve an acidic proton shared between the carboxy and amino function. Dipeptides adopt one of two intramolecular-hydrogen bonded conformations C_5 or. Upon complexation with a divalent cation, the accessible conformational space shrinks and intramolecular hydrogen bonding is prevented due to strong electrostatic interaction of backbone and side chain functional groups with cations. Clear correlations emerge from the binding energies of the six divalent ions with amino acids and dipeptides. Cd^{2+} and Hg^{2+} show the largest binding energies—a potential correlation with their known high acute toxicities. Ca^{2+} and Pb^{2+} reveal almost identical binding energies across the entire series of amino acids and dipeptides. This observation validates past indications that ion-mimicry of calcium and lead should play an important role in a toxicological context.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Computational Physics, Fritz Haber Institute of the Max Planck Society, Duke University, Aalto University

Contributors: Ropo, M., Blum, V., Baldauf, C.

Publication date: 3 Nov 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 35772

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

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URLs:

<http://urn.fi/URN:NBN:fi:tty-201612204881>

URLs:

<http://www.scopus.com/inward/record.url?scp=84994673495&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84994673495

Research output: Contribution to journal › Article › Scientific › peer-review

Traffic is a major source of atmospheric nanocluster aerosol

In densely populated areas, traffic is a significant source of atmospheric aerosol particles. Owing to their small size and complicated chemical and physical characteristics, atmospheric particles resulting from traffic emissions pose a significant risk to human health and also contribute to anthropogenic forcing of climate. Previous research has established that vehicles directly emit primary aerosol particles and also contribute to secondary aerosol particle formation by emitting aerosol precursors. Here, we extend the urban atmospheric aerosol characterization to cover nanocluster aerosol (NCA) particles and show that a major fraction of particles emitted by road transportation are in a previously unmeasured size range of 1.3–3.0 nm. For instance, in a semiurban roadside environment, the NCA represented 20–54% of the total particle concentration in ambient air. The observed NCA concentrations varied significantly depending on the traffic rate and wind direction. The emission factors of NCA for traffic were $2.4 \cdot 10^{15} \text{ (kg}_{\text{fuel}})^{-1}$ in a roadside environment, $2.6 \cdot 10^{15} \text{ (kg}_{\text{fuel}})^{-1}$ in a street canyon, and $2.9 \cdot 10^{15} \text{ (kg}_{\text{fuel}})^{-1}$ in an on-road study throughout Europe. Interestingly, these emissions were not associated with all vehicles. In engine laboratory experiments, the emission factor of exhaust NCA varied from a relatively low value of $1.6 \cdot 10^{12} \text{ (kg}_{\text{fuel}})^{-1}$ to a high value of $4.3 \cdot 10^{15} \text{ (kg}_{\text{fuel}})^{-1}$. These NCA emissions directly affect particle concentrations and human exposure to nanosized aerosol in urban areas, and potentially may act as nanosized condensation nuclei for the condensation of atmospheric low-volatile organic compounds.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: The Instrumentation, Emissions, and Atmospheric Aerosols Group, Finnish Meteorological Institute, Helsinki Region Environmental Services Authority, University of Helsinki, Turku University of Applied Sciences

Contributors: Rönkkö, T., Kuuluvainen, H., Karjalainen, P., Keskinen, J., Hillamo, R., Niemi, J. V., Pirjola, L., Timonen, H. J., Saarikoski, S., Saukko, E., Järvinen, A., Silvennoinen, H., Rostedt, A., Olin, M., Yli-Ojanperä, J., Nousiainen, P., Kousa, A., Dal Maso, M.

Number of pages: 6

Pages: 7549-7554

Publication date: 18 Jul 2017

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 114

Issue number: 29

ISSN (Print): 0027-8424

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Scopus rating (2017): CiteScore 17.1 SJR 6.092 SNIP 2.655

Original language: English

ASJC Scopus subject areas: General

Keywords: Air pollution, Atmospheric aerosol, Combustion-derived nanoparticles, Nanocluster aerosol, Traffic emission

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<http://urn.fi/URN:NBN:fi:tty-201712192416>

Bibliographical note

INT=FYS, "Silvennoinen, Henna"

Source: Scopus

Source ID: 85024373359

Research output: Contribution to journal › Article › Scientific › peer-review

Infiltrated bunch of solitons in Bi-doped frequency-shifted feedback fibre laser operated at 1450 nm

Mode-locked fibre laser as a dissipative system is characterized by rich forms of soliton interaction, which take place via internal energy exchange through noisy background in the presence of dispersion and nonlinearity. The result of soliton interaction was either stationary-localized or chaotically-oscillated soliton complexes, which have been shown before as stand-alone in the cavity. Here we report on a new form of solitons complex observed in Bi-doped mode-locked fibre laser operated at 1450 nm. The solitons are arranged in two different group types contemporizing in the cavity: one pulse group propagates as bound solitons with fixed phase relation and interpulse position eventuated in 30 dB spectrum modulation

depth; while the other pulses form a bunch with continuously and chaotically moving solitons. The article describes both experimental and theoretical considerations of this effect.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Photonics, Research group: Ultrafast and intense lasers, Ulyanovsk State University, Russian Academy of Sciences

Contributors: Rissanen, J., Korobko, D. A., Zolotovskiy, I. O., Melkumov, M., Khopin, V. F., Gumenyuk, R.

Publication date: 10 Mar 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Article number: 44194

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Infiltrated bunch of solitons in Bi-doped frequency-shifted feedback fibre laser operated at 1450 nm

DOIs:

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URLs:

<http://urn.fi/URN:NBN:fi:ty-201703281226>

Source: Scopus

Source ID: 85014889267

Research output: [Contribution to journal](#) > [Article](#) > [Scientific](#) > [peer-review](#)

Superdiffusion dominates intracellular particle motion in the supercrowded cytoplasm of pathogenic *Acanthamoeba castellanii*

Acanthamoebae are free-living protists and human pathogens, whose cellular functions and pathogenicity strongly depend on the transport of intracellular vesicles and granules through the cytosol. Using high-speed live cell imaging in combination with single-particle tracking analysis, we show here that the motion of endogenous intracellular particles in the size range from a few hundred nanometers to several micrometers in *Acanthamoeba castellanii* is strongly superdiffusive and influenced by cell locomotion, cytoskeletal elements, and myosin II. We demonstrate that cell locomotion significantly contributes to intracellular particle motion, but is clearly not the only origin of superdiffusivity. By analyzing the contribution of microtubules, actin, and myosin II motors we show that myosin II is a major driving force of intracellular motion in *A. castellanii*. The cytoplasm of *A. castellanii* is supercrowded with intracellular vesicles and granules, such that significant intracellular motion can only be achieved by actively driven motion, while purely thermally driven diffusion is negligible.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Institute for Physics and Astronomy, University of Potsdam, Institute for Materials Science, Biocompatible Nanomaterials, Christian-Albrechts-Universität zu Kiel, Zoological Institute, Comparative Immunobiology, Korea Institute for Advanced Study

Contributors: Reverey, J. F., Jeon, J., Bao, H., Leippe, M., Metzler, R., Selhuber-Unkel, C.

Publication date: 30 Jun 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 11690

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep11690

URLs:

<http://www.scopus.com/inward/record.url?scp=84934784474&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

EXT="Jeon, Jae-Hyung"

Source: Scopus

Source ID: 84934784474

Research output: Contribution to journal › Article › Scientific › peer-review

Highly-Sensitive Refractive Index Sensing by Near-infrared Metatronic Nanocircuits

In this work, we present a highly-sensitive refractive index sensor based on metatronic nanocircuits operating at near-infrared spectral range. The structure is designed based on simple nanorod geometry and fabricated by nanopatterning of transparent conducting oxides. The functionality of these polarization dependent metatronic nanocircuits is enhanced by applying tunable response. This feature is investigated by depositing NH₂ (Amine) groups via plasma polymerization technique on top of indium-tin-oxide nanorods. The dielectric constant of Amine groups is a function of their thickness, which can be controlled by the RF power and the time duration of the applied plasma polymerization process. The resonance wavelengths of nanocircuits shift to higher wavelength, as the dielectric constant of the deposited material increases. An excellent agreement between the design and experimental results are obtained. Our metatronic based nanosensor offers a high-sensitive performance of 1587 nm/RIU with a satisfactory figure of merit for this class of sensors.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Photonics, Bilkent University, University of Hacettepe, Electronics and Telecommunication Research Institute (ETRI), Nanotechnology Research Center

Contributors: Rashed, A. R., Gudulluoglu, B., Yun, H. W., Habib, M., Boyaci, I. H., Hong, S. H., Ozbay, E., Caglayan, H.

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 11457

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

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URLs:

<http://urn.fi/URN:NBN:fi:tty-201808232197>

Source: Scopus

Source ID: 85050821443

Research output: Contribution to journal › Article › Scientific › peer-review

A Highly Efficient Sensor Platform Using Simply Manufactured Nanodot Patterned Substrates

Block copolymer (BCP) self-assembly is a low-cost means to nanopattern surfaces. Here, we use these nanopatterns to directly print arrays of nanodots onto a conducting substrate (Indium Tin Oxide (ITO) coated glass) for application as an electrochemical sensor for ethanol (EtOH) and hydrogen peroxide (H₂O₂) detection. The work demonstrates that BCP systems can be used as a highly efficient, flexible methodology for creating functional surfaces of materials. Highly dense iron oxide nanodots arrays that mimicked the original BCP pattern were prepared by an 'insitu' BCP inclusion methodology using poly(styrene)-block-poly(ethylene oxide) (PS-b-PEO). The electrochemical behaviour of these densely packed arrays of iron oxide nanodots fabricated by two different molecular weight PS-b-PEO systems was studied. The dual detection of EtOH and H₂O₂ was clearly observed. The as-prepared nanodots have good long term thermal and chemical stability at the substrate and demonstrate promising electrocatalytic performance.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Frontier Photonics, Tyndall National Institute at National University of Ireland, Cork, Centre for Research on Adaptive Nanostructures and Nanodevices (CRANN), Trinity College Dublin

Contributors: Rasappa, S., Ghoshal, T., Borah, D., Senthamaraikannan, R., Holmes, J. D., Morris, M. A.

Publication date: 20 Aug 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 13270

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep13270

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<http://www.scopus.com/inward/record.url?scp=84939781258&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84939781258

Research output: Contribution to journal > Article > Scientific > peer-review

Non-toxic printed supercapacitors operating in sub-zero conditions

Aqueous supercapacitors offer a safe alternative for intermediate energy storage in energy harvesting applications, but their performance is limited to relatively warm temperatures. We report the performance of glycerol as a non-toxic anti-freeze for a water-based electrolyte from room temperature to -30°C at various concentrations. The supercapacitors are manufactured with graphite and activated carbon as current collector and electrode on a flexible polyester (PET) substrate by stencil printing, with a sodium chloride solution as the electrolyte. The devices are characterized at various constant temperatures for electrical performance, as well as in room temperature for mass loss and development of performance over time. It is shown that supercapacitors with glycerol function well in the decreased temperatures compared to water: the capacitance experiences only a slight decrease and the leakage current is significantly reduced. The equivalent series resistance is affected the most by the reduced temperatures, and should be considered the primary limiting factor in low-temperature applications. Electrolytes with 30-40% glycerol perform the best in commercial freezer temperatures, but below -20°C a higher concentration of 45% glycerol retains better function. The results show great promise for a non-toxic alternative for improving the temperature range of printed supercapacitors.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Electrical Engineering, Research group: Laboratory for Future Electronics

Contributors: Railanmaa, A., Lehtimäki, S., Keskinen, J., Lupo, D.

Publication date: 1 Oct 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 14059

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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DOIs:

10.1038/s41598-019-50570-w

URLs:

<http://urn.fi/URN:NBN:fi:tuni-201910153858>

Source: Scopus

Source ID: 85072847480

Skin-conformable printed supercapacitors and their performance in wear

Wearable sensors and electronic systems are of great interest these days, but their viability depends on the availability of compatible energy storage solutions. Such sensors can either be integrated into clothing or attached directly to the skin, each case presenting a different set of requirements for the devices. In this work, we examine the performance of printed supercapacitors while attached to the skin. The devices are manufactured from benign materials, such as water, carbon and sodium chloride, and worn on the forearm or chest for 24 h for durability testing. The supercapacitors exhibit excellent mechanical durability and stay well attached under all test conditions. Electrically, the supercapacitors exhibit reliable capacitive function throughout the test period; other key parameters such as equivalent series resistance and leakage current are affected but to a minimal extent. The movement and deformation of the supercapacitor show good compatibility with the skin, as shown by the Digital Image Correlation full field strain measurements on and around the capacitor. The supercapacitors deform with the skin and do not hinder normal movement or function.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Electrical Engineering, Research group: Laboratory for Future Electronics, Materials Science and Environmental Engineering, Research group: Materials Characterization, Research group: Wireless Communications and Positioning

Contributors: Railanmaa, A., Soltani, A., Lehtimäki, S., Pournoori, N., Keskinen, J., Hokka, M., Lupo, D.

Number of pages: 9

Publication date: 2020

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 10

Issue number: 1

Article number: 15194

ISSN (Print): 2045-2322

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Skin-conformable printed supercapacitors 2020

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URLs:

<http://urn.fi/URN:NBN:fi:tuni-202009287144>

Source: Scopus

Source ID: 85091129191

Research output: Contribution to journal › Article › Scientific › peer-review

Variance-corrected Michaelis-Menten equation predicts transient rates of single-enzyme reactions and response times in bacterial gene-regulation

Many chemical reactions in biological cells occur at very low concentrations of constituent molecules. Thus, transcriptional gene-regulation is often controlled by poorly expressed transcription-factors, such as E.coli lac repressor with few tens of copies. Here we study the effects of inherent concentration fluctuations of substrate-molecules on the seminal Michaelis-Menten scheme of biochemical reactions. We present a universal correction to the Michaelis-Menten equation for the reaction-rates. The relevance and validity of this correction for enzymatic reactions and intracellular gene-regulation is demonstrated. Our analytical theory and simulation results confirm that the proposed variance-corrected Michaelis-Menten equation predicts the rate of reactions with remarkable accuracy even in the presence of large non-equilibrium concentration fluctuations. The major advantage of our approach is that it involves only the mean and variance of the substrate-molecule concentration. Our theory is therefore accessible to experiments and not specific to the exact source of the concentration fluctuations.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Computational Physics, Institute for Physics and Astronomy, University of Potsdam

Contributors: Pulkkinen, O., Metzler, R.

Publication date: 4 Dec 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 17820

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

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Source: Scopus

Source ID: 84949239330

Research output: Contribution to journal › Article › Scientific › peer-review

Added value of autoregulation and multi-step kinetics of transcription initiation

Bacterial gene expression regulation occurs mostly during transcription, which has two main rate-limiting steps: the close complex formation, when the RNA polymerase binds to an active promoter, and the subsequent open complex formation, after which it follows elongation. Tuning these steps' kinetics by the action of e.g. transcription factors, allows for a wide diversity of dynamics. For example, adding autoregulation generates single-gene circuits able to perform more complex tasks. Using stochastic models of transcription kinetics with empirically validated parameter values, we investigate how autoregulation and the multi-step transcription initiation kinetics of single-gene autoregulated circuits can be combined to fine-tune steady state mean and cell-to-cell variability in protein expression levels, as well as response times. Next, we investigate how they can be jointly tuned to control complex behaviours, namely, time counting, switching dynamics and memory storage. Overall, our finding suggests that, in bacteria, jointly regulating a single-gene circuit's topology and the transcription initiation multi-step dynamics allows enhancing complex task performance.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Laboratory of Biosystem Dynamics-LBD

Contributors: Prajapat, M. K., Ribeiro, A. S.

Publication date: 1 Nov 2018

Peer-reviewed: Yes

Publication information

Journal: Royal Society Open Science

Volume: 5

Issue number: 11

Article number: 181170

ISSN (Print): 2054-5703

Ratings:

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Electronic versions:

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10.1098/rsos.181170

URLs:

<http://urn.fi/URN:NBN:fi:tty-201901081026>

Source: Scopus

Source ID: 85058415001

Research output: Contribution to journal › Article › Scientific › peer-review

Information transfer in QT-RR dynamics: Application to QT-correction

The relation between the electrical properties of the heart and the beating rate is essential for the heart functioning. This relation is central when calculating the "corrected QT interval" — an important measure of the risk of potentially lethal arrhythmias. We use the transfer entropy method from information theory to quantitatively study the mutual dynamics of the ventricular action potential duration (the QT interval) and the length of the beat-to-beat (RR) interval. We show that for healthy individuals there is a strong asymmetry in the information transfer: the information flow from RR to QT dominates over the opposite flow (from QT to RR), i.e. QT depends on RR to a larger extent than RR on QT. Moreover, the history of the intervals has a strong effect on the information transfer: at sufficiently long QT history length the information flow

asymmetry inverts and the RR influence on QT dynamics weakens. Finally, we demonstrate that the widely used QT correction methods cannot properly capture the changes in the information flows between QT and RR. We conclude that our results obtained through a model-free informational perspective can be utilised to improve and test the QT correction schemes in clinics.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research area: Computational Physics, Research group: Quantum Control and Dynamics, Firstbeat Technologies Ltd, Tampere University Hospital

Contributors: Potapov, I., Latukka, J., Kim, J., Luukko, P., Aalto-Setälä, K., Räsänen, E.

Number of pages: 9

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 14992

ISSN (Print): 2045-2322

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Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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<http://urn.fi/URN:NBN:fi:tty-201811222752>

Source: Scopus

Source ID: 85054772453

Research output: Contribution to journal > Article > Scientific > peer-review

Selective effect of cell membrane on synaptic neurotransmission

Atomistic molecular dynamics simulations were performed with 13 non-peptidic neurotransmitters (NTs) in three different membrane environments. The results provide compelling evidence that NTs are divided into membrane-binding and membrane-nonbinding molecules. NTs adhere to the postsynaptic membrane surface whenever the ligand-binding sites of their synaptic receptors are buried in the lipid bilayer. In contrast, NTs that have extracellular ligand-binding sites do not have a similar tendency to adhere to the membrane surface. This finding is a seemingly simple yet important addition to the paradigm of neurotransmission, essentially dividing it into membrane-independent and membrane-dependent mechanisms. Moreover, the simulations also indicate that the lipid composition especially in terms of charged lipids can affect the membrane partitioning of NTs. The revised paradigm, highlighting the importance of cell membrane and specific lipids for neurotransmission, should be of interest to neuroscientists, drug industry and the general public alike.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Computational Physics, Research group: Biological Physics and Soft Matter, Department of Chemistry and Biochemistry, University of California San Diego, MEMPHYS - Centre for Biomembrane Physics, University of Southern Denmark, University of Helsinki

Contributors: Postila, P. A., Vattulainen, I., Róg, T.

Publication date: 19 Jan 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 19345

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Selective effect of cell membrane on synaptic neurotransmission

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URLs:

<http://urn.fi/URN:NBN:fi:tty-201604123805>

Source: Scopus

Source ID: 84955442236

Research output: Contribution to journal > Article > Scientific > peer-review

Atomistic determinants of co-enzyme Q reduction at the Q_i-site of the cytochrome bc₁ complex

The cytochrome (cyt) bc₁ complex is an integral component of the respiratory electron transfer chain sustaining the energy needs of organisms ranging from humans to bacteria. Due to its ubiquitous role in the energy metabolism, both the oxidation and reduction of the enzyme's substrate co-enzyme Q has been studied vigorously. Here, this vast amount of data is reassessed after probing the substrate reduction steps at the Q_i-site of the cyt bc₁ complex of *Rhodobacter capsulatus* using atomistic molecular dynamics simulations. The simulations suggest that the Lys251 side chain could rotate into the Q_i-site to facilitate binding of half-protonated semiquinone-a reaction intermediate that is potentially formed during substrate reduction. At this bent pose, the Lys251 forms a salt bridge with the Asp252, thus making direct proton transfer possible. In the neutral state, the lysine side chain stays close to the conserved binding location of cardiolipin (CL). This back-and-forth motion between the CL and Asp252 indicates that Lys251 functions as a proton shuttle controlled by pH-dependent negative feedback. The CL/K/D switching, which represents a refinement to the previously described CL/K pathway, fine-tunes the proton transfer process. Lastly, the simulation data was used to formulate a mechanism for reducing the substrate at the Q_i-site.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Structural Bioinformatics Laboratory, Abo Akademi University, Department of Chemistry and Biochemistry, University of California San Diego, Institute of Science and Technology Austria, Uniwersytet Jagiellonski w Krakowie, University of Helsinki, MEMPHYS, University of Southern Denmark

Contributors: Postila, P. A., Kaszuba, K., Kuleta, P., Vattulainen, I., Sarewicz, M., Osyczka, A., Róg, T.

Publication date: 26 Sep 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 33607

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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10.1038/srep33607

URLs:

<http://urn.fi/URN:NBN:fi:tty-201610204618>

Source: Scopus

Source ID: 84988841494

Research output: Contribution to journal > Article > Scientific > peer-review

Interleukin-6 and microRNA profiles induced by oral bacteria in human atheroma derived and healthy smooth muscle cells

Background: Atherosclerosis is an inflammatory disease with possible contributions from bacterial antigens. We aimed to investigate the role of oral bacteria as inducers of inflammatory cascades in smooth muscle cells from carotid endarterectomy patients (AthSMCs) and healthy controls (HSMCs). **Findings:** Inactivated *Streptococcus mitis*, *S. sanguinis*, *S. gorgonii*, *Aggregatibacter actinomycetemcomitans* and *Porphyromonas gingivalis* were used to stimulate inflammation in HSMCs and AthSMCs. Tumor necrosis factor- α (TNF α) was used as a positive control in all stimulations. Interleukin-6 (IL-6) levels were determined from cell culture supernatants and microRNA expression profiles from cells after 24 h of bacterial stimulation. Genome wide expression (GWE) analyses were performed after 5 h stimulation. All studied bacteria induced pro inflammatory IL-6 production in both SMCs. The most powerful inducer of IL-6 was *A. actinomycetemcomitans* ($p < 0.001$). Of the 84 studied miRNAs, expression of 9 miRNAs differed significantly ($p \leq 0.001$) between HSMCs and AthSMCs stimulated with inactivated bacteria or TNF α . The data was divided into two groups: high

IL-6 producers (*A. actinomyctemcomitans* and TNF α) and low IL-6 producers (streptococcal strains and *P. gingivalis*). The expression of 4 miRNAs (miR-181-5p, -186-5p, -28-5p and -155-5p) differed statistically significantly ($p < 0.001$) between healthy HSMCs and AthSMCs in the low IL-6 producer group. According to multidimensional scaling, two gene expression clusters were seen: one in HSMCs and one AthSMCs. Conclusions: Our results suggest that inactivated oral bacteria induce inflammation that is differently regulated in healthy and atherosclerotic SMCs.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Kennedy Institute of Rheumatology, School of Management (JKK), German Research Center for Environmental Health, Lounatmaa Ltd

Contributors: Pessi, T., Viiri, L. E., Raitoharju, E., Astola, N., Seppälä, I., Waldenberger, M., Lounatmaa, K., Davies, A. H., Lehtimäki, T., Karhunen, P. J., Monaco, C.

Publication date: 1 Dec 2015

Peer-reviewed: Yes

Publication information

Journal: SpringerPlus

Volume: 4

Issue number: 1

ISSN (Print): 2193-1801

Ratings:

Scopus rating (2015): CiteScore 1.2 SJR 0.433 SNIP 0.638

Original language: English

ASJC Scopus subject areas: General

Keywords: Atherosclerosis, Genome wide expression, Inflammation, microRNA, Oral bacteria, Smooth muscle cells

DOIs:

10.1186/s40064-015-0993-8

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<http://www.scopus.com/inward/record.url?scp=84928969616&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84928969616

Research output: Contribution to journal > Article > Scientific > peer-review

An ensemble of classifiers based on different texture descriptors for texture classification

Here we propose a system that incorporates two different state-of-the-art classifiers (support vector machine and gaussian process classifier) and two different descriptors (multi local quinary patterns and multi local phase quantization with ternary coding) for texture classification. Both the tested descriptors are an ensemble of stand-alone descriptors obtained using different parameters setting (the same set is used in each dataset). For each stand-alone descriptor we train a different classifier, the set of scores of each classifier is normalized to mean equal to zero and standard deviation equal to one, then all the score sets are combined by the sum rule. Our experimental section shows that we succeed in building a high performance ensemble that works well on different datasets without any ad hoc parameters tuning. The fusion among the different systems permits to outperform SVM where the parameters and kernels are tuned separately in each dataset, while in the proposed ensemble the linear SVM, with the same parameter cost in all the datasets, is used.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), University of Bologna, Università degli Studi di Padova, Italy

Contributors: Paci, M., Nanni, L., Severi, S.

Number of pages: 10

Pages: 235-244

Publication date: Jul 2013

Peer-reviewed: Yes

Publication information

Journal: Journal of King Saud University - Science

Volume: 25

Issue number: 3

ISSN (Print): 1018-3647

Ratings:

Scopus rating (2013): CiteScore 2 SJR 0.295 SNIP 0.74

Original language: English

ASJC Scopus subject areas: General

Keywords: Ensemble of classifiers, Machine learning, Non-binary coding, Support vector machine, Texture descriptors
DOIs:
10.1016/j.jksus.2012.12.001
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<http://www.scopus.com/inward/record.url?scp=84878964801&partnerID=8YFLogxK> (Link to publication in Scopus)
Source: Scopus
Source ID: 84878964801
Research output: Contribution to journal › Article › Scientific › peer-review

1700 nm dispersion managed mode-locked bismuth fiber laser

We demonstrate the first 1.7 μm bismuth-doped fiber laser generating ultrashort pulses via passive mode-locking. Pulse operation has been achieved for both anomalous and normal dispersion of the laser cavity owing to broadband characteristics of carbon nanotube saturable absorber. The laser delivered 1.65 ps pulses in net anomalous dispersion regime. In normal dispersion regime, the laser delivered 14 ps pulses which could be compressed to 1.2 ps using external fiber compressor.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Optoelectronics Research Centre, Research group: Ultrafast and intense lasers
Contributors: Noronen, T., Firstov, S., Dianov, E., Okhotnikov, O. G.
Publication date: 21 Apr 2016
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports
Volume: 6
Article number: 24876
ISSN (Print): 2045-2322
Ratings:
Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364
Original language: English
ASJC Scopus subject areas: General
Electronic versions:
1700 nm dispersion managed mode-locked bismuth fiber laser
DOIs:
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Source: Scopus
Source ID: 84964285695
Research output: Contribution to journal › Article › Scientific › peer-review

Ricci-flow based conformal mapping of the proximal femur to identify exercise loading effects

The causal relationship between habitual loading and adaptive response in bone morphology is commonly explored by analysing the spatial distribution of mechanically relevant features. In this study, 3D distribution of features in the proximal femur of 91 female athletes (5 exercise loading groups representing habitual loading) is contrasted with 20 controls. A femur specific Ricci-flow based conformal mapping procedure was developed for establishing correspondence among the periosteal surfaces. The procedure leverages the invariance of the conformal mapping method to isometric shape differences to align surfaces in the 2D parametric domain, to produce dense correspondences across an isotopological set of surfaces. This is implemented through a multi-parametrisation approach to detect surface features and to overcome the issue of inconsistency in the anatomical extent present in the data. Subsequently, the group-wise distribution of two mechanically relevant features was studied - cortical thickness and surface principal strains (simulation results of a sideways fall). Statistical inferences over the surfaces were made by contrasting the athlete groups with the controls through statistical parametric mapping. With the aid of group-wise and composite-group maps, proximal femur regions affected by specific loading groups were identified with a high degree of spatial localisation.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Faculty of Biomedical Sciences and Engineering, Civil Engineering, Research group: Computational Biophysics and Imaging Group, University of Calgary, Geometric Energy Corporation, Jyväskylä yliopisto, GeroCenter Foundation for Aging Research and Development, Jyväskylä Central Hospital, UKK Institute Finland

Contributors: Narra, N., Abe, S., Dimitrov, V., Nikander, R., Kouhia, R., Sievänen, H., Hyttinen, J.
Publication date: 2018
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports
Volume: 8
Issue number: 1
Article number: 4823
ISSN (Print): 2045-2322
Ratings:
Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274
Original language: English
ASJC Scopus subject areas: General
Electronic versions:
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Bibliographical note

EXT="Sievänen, Harri"
Source: Scopus
Source ID: 85044246635
Research output: Contribution to journal › Article › Scientific › peer-review

Dynamical heart beat correlations during running

Fluctuations of the human heart beat constitute a complex system that has been studied mostly under resting conditions using conventional time series analysis methods. During physical exercise, the variability of the fluctuations is reduced, and the time series of beat-to-beat RR intervals (RRIs) become highly non-stationary. Here we develop a dynamical approach to analyze the time evolution of RRI correlations in running across various training and racing events under real-world conditions. In particular, we introduce dynamical detrended fluctuation analysis and dynamical partial autocorrelation functions, which are able to detect real-time changes in the scaling and correlations of the RRIs as functions of the scale and the lag. We relate these changes to the exercise intensity quantified by the heart rate (HR). Beyond subject-specific HR thresholds the RRIs show multiscale anticorrelations with both universal and individual scale-dependent structure that is potentially affected by the stride frequency. These preliminary results are encouraging for future applications of the dynamical statistical analysis in exercise physiology and cardiology, and the presented methodology is also applicable across various disciplines.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Physics, Research group: Quantum Control and Dynamics, Massachusetts Institute of Technology, Laboratoire de physique théorique et modèles statistiques
Contributors: Molkkari, M., Angelotti, G., Emig, T., Räsänen, E.
Number of pages: 9
Publication date: 2020
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports
Volume: 10
Issue number: 1
Article number: 13627
ISSN (Print): 2045-2322
Original language: English
ASJC Scopus subject areas: General
Electronic versions:
Dynamical heart beat correlations 2020
DOIs:
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URLs:
<http://urn.fi/URN:NBN:fi:tuni-202008246605>

Source: Scopus

Source ID: 85089376733

Research output: Contribution to journal › Article › Scientific › peer-review

Glucosylceramide modifies the LPS-induced inflammatory response in macrophages and the orientation of the LPS/TLR4 complex in silico

Toll-like receptor 4 (TLR4) is activated by bacterial lipopolysaccharide (LPS), which drives the production of proinflammatory cytokines. Earlier studies have indicated that cholesterol- and glycosphingolipid-rich subregions of the plasma membrane (lipid domains) are important for TLR4-mediated signaling. We report that inhibition of glucosylceramide (GluCer) synthase, which resulted in decreased concentrations of the glycosphingolipid GluCer in lipid domains, reduced the LPS-induced inflammatory response in both mouse and human macrophages. Atomistic molecular dynamics simulations of the TLR4 dimer complex (with and without LPS in its MD-2 binding pockets) in membranes (in the presence and absence of GluCer) showed that: (1) LPS induced a tilted orientation of TLR4 and increased dimer integrity; (2) GluCer did not affect the integrity of the LPS/TLR4 dimer but reduced the LPS-induced tilt; and (3) GluCer increased electrostatic interactions between the membrane and the TLR4 extracellular domain, which could potentially modulate the tilt. We also showed that GCS inhibition reduced the interaction between TLR4 and the intracellular adaptor protein Mal. We conclude that the GluCer-induced effects on LPS/TLR4 orientation may influence the signaling capabilities of the LPS/TLR4 complex by affecting its interaction with downstream signaling proteins.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: Biological Physics and Soft Matter, University of Gothenburg and Sahlgrenska University Hospital, Indian Institute of Science Education and Research Bhopal, University of Southern Denmark

Contributors: Mobarak, E., Håversen, L., Manna, M., Rutberg, M., Levin, M., Perkins, R., Rog, T., Vattulainen, I., Borén, J.

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 13600

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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Source: Scopus

Source ID: 85053216123

Research output: Contribution to journal › Article › Scientific › peer-review

Comparative proteomics reveals human pluripotent stem cell-derived limbal epithelial stem cells are similar to native ocular surface epithelial cells

Limbal epithelial stem cells (LESCs) are tissue-specific stem cells responsible for renewing the corneal epithelium. Acute trauma or chronic disease affecting LESCs may disrupt corneal epithelial renewal, causing vision threatening and painful ocular surface disorders, collectively referred to as LESL deficiency (LESLD). These disorders cannot be treated with traditional corneal transplantation and therefore alternative cell sources for successful cell-based therapy are needed. LESCs derived from human pluripotent stem cells (hPSCs) are a prospective source for ocular surface reconstruction, yet critical evaluation of these cells is crucial before considering clinical applications. In order to quantitatively evaluate hPSC-derived LESCs, we compared protein expression in native human corneal cells to that in hPSC-derived LESCs using isobaric tag for relative and absolute quantitation (iTRAQ) technology. We identified 860 unique proteins present in all samples, including proteins involved in cell cycling, proliferation, differentiation and apoptosis, various LESL niche components, and limbal and corneal epithelial markers. Protein expression profiles were nearly identical in LESCs derived from two different hPSC lines, indicating that the differentiation protocol is reproducible, yielding homogeneous cell populations. Their protein expression profile suggests that hPSC-derived LESCs are similar to the human ocular surface epithelial cells, and possess LESL-like characteristics.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Bolyai Institute, University of Szeged, Singapore Eye Research Institute, Tampere University Hospital

Contributors: Mikhailova, A., Jylhä, A., Rieck, J., Nättinen, J., Ilmarinen, T., Veréb, Z., Aapola, U., Beuerman, R., Petrovski, G., Uusitalo, H., Skottman, H.

Publication date: 1 Oct 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 14684

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

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URLs:

<http://www.scopus.com/inward/record.url?scp=84943143725&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84943143725

Research output: Contribution to journal › Article › Scientific › peer-review

Caustics and rogue waves in an optical sea

There are many examples in physics of systems showing rogue wave behaviour, the generation of high amplitude events at low probability. Although initially studied in oceanography, rogue waves have now been seen in many other domains, with particular recent interest in optics. Although most studies in optics have focussed on how nonlinearity can drive rogue wave emergence, purely linear effects have also been shown to induce extreme wave amplitudes. In this paper, we report a detailed experimental study of linear rogue waves in an optical system, using a spatial light modulator to impose random phase structure on a coherent optical field. After free space propagation, different random intensity patterns are generated, including partially-developed speckle, a broadband caustic network, and an intermediate pattern with characteristics of both speckle and caustic structures. Intensity peaks satisfying statistical criteria for rogue waves are seen especially in the case of the caustic network, and are associated with broader spatial spectra. In addition, the electric field statistics of the intermediate pattern shows properties of an optical sea with near-Gaussian statistics in elevation amplitude, and trough-to-crest statistics that are near-Rayleigh distributed but with an extended tail where a number of rogue wave events are observed.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research group: Nonlinear Fiber Optics, Frontier Photonics, School of Mathematical Sciences, Institut FEMTO-ST, UMR 6174 CNRS-Université de Franche-Comté, University College Dublin

Contributors: Mathis, A., Froehly, L., Toenger, S., Dias, F., Genty, G., Dudley, J. M.

Publication date: 6 Aug 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 12822

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep12822

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Source: Scopus

Source ID: 84938885285

Research output: Contribution to journal › Article › Scientific › peer-review

Tooth wear and dentoalveolar remodeling are key factors of morphological variation in the Dmanisi mandibles

The Plio-Pleistocene hominin sample from Dmanisi (Georgia), dated to 1.77 million years ago, is unique in offering detailed insights into patterns of morphological variation within a paleodeme of early Homo. Cranial and dentoalveolar morphologies exhibit a high degree of diversity, but the causes of variation are still relatively unexplored. Here we show that wear-related dentoalveolar remodeling is one of the principal mechanisms causing mandibular shape variation in fossil Homo and in modern human hunter-gatherer populations. We identify a consistent pattern of mandibular morphological alteration, suggesting that dental wear and compensatory remodeling mechanisms remained fairly constant throughout the evolution of the genus Homo. With increasing occlusal and interproximal tooth wear, the teeth continue to erupt, the posterior dentition tends to drift in a mesial direction, and the front teeth become more upright. The resulting changes in dentognathic size and shape are substantial and need to be taken into account in comparative taxonomic analyses of isolated hominin mandibles. Our data further show that excessive tooth wear eventually leads to a breakdown of the normal remodeling mechanisms, resulting in dentognathic pathologies, tooth loss, and loss of masticatory function. Complete breakdown of dentognathic homeostasis, however, is unlikely to have limited the life span of early Homo because this effect was likely mediated by the preparation of soft foods.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Georgian National Museum, University of Zurich, School of Management (JKK)

Contributors: Margvelashvili, A., Zollikofer, C. P. E., Lordkipanidze, D., Peltomäki, T., De León, M. S. P.

Number of pages: 6

Pages: 17278-17283

Publication date: 22 Oct 2013

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 110

Issue number: 43

ISSN (Print): 0027-8424

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Scopus rating (2013): CiteScore 17.4 SJR 7.073 SNIP 2.721

Original language: English

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Keywords: Aging, Compensatory mechanisms, Early Pleistocene Homo, Local periodontitis, Toothpick

DOIs:

10.1073/pnas.1316052110

URLs:

<http://www.scopus.com/inward/record.url?scp=84886412299&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84886412299

Research output: Contribution to journal › Article › Scientific › peer-review

Rate-limiting steps in transcription dictate sensitivity to variability in cellular components

Cell-to-cell variability in cellular components generates cell-to-cell diversity in RNA and protein production dynamics. As these components are inherited, this should also cause lineage-to-lineage variability in these dynamics. We conjectured that these effects on transcription are promoter initiation kinetics dependent. To test this, first we used stochastic models to predict that variability in the numbers of molecules involved in upstream processes, such as the intake of inducers from the environment, acts only as a transient source of variability in RNA production numbers, while variability in the numbers of a molecular species controlling transcription of an active promoter acts as a constant source. Next, from single-cell, single-RNA level time-lapse microscopy of independent lineages of *Escherichia coli* cells, we demonstrate the existence of lineage-to-lineage variability in gene activation times and mean RNA production rates, and that these variabilities differ between promoters and inducers used. Finally, we provide evidence that this can be explained by differences in the kinetics of the rate-limiting steps in transcription between promoters and induction schemes. We conclude that cell-to-cell and consequent lineage-to-lineage variability in RNA and protein numbers are both promoter sequence-dependent and subject to regulation.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Laboratory of Biosystem Dynamics-LBD, University of Oxford
Contributors: Mäkelä, J., Kandavalli, V., Ribeiro, A. S.
Publication date: 1 Dec 2017
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 10588

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Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

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URLs:

<http://urn.fi/URN:NBN:fi:tty-201709261964>

Source: Scopus

Source ID: 85028918063

Research output: Contribution to journal > Article > Scientific > peer-review

Human iPSC derived disease model of MERTK-associated retinitis pigmentosa

Retinitis pigmentosa (RP) represents a genetically heterogeneous group of retinal dystrophies affecting mainly the rod photoreceptors and in some instances also the retinal pigment epithelium (RPE) cells of the retina. Clinical symptoms and disease progression leading to moderate to severe loss of vision are well established and despite significant progress in the identification of causative genes, the disease pathology remains unclear. Lack of this understanding has so far hindered development of effective therapies. Here we report successful generation of human induced pluripotent stem cells (iPSC) from skin fibroblasts of a patient harboring a novel Ser331Cysfs*5 mutation in the MERTK gene. The patient was diagnosed with an early onset and severe form of autosomal recessive RP (arRP). Upon differentiation of these iPSC towards RPE, patient-specific RPE cells exhibited defective phagocytosis, a characteristic phenotype of MERTK deficiency observed in human patients and animal models. Thus we have created a faithful cellular model of arRP incorporating the human genetic background which will allow us to investigate in detail the disease mechanism, explore screening of a variety of therapeutic compounds/reagents and design either combined cell and gene- based therapies or independent approaches.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Integrated Technologies for Tissue Engineering Research (ITTE), Parque Científico y Tecnológico Cartuja, Campus de San Vicente Del Raspeig, ISCIII, Research Center 'Principe Felipe'

Contributors: Lukovic, D., Castro, A. A., Delgado, A. B. G., Bernal, M. D. L. A. M., Pelaez, N. L., Lloret, A. D., Espejo, R. P., Kamenarova, K., Sánchez, L. F., Cuenca, N., Cortón, M., Fernandez, A. A., Sorkio, A., Skottman, H., Ayuso, C., Erceg, S., Bhattacharya, S. S.

Publication date: 11 Aug 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 12910

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep12910

URLs:

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Source: Scopus

Source ID: 84939144654

Research output: Contribution to journal › Article › Scientific › peer-review

Transient formation of water-conducting states in membrane transporters

Membrane transporters rely on highly coordinated structural transitions between major conformational states for their function, to prevent simultaneous access of the substrate binding site to both sides of the membrane—a mode of operation known as the alternating access model. Although this mechanism successfully accounts for the efficient exchange of the primary substrate across the membrane, accruing evidence on significant water transport and even uncoupled ion transport mediated by transporters has challenged the concept of perfect mechanical coupling and coordination of the gating mechanism in transporters, which might be expected from the alternating access model. Here, we present a large set of extended equilibrium molecular dynamics simulations performed on several classes of membrane transporters in different conformational states, to test the presence of the phenomenon in diverse transporter classes and to investigate the underlying molecular mechanism of water transport through membrane transporters. The simulations reveal spontaneous formation of transient water-conducting (channel-like) states allowing passive water diffusion through the lumen of the transporters. These channel-like states are permeable to water but occluded to substrate, thereby not hindering the uphill transport of the primary substrate, i.e., the alternating access model remains applicable to the substrate. The rise of such water-conducting states during the large-scale structural transitions of the transporter protein is indicative of imperfections in the coordinated closing and opening motions of the cytoplasmic and extracellular gates. We propose that the observed water-conducting states likely represent a universal phenomenon in membrane transporters, which is consistent with their reliance on large-scale motion for function.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Computational Science X (CompX), Univ Illinois, University of Illinois System, University of Illinois Urbana-Champaign, Frederick Seitz Mat Res Lab, Dept Mat Sci & Engr, Department of Biochemistry

Contributors: Li, J., Shaikh, S. A., Enkavi, G., Wen, P. C., Huang, Z., Tajkhorshid, E.

Number of pages: 6

Pages: 7696-7701

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Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 110

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Ratings:

Scopus rating (2013): CiteScore 17.4 SJR 7.073 SNIP 2.721

Original language: English

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Keywords: ABC transporters, LeuT-fold transporters, Major facilitator superfamily, Neurotransmitter transporters

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Source: Scopus

Source ID: 84877317987

Research output: Contribution to journal › Article › Scientific › peer-review

Structure and permeation mechanism of a mammalian urea transporter

As an adaptation to infrequent access to water, terrestrial mammals produce urine that is hyperosmotic to plasma. To prevent osmotic diuresis by the large quantity of urea generated by protein catabolism, the kidney epithelia contain facilitative urea transporters (UTs) that allow rapid equilibration between the urinary space and the hyperosmotic interstitium. Here we report the first X-ray crystal structure of a mammalian UT, UT-B, at a resolution of 2.36 Å. UT-B is a homotrimer and each protomer contains a urea conduction pore with a narrow selectivity filter. Structural analyses and molecular dynamics simulations showed that the selectivity filter has two urea binding sites separated by an approximately 5.0 kcal/mol energy barrier. Functional studies showed that the rate of urea conduction in UT-B is increased by hypoosmotic stress, and that the site of osmoregulation coincides with the location of the energy barrier.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Computational Science X (CompX), Columbia University, College of Physicians and Surgeons, Department of Biochemistry, Univ Illinois, University of Illinois System, University of Illinois Urbana-Champaign, Frederick Seitz Mat Res Lab, Dept Mat Sci & Engr, Columbia University in the City of New York
Contributors: Levin, E. J., Cao, Y., Enkavi, G., Quick, M., Pan, Y., Tajkhorshid, E., Zhou, M.
Number of pages: 6
Pages: 11194-11199
Publication date: 10 Jul 2012
Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 109

Issue number: 28

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2012): CiteScore 17.3 SJR 6.868 SNIP 2.679

Original language: English

ASJC Scopus subject areas: General

Keywords: Channels, Membrane proteins, Osmosensing, Renal physiology

DOIs:

10.1073/pnas.1207362109

URLs:

<http://www.scopus.com/inward/record.url?scp=84863944898&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84863944898

Research output: Contribution to journal › Article › Scientific › peer-review

Multicomponent new particle formation from sulfuric acid, ammonia, and biogenic vapors

A major fraction of atmospheric aerosol particles, which affect both air quality and climate, form from gaseous precursors in the atmosphere. Highly oxygenated organic molecules (HOMs), formed by oxidation of biogenic volatile organic compounds, are known to participate in particle formation and growth. However, it is not well understood how they interact with atmospheric pollutants, such as nitrogen oxides (NO_x) and sulfur oxides (SO_x) from fossil fuel combustion, as well as ammonia (NH_3) from livestock and fertilizers. Here, we show how NO_x suppresses particle formation, while HOMs, sulfuric acid, and NH_3 have a synergistic enhancing effect on particle formation. We postulate a novel mechanism, involving HOMs, sulfuric acid, and ammonia, which is able to closely reproduce observations of particle formation and growth in daytime boreal forest and similar environments. The findings elucidate the complex interactions between biogenic and anthropogenic vapors in the atmospheric aerosol system.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Yliopisto-lehti: Helsingin yliopiston tiedelehti, Paul Scherrer Institut, Finnish Meteorological Institute, Der Technischen Universität Wien Fakultät für Elektrotechnik und Informationstechnik, Universidade de Lisboa, Goethe-University Frankfurt, University of Innsbruck, Ionicon GesmbH, Harvard University, Université Clermont Auvergne, University of Eastern Finland, Carnegie Mellon University, University of California, University of Colorado at Boulder, University of Leeds, HCl e 486.1, Beijing University of Chemical Technology, California Institute of Technology, Pusan National University, European Organization for Nuclear Research, Stockholm University, Department of Applied Physics, University of Manchester, National Research Council, Nanjing University, Collaborative Innovation Center of Climate Change, IDL, Aero-dyne Research Inc., Helsinki Institute of Physics

Contributors: Lehtipalo, K., Yan, C., Dada, L., Bianchi, F., Xiao, M., Wagner, R., Stolzenburg, D., Ahonen, L. R., Amorim, A., Baccarini, A., Bauer, P. S., Baumgartner, B., Bergen, A., Bernhammer, A. K., Breitenlechner, M., Brilke, S., Buchholz, A., Mazon, S. B., Chen, D., Chen, X., Dias, A., Dommen, J., Draper, D. C., Duplissy, J., Ehn, M., Finkenzeller, H., Fischer, L., Frege, C., Fuchs, C., Garmash, O., Gordon, H., Hakala, J., He, X., Heikkinen, L., Heinritzi, M., Helm, J. C., Hofbauer, V., Hoyle, C. R., Jokinen, T., Kangasluoma, J., Kerminen, V. M., Kim, C., Kirkby, J., Kontkanen, J., Kürten, A., Lawler, M. J., Mai, H., Mathot, S., Nieminen, T., Virtanen, A.

Publication date: 12 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Science Advances

Volume: 4

Issue number: 12

Article number: eaau5363

ISSN (Print): 2375-2548

Ratings:

Scopus rating (2018): CiteScore 15 SJR 6.267 SNIP 3.215
Original language: English
ASJC Scopus subject areas: General
Electronic versions:
eaa5363.full
DOIs:
10.1126/sciadv.aau5363
URLs:
<http://urn.fi/URN:NBN:fi:tty-201901181113>
Source: Scopus
Source ID: 85058725307
Research output: Contribution to journal > Article > Scientific > peer-review

Quasi two-dimensional astigmatic solitons in soft chiral metastructures

We investigate a non-homogeneous layered structure encompassing dual spatial dispersion: continuous diffraction in one transverse dimension and discrete diffraction in the orthogonal one. Such dual diffraction can be balanced out by one and the same nonlinear response, giving rise to light self-confinement into astigmatic spatial solitons: self-focusing can compensate for the spreading of a bell-shaped beam, leading to quasi-2D solitary wavepackets which result from 1D transverse self-localization combined with a discrete soliton. We demonstrate such intensity-dependent beam trapping in chiral soft matter, exhibiting one-dimensional discrete diffraction along the helical axis and one-dimensional continuous diffraction in the orthogonal plane. In nematic liquid crystals with suitable birefringence and chiral arrangement, the reorientational nonlinearity is shown to support bell-shaped solitary waves with simple astigmatism dependent on the medium birefringence as well as on the dual diffraction of the input wavepacket. The observations are in agreement with a nonlinear nonlocal model for the all-optical response.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Department of Physics, Politechnika Warszawska, Nonlinear Optics and OptoElectronics Lab, University "Roma Tre", Aerosol Physics Laboratory
Contributors: Laudyn, U. A., Jung, P. S., Karpierz, M. A., Assanto, G.
Publication date: 15 Mar 2016
Peer-reviewed: Yes

Publication information

Journal: Scientific Reports
Volume: 6
Article number: 22923
ISSN (Print): 2045-2322
Ratings:
Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364
Original language: English
ASJC Scopus subject areas: General
Electronic versions:
Quasi two-dimensional astigmatic solitons in soft chiral metastructures
DOIs:
10.1038/srep22923
URLs:
<http://urn.fi/URN:NBN:fi:tty-201607294342>
Source: Scopus
Source ID: 84961183522
Research output: Contribution to journal > Article > Scientific > peer-review

Curved optical solitons subject to transverse acceleration in reorientational soft matter

We demonstrate that optical spatial solitons with non-rectilinear trajectories can be made to propagate in a uniaxial dielectric with a transversely modulated orientation of the optic axis. Exploiting the reorientational nonlinearity of nematic liquid crystals and imposing a linear variation of the background alignment of the molecular director, we observe solitons whose trajectories have either a monotonic or a non-monotonic curvature in the observation plane of propagation, depending on either the synergistic or counteracting roles of wavefront distortion and birefringent walk-off, respectively. The observed effect is well modelled in the weakly nonlinear regime using momentum conservation of the self-collimated beams in the presence of the spatial nonlocality of the medium response. Since reorientational solitons can act as passive waveguides for other weak optical signals, these results introduce a wealth of possibilities for all-optical signal routing and light-induced photonic interconnects.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Photonics, Politechnika Warszawska, University of Edinburgh, University of Rome Roma Tre, University "Roma Tre", Laboratory of Photonics

Contributors: Laudyn, U. A., Kwaśny, M., Sala, F. A., Karpierz, M. A., Smyth, N. F., Assanto, G.

Publication date: 1 Dec 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 12385

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-017-12242-5

DOIs:

10.1038/s41598-017-12242-5

URLs:

<http://urn.fi/URN:NBN:fi:tty-201710182018>

Source: Scopus

Source ID: 85030096555

Research output: Contribution to journal › Article › Scientific › peer-review

Using multi-step proposal distribution for improved MCMC convergence in Bayesian network structure learning

Bayesian networks have become popular for modeling probabilistic relationships between entities. As their structure can also be given a causal interpretation about the studied system, they can be used to learn, for example, regulatory relationships of genes or proteins in biological networks and pathways. Inference of the Bayesian network structure is complicated by the size of the model structure space, necessitating the use of optimization methods or sampling techniques, such as Markov Chain Monte Carlo (MCMC) methods. However, convergence of MCMC chains is in many cases slow and can become even a harder issue as the dataset size grows. We show here how to improve convergence in the Bayesian network structure space by using an adjustable proposal distribution with the possibility to propose a wide range of steps in the structure space, and demonstrate improved network structure inference by analyzing phosphoprotein data from the human primary T cell signaling network.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Signal Processing, Aalto University, Department of Computer Science and Information Systems

Contributors: Larjo, A., Lähdesmäki, H.

Publication date: 27 Dec 2015

Peer-reviewed: Yes

Publication information

Journal: Eurasip Journal on Bioinformatics and Systems Biology

Volume: 2015

Issue number: 1

Article number: 6

ISSN (Print): 1687-4145

Ratings:

Scopus rating (2015): CiteScore 1.8 SJR 0.314 SNIP 0.371

Original language: English

ASJC Scopus subject areas: Medicine(all), Computer Science(all), Signal Processing, Statistics and Probability, General

Keywords: Bayesian network, MCMC, Proposal distribution, Structure learning

DOIs:

10.1186/s13637-015-0024-7

Bibliographical note

EXT="Lähdesmäki, Harri"

Source: Scopus

Source ID: 84932633872

Research output: Contribution to journal › Article › Scientific › peer-review

Real-time characterization of spectral instabilities in a mode-locked fibre laser exhibiting soliton-similariton dynamics

The study of dissipative solitons in mode-locked lasers reveals a rich landscape of interaction dynamics resulting from the interplay of nonlinearity, dispersion and dissipation. Here, we characterize a range of instabilities in a dissipative soliton fibre laser in a regime where both conventional soliton and similariton propagation play significant roles in the intracavity pulse shaping. Specifically, we use the Dispersive Fourier Transform technique to perform real-time spectral measurements of buildup dynamics from noise to the generation of stable single pulses, phase evolution dynamics of bound state "similariton molecules", and several examples of intermittent instability and explosion dynamics. These results show that the instabilities previously seen in other classes of passively mode-locked fibre lasers are also observed in the presence of strong nonlinear attraction of similariton evolution in an optical fibre amplifier.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: Ultrafast Optics, UMR 6174

Contributors: Lapre, C., Billet, C., Meng, F., Ryczkowski, P., Sylvestre, T., Finot, C., Genty, G., Dudley, J. M.

Publication date: 27 Sep 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-50022-5

DOIs:

10.1038/s41598-019-50022-5

URLs:

<http://urn.fi/URN:NBN:fi:tuni-201910073729>

Source: Scopus

Source ID: 85072699830

Research output: Contribution to journal › Article › Scientific › peer-review

Gaussian Light Model in Brightfield Optical Projection Tomography

This study focuses on improving the reconstruction process of the brightfield optical projection tomography (OPT). OPT is often described as the optical equivalent of X-ray computed tomography, but based on visible light. The detection optics used to collect light in OPT focus on a certain distance and induce blurring in those features out of focus. However, the conventionally used inverse Radon transform assumes an absolute focus throughout the propagation axis. In this study, we model the focusing properties of the detection by coupling Gaussian beam model (GBM) with the Radon transform. The GBM enables the construction of a projection operator that includes modeling of the blurring caused by the light beam. We also introduce the concept of a stretched GBM (SGBM) in which the Gaussian beam is scaled in order to avoid the modeling errors related to the determination of the focal plane. Furthermore, a thresholding approach is used to compress memory usage. We tested the GBM and SGBM approaches using simulated and experimental data in mono- and multifocal modes. When compared with the traditionally used filtered backprojection algorithm, the iteratively computed reconstructions, including the Gaussian models GBM and SGBM, provided smoother images with higher contrast.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: BioMediTech, Research group: Computational Biophysics and Imaging Group, Computing Sciences,

Research group: Inverse Problems, HAMK Smart Research Unit, Häme University of Applied Sciences, Champalimaud Foundation

Contributors: Koskela, O., Montonen, T., Belay, B., Figueiras, E., Pursiainen, S., Hyttinen, J.

Publication date: 26 Sep 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-50469-6

DOIs:

10.1038/s41598-019-50469-6

URLs:

<http://urn.fi/URN:NBN:fi:tuni-201910073730>

Source: Scopus

Source ID: 85072700777

Research output: Contribution to journal › Article › Scientific › peer-review

Personalized Monitoring and Advance Warning System for Cardiac Arrhythmias

Each year more than 7 million people die from cardiac arrhythmias. Yet no robust solution exists today to detect such heart anomalies right at the moment they occur. The purpose of this study was to design a personalized health monitoring system that can detect early occurrences of arrhythmias from an individual's electrocardiogram (ECG) signal. We first modelled the common causes of arrhythmias in the signal domain as a degradation of normal ECG beats to abnormal beats. Using the degradation models, we performed abnormal beat synthesis which created potential abnormal beats from the average normal beat of the individual. Finally, a Convolutional Neural Network (CNN) was trained using real normal and synthesized abnormal beats. As a personalized classifier, the trained CNN can monitor ECG beats in real time for arrhythmia detection. Over 34 patients' ECG records with a total of 63,341 ECG beats from the MIT-BIH arrhythmia benchmark database, we have shown that the probability of detecting one or more abnormal ECG beats among the first three occurrences is higher than 99.4% with a very low false-alarm rate.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Signal Processing, Research group: Multimedia Research Group - MRG, Qatar University, Electrical and Electronics Engineering Department, Izmir University of Economics

Contributors: Kiranyaz, S., Ince, T., Gabbouj, M.

Publication date: 1 Dec 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 9270

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-017-09544-z

DOIs:

10.1038/s41598-017-09544-z

URLs:

<http://urn.fi/URN:NBN:fi:tty-201709041866>

Bibliographical note

EXT="Ince, Turker"

EXT="Kiranyaz, Serkan"

Source: Scopus

Source ID: 85028043328

Scaling and correlation properties of RR and QT intervals at the cellular level

We study complex scaling properties of RR and QT intervals of electrocardiograms (ECGs) with their equivalences at the cellular level, that is, inter-beat intervals (IBI) and field potential durations (FPD) of spontaneously beating human-induced pluripotent stem cell-derived cardiomyocyte (hiPSC-CM) aggregates. Our detrended fluctuation analysis and Poincaré plots reveal remarkable similarities between the ECG and hiPSC-CM data. In particular, no statistically significant difference was found in the short- and long-term scaling exponents α_1 and α_2 of RR and QT intervals and their cellular equivalences. Previously unknown scaling properties of FPDs of hiPSC-CM aggregates reveal that the increasing scaling exponent of QT intervals as a function of the time scale, is an intrinsic feature at the cellular level.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: Quantum Control and Dynamics, BioMediTech, Heart Group, BioMediTech Institute and Faculty of Medicine and Life Science, University of Tampere, The Heart Center, Tampere University Hospital

Contributors: Kim, J., Shah, D., Potapov, I., Latukka, J., Aalto-Setälä, K., Räsänen, E.

Publication date: 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 3651

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/s41598-019-40247-9

URLs:

<http://urn.fi/URN:NBN:fi:tuni-201909113258>

Bibliographical note

INT=bmte,"Shah, Disheet"

INT=phys,"Latukka, Joonas"

INT=bmte,"Aalto-Setälä, Katriina"

Source: Scopus

Source ID: 85062601252

Research output: Contribution to journal › Article › Scientific › peer-review

Optimized dispersion quality of aqueous carbon nanotube colloids as a function of sonochemical yield and surfactant/CNT ratio

In this paper, we propose and verify a theoretical model of the development of dispersion quality of aqueous carbon nanotube (CNT) colloid as a function of sonochemical yield of the sonication process. Four different surfactants; Triton X-100, Pluronic F-127, CTAB and SDS were studied. From these four SDS had the lowest dispersion performance which was surprising. Optical dispersion quality results fits well with proposed theoretical model.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science, Research group: Plastics and Elastomer Technology, Univ of Oulu

Contributors: Keinänen, P., Siljander, S., Koivula, M., Sethi, J., Sarlin, E., Vuorinen, J., Kanerva, M.

Number of pages: 15

Publication date: 1 Sep 2018

Peer-reviewed: Yes

Publication information

Journal: Heliyon

Volume: 4

Issue number: 9

Article number: e00787

ISSN (Print): 2405-8440

Ratings:

Scopus rating (2018): CiteScore 1.1 SJR 0.426 SNIP 0.662

Original language: English

ASJC Scopus subject areas: General

Keywords: Materials science, Physical chemistry

Electronic versions:

1-s2.0-S2405844018313070-main

DOIs:

10.1016/j.heliyon.2018.e00787

URLs:

<http://urn.fi/URN:NBN:fi:tty-201810262483>

Bibliographical note

INT=mol,"Koivula, Mikko"

Source: Scopus

Source ID: 85048933821

Research output: Contribution to journal › Article › Scientific › peer-review

Väitöstilaisuus yliopiston imagonluojana

General information

Publication status: Published

MoE publication type: B1 Article in a scientific magazine

Organisations: Civil Engineering

Contributors: Katko, T. S.

Number of pages: 2

Pages: 63-64

Publication date: May 2017

Peer-reviewed: No

Publication information

Journal: Tiedepolitiikka

Volume: 42

Issue number: 1

ISSN (Print): 0782-0674

Original language: Finnish

ASJC Scopus subject areas: General

URLs:

http://www.tiedeliitto.net/tiedepolitiikka_lehti/tp1_17.htm

Research output: Contribution to journal › Comment/debate › Scientific

N-Glycosylation as determinant of epidermal growth factor receptor conformation in membranes

The epidermal growth factor receptor (EGFR) regulates several critical cellular processes and is an important target for cancer therapy. In lieu of a crystallographic structure of the complete receptor, atomistic molecular dynamics (MD) simulations have recently shown that they can excel in studies of the full-length receptor. Here we present atomistic MD simulations of the monomeric N-glycosylated human EGFR in biomimetic lipid bilayers that are, in parallel, also used for the reconstitution of full-length receptors. This combination enabled us to experimentally validate our simulations, using ligand binding assays and antibodies to monitor the conformational properties of the receptor reconstituted into membranes. We find that N-glycosylation is a critical determinant of EGFR conformation, and specifically the orientation of the EGFR ectodomain relative to the membrane. In the absence of a structure for full-length, posttranslationally modified membrane receptors, our approach offers new means to structurally define and experimentally validate functional properties of cell surface receptors in biomimetic membrane environments.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Tampere University of Technology, Research area: Computational Physics,

Research group: Biological Physics and Soft Matter, Computational Science X (CompX), University of Southern Denmark,

Paul Langerhans Institute Dresden of the Helmholtz Centre Munich, University Clinic Carl Gustav Carus, TU Dresden,

German Center for Diabetes Research (DZD e.V.), Max Planck Institute for Molecular Cell Biology and Genetics

Contributors: Kaszuba, K., Grzybek, M., Orłowski, A., Danne, R., Róg, T., Simons, K., Coskun, Ü., Vattulainen, I.

Number of pages: 6

Pages: 4334-4339

Publication date: 7 Apr 2015

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 112

Issue number: 14

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2015): CiteScore 17.8 SJR 6.814 SNIP 2.664

Original language: English

ASJC Scopus subject areas: General

Keywords: EGFR, Lipid-protein interaction, Lipids, MD simulation, Proteoliposomes

DOIs:

10.1073/pnas.1503262112

URLs:

<http://www.scopus.com/inward/record.url?scp=84929500864&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

AUX=fys,"Orlowski, Adam"

Source: Scopus

Source ID: 84929500864

Research output: Contribution to journal › Article › Scientific › peer-review

Changes in hemodynamics associated with metabolic syndrome are more pronounced in women than in men

The increase in cardiovascular risk associated with metabolic syndrome (MS) seems higher in women than in men. We examined hemodynamics during head-up tilt in 252 men and 250 women without atherosclerosis, diabetes, or antihypertensive medication, mean age 48 years, using whole-body impedance cardiography and radial pulse wave analysis. MS was defined according to Alberti et al. 2009. Men and women with MS presented with corresponding elevations of systolic and diastolic blood pressure (10–14%, $p \leq 0.001$) versus controls. Supine pulse wave velocity (16–17%, $p < 0.001$) and systemic vascular resistance (7–9%, $p \leq 0.026$), and upright cardiac output (6–11%, $p \leq 0.008$) were higher in both MS groups than controls. Elevation of supine aortic characteristic impedance was higher in women than in men with MS (16% vs. 8%, $p = 0.026$), and in contrast to men, no upright impedance reduction was observed in women. When upright, women but not men with MS showed faster return of reflected pressure wave ($p = 0.036$), and smaller decrease in left cardiac work ($p = 0.035$) versus controls. The faster upright return of reflected pressure, lower upright decrease in left cardiac work, and higher elevation of aortic characteristic impedance may contribute to the greater increase in MS-related cardiovascular risk in women than in men.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: BioMediTech, Tampere University, Tampere University Hospital

Contributors: Kangas, P., Tikkakoski, A., Kettunen, J., Eräranta, A., Huhtala, H., Kähönen, M., Sipilä, K., Mustonen, J., Pörsti, I.

Number of pages: 11

Publication date: 5 Dec 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 18377

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-54926-0

DOIs:

10.1038/s41598-019-54926-0

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202001131193>

Source: Scopus

Source ID: 85076028803

Research output: Contribution to journal › Article › Scientific › peer-review

Automatization and stress analysis data of CoCr laser weld fatigue tests

This work includes raw and analyzed test data when using a recently developed fatigue test method for miniature laser welds in cobalt-chromium (CoCr) alloy joints [1]: 10.1016/j.jmbbm.2019.07.004. The automatization of fatigue tests is crucial for saving costs and personnel resources and that is the reason why the automatization threshold and the resulting spectrum data related to CoCr welds are provided here. The finite element method based stress computation output is provided related to shearing-mode tests to support the dataset as a whole. In addition, the compositional data of the parent material and the laser weld are given.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, Research group: Plastics and Elastomer Technology, Orton Orthopaedic Hospital, Surface and Corrosion Science

Contributors: Kanerva, M., Besharat, Z., Pärnänen, T., Jokinen, J., Honkanen, M., Sarlin, E., Göthelid, M., Schlenzka, D.

Publication date: 1 Oct 2019

Peer-reviewed: Yes

Publication information

Journal: Data in Brief

Volume: 26

Article number: 104374

ISSN (Print): 2352-3409

Ratings:

Scopus rating (2019): CiteScore 1.5 SJR 0.105

Original language: English

ASJC Scopus subject areas: General

Keywords: Automatization, CoCr, Fatigue, Laser, Testing, Welding

DOIs:

10.1016/j.dib.2019.104374

Bibliographical note

EXT="Pärnänen, T."

Source: Scopus

Source ID: 85072173471

Research output: Contribution to journal › Article › Scientific › peer-review

Entropy analysis of word-length series of natural language texts: Effects of text language and genre

We estimate the n-gram entropies of natural language texts in word-length representation and find that these are sensitive to text language and genre. We attribute this sensitivity to changes in the probability distribution of the lengths of single words and emphasize the crucial role of the uniformity of probabilities of having words with length between five and ten. Furthermore, comparison with the entropies of shuffled data reveals the impact of word length correlations on the estimated n-gram entropies.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Multi-scaled biodata analysis and modelling (MultiBAM), University of Athens, Institute of Microelectronics, Athens, Institute for Language and Speech Processing, Athena R.C.

Contributors: Kalimeri, M., Constantoudis, V., Papadimitriou, C., Karamanos, K., Diakonos, F. K., Papageorgiou, H.

Publication date: Sep 2012

Peer-reviewed: Yes

Publication information

Journal: INTERNATIONAL JOURNAL OF BIFURCATION AND CHAOS

Volume: 22

Issue number: 9

Article number: 1250223

ISSN (Print): 0218-1274

Ratings:

Scopus rating (2012): CiteScore 1.6 SJR 0.551 SNIP 0.79

Original language: English

ASJC Scopus subject areas: Applied Mathematics, General, Engineering(all), Modelling and Simulation

Keywords: N-gram entropies, Quantitative linguistics, Symbolic dynamics, Time series, Word-length representation

DOIs:

10.1142/S0218127412502239

URLs:

<http://www.scopus.com/inward/record.url?scp=84867518276&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

EXT="Kalimeri, Maria"

Source: Scopus

Source ID: 84867518276

Research output: Contribution to journal > Article > Scientific > peer-review

Parkinson's disease detection from 20-step walking tests using inertial sensors of a smartphone: Machine learning approach based on an observational case-control study

Parkinson's disease (PD) is a neurodegenerative disease inducing dystrophy of the motor system. Automatic movement analysis systems have potential in improving patient care by enabling personalized and more accurate adjust of treatment. These systems utilize machine learning to classify the movement properties based on the features derived from the signals. Smartphones can provide an inexpensive measurement platform with their built-in sensors for movement assessment. This study compared three feature selection and nine classification methods for identifying PD patients from control subjects based on accelerometer and gyroscope signals measured with a smartphone during a 20-step walking test. Minimum Redundancy Maximum Relevance (mRMR) and sequential feature selection with both forward (SFS) and backward (SBS) propagation directions were used in this study. The number of selected features was narrowed down from 201 to 4-15 features by applying SFS and mRMR methods. From the methods compared in this study, the highest accuracy for individual steps was achieved with SFS (7 features) and Naive Bayes classifier (accuracy 75.3%), and the second highest accuracy with SFS (4 features) and k Nearest neighbours (accuracy 75.1%). Leave-one-subject-out cross-validation was used in the analysis. For the overall classification of each subject, which was based on the majority vote of the classified steps, k Nearest Neighbors provided the most accurate result with an accuracy of 84.5% and an error rate of 15.5%. This study shows the differences in feature selection methods and classifiers and provides generalizations for optimizing methodologies for smartphone-based monitoring of PD patients. The results are promising for further developing the analysis system for longer measurements carried out in free-living conditions.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: BioMediTech, Research group: Personal Health Informatics-PHI, Information and Knowledge Management, Research group: Sensor Technology and Biomeasurements (STB), Massachusetts Institute of Technology, Harvard University, Technical University of Munich, University of Helsinki, Tampere University of Applied Science, University of Turku, Satakunta Hospital District

Contributors: Juutinen, M., Wang, C., Zhu, J., Haladjian, J., Ruokolainen, J., Puustinen, J., Vehkaoja, A.

Number of pages: 19

Publication date: 2020

Peer-reviewed: Yes

Publication information

Journal: PLoS ONE

Volume: 15

Issue number: 7

Article number: e0236258

ISSN (Print): 1932-6203

Original language: English

ASJC Scopus subject areas: Biochemistry, Genetics and Molecular Biology(all), Agricultural and Biological Sciences(all),

General

Electronic versions:

Parkinson's disease detection 2020

DOIs:

10.1371/journal.pone.0236258

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202008246594>

Source: Scopus

Source ID: 85088507476

Research output: Contribution to journal > Article > Scientific > peer-review

Physical chemistry: Water's wafer-thin surface

General information

Publication status: Published

Organisations: Computational Science X (CompX), Institute of Organic Chemistry and Biochemistry, Academy of Sciences of the Czech Republic

Contributors: Jungwirth, P.

Number of pages: 2

Pages: 168-169

Publication date: 8 Jun 2011

Peer-reviewed: Yes

Publication information

Journal: Nature

Volume: 474

Issue number: 7350

ISSN (Print): 0028-0836

Ratings:

Scopus rating (2011): CiteScore 53.1 SJR 17.598 SNIP 8.652

Original language: English

ASJC Scopus subject areas: Medicine(all), General

DOIs:

10.1038/474168a

URLs:

<http://www.scopus.com/inward/record.url?scp=79958292415&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 79958292415

Research output: Contribution to journal › Short survey › Scientific › peer-review

Brain hemodynamic activity during viewing and re-viewing of comedy movies explained by experienced humor

Humor is crucial in human social interactions. To study the underlying neural processes, three comedy clips were shown twice to 20 volunteers during functional magnetic resonance imaging (fMRI). Inter-subject similarities in humor ratings, obtained immediately after fMRI, explained inter-subject correlation of hemodynamic activity in right frontal pole and in a number of other brain regions. General linear model analysis also indicated activity in right frontal pole, as well as in additional cortical areas and subcortically in striatum, explained by humorousness. The association of the right frontal pole with experienced humorousness is a novel finding, which might be related to humor unfolding over longer time scales in the movie clips. Specifically, frontal pole has been shown to exhibit longer temporal receptive windows than, e.g., sensory areas, which might have enabled processing of humor in the clips based on holding information and reinterpreting that in light of new information several (even tens of) seconds later. As another novel finding, medial and lateral prefrontal areas, frontal pole, posterior-inferior temporal areas, posterior parietal areas, posterior cingulate, striatal structures and amygdala showed reduced activity upon re-viewing of the clips, suggesting involvement in processing of humor related to novelty of the comedic events.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Signal Processing, Aalto University, Department of Bioengineering and Aerospace Engineering, Universidad Carlos III de Madrid, Instituto de Investigación Sanitaria Gregorio Marañón, National Yang Ming University, National Taiwan University

Contributors: Jääskeläinen, I. P., Pajula, J., Tohka, J., Lee, H. J., Kuo, W. J., Lin, F. H.

Publication date: 21 Jun 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 27741

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Brain hemodynamic activity

DOIs:

10.1038/srep27741

URLs:

<http://urn.fi/URN:NBN:fi:tty-201607214332>

Bibliographical note

EXT="Tohka, Jussi"

Source: Scopus

Source ID: 84975797456

Research output: Contribution to journal › Article › Scientific › peer-review

Genetic similarity of biological samples to counter bio-hacking of DNA-sequencing functionality

We present the work towards strengthening the security of DNA-sequencing functionality of future bioinformatics systems against bio-computing attacks. Recent research has shown how using common tools, a perpetrator can synthesize biological material, which upon DNA-analysis opens a cyber-backdoor for the perpetrator to hijack control of a computational resource from the DNA-sequencing pipeline. As DNA analysis finds its way into practical everyday applications, the threat of bio-hacking increases. Our wetlab experiments establish that malicious DNA can be synthesized and inserted into *E. coli*, a common contaminant. Based on that, we propose a new attack, where a hacker to reach the target hides the DNA with malicious code on common surfaces (e.g., lab coat, bench, rubber glove). We demonstrated that the threat of bio-hacking can be mitigated using dedicated input control techniques similar to those used to counter conventional injection attacks. This article proposes to use genetic similarity of biological samples to identify material that has been generated for bio-hacking. We considered freely available genetic data from 506 mammary, lymphocyte and erythrocyte samples that have a bio-hacking code inserted. During the evaluation we were able to detect up to 95% of malicious DNAs confirming suitability of our method.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research group: Emerging Technologies for Nano-Bio-Info-Cogno, Electrical Engineering, McAfee Ireland Ltd., Waterford Institute of Technology, Telecommunications Software and Systems Group (TSSG)

Contributors: Islam, M. S., Ivanov, S., Robson, E., Dooley-Cullinane, T., Coffey, L., Doolin, K., Balasubramaniam, S.

Publication date: 1 Dec 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 8684

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-44995-6

DOIs:

10.1038/s41598-019-44995-6

URLs:

<http://urn.fi/URN:NBN:fi:tty-201907011921>

Source: Scopus

Source ID: 85067546093

Research output: Contribution to journal › Article › Scientific › peer-review

Genome-wide modeling of transcription kinetics reveals patterns of RNA production delays

Genes with similar transcriptional activation kinetics can display very different temporal mRNA profiles because of differences in transcription time, degradation rate, and RNA-processing kinetics. Recent studies have shown that a splicing-associated RNA production delay can be significant. To investigate this issue more generally, it is useful to develop methods applicable to genome-wide datasets. We introduce a joint model of transcriptional activation and mRNA accumulation that can be used for inference of transcription rate, RNA production delay, and degradation rate given data from high-throughput sequencing time course experiments. We combine a mechanistic differential equation model with a nonparametric statistical modeling approach allowing us to capture a broad range of activation kinetics, and we use Bayesian parameter estimation to quantify the uncertainty in estimates of the kinetic parameters. We apply the model to

data from estrogen receptor α activation in the MCF-7 breast cancer cell line. We use RNA polymerase II ChIP-Seq time course data to characterize transcriptional activation and mRNA-Seq time course data to quantify mature transcripts. We find that 11% of genes with a good signal in the data display a delay of more than 20 min between completing transcription and mature mRNA production. The genes displaying these long delays are significantly more likely to be short. We also find a statistical association between high delay and late intron retention in pre-mRNA data, indicating significant splicing-associated production delays in many genes.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research Community on Data-to-Decision (D2D), University of Helsinki, Aalto University, Institute for Molecular Biology, Radboud University Nijmegen, Genomatix Software GmbH, University of Sheffield, University of Manchester

Contributors: Honkela, A., Peltonen, J., Topa, H., Charapitsa, I., Matarese, F., Grote, K., Stunnenberg, H. G., Reid, G., Lawrence, N. D., Rattray, M.

Number of pages: 6

Pages: 13115-13120

Publication date: 20 Oct 2015

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 112

Issue number: 42

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2015): CiteScore 17.8 SJR 6.814 SNIP 2.664

Original language: English

ASJC Scopus subject areas: General

Keywords: Gaussian process inference, Gene expression, Gene transcription, RNA processing, RNA splicing

DOIs:

10.1073/pnas.1420404112

URLs:

<http://www.scopus.com/inward/record.url?scp=84947244766&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84947244766

Research output: Contribution to journal > Article > Scientific > peer-review

Structure-phenotype correlations of human CYP21A2 mutations in congenital adrenal hyperplasia

Mutations in the cytochrome p450 (CYP)21A2 gene, which encodes the enzyme steroid 21-hydroxylase, cause the majority of cases in congenital adrenal hyperplasia, an autosomal recessive disorder. To date, more than 100 CYP21A2 mutations have been reported. These mutations can be associated either with severe salt-wasting or simple virilizing phenotypes or with milder nonclassical phenotypes. Not all CYP21A2 mutations have, however, been characterized biochemically, and the clinical consequences of these mutations remain unknown. Using the crystal structure of its bovine homolog as a template, we have constructed a humanized model of CYP21A2 to provide comprehensive structural explanations for the clinical manifestations caused by each of the known disease-causing mis-sense mutations in CYP21A2. Mutations that affect membrane anchoring, disrupt heme and/or substrate binding, or impair stability of CYP21A2 cause complete loss of function and salt-wasting disease. In contrast, mutations altering the transmembrane region or conserved hydrophobic patches cause up to a 98% reduction in enzyme activity and simple virilizing disease. Mild nonclassical disease can result from interference in oxidoreductase interactions, salt-bridge and hydrogen-bonding networks, and nonconserved hydrophobic clusters. A simple in silico evaluation of previously uncharacterized gene mutations could, thus, potentially help predict the often diverse phenotypes of a monogenic disorder.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Computational Science X (CompX), Queen's University, Belfast, Northern Ireland, Forschungszentrum Jülich GmbH, Forschungszentrum Jülich (FZJ), Mount Sinai School of Medicine

Contributors: Haider, S., Islam, B., D'Atri, V., Sgobba, M., Poojari, C., Sun, L., Yuen, T., Zaidi, M., New, M. I.

Number of pages: 6

Pages: 2605-2610

Publication date: 12 Feb 2013

Peer-reviewed: Yes

Publication information

Journal: Proceedings of the National Academy of Sciences of the United States of America

Volume: 110

Issue number: 7

ISSN (Print): 0027-8424

Ratings:

Scopus rating (2013): CiteScore 17.4 SJR 7.073 SNIP 2.721

Original language: English

ASJC Scopus subject areas: General

Keywords: CYP21A2 structural analysis, Molecular modeling, Structure-phenotype correlation

DOIs:

10.1073/pnas.1221133110

URLs:

<http://www.scopus.com/inward/record.url?scp=84873734979&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84873734979

Research output: Contribution to journal > Article > Scientific > peer-review

The evolutionary history of lethal metastatic prostate cancer

Cancers emerge from an ongoing Darwinian evolutionary process, often leading to multiple competing subclones within a single primary tumour. This evolutionary process culminates in the formation of metastases, which is the cause of 90% of cancer-related deaths. However, despite its clinical importance, little is known about the principles governing the dissemination of cancer cells to distant organs. Although the hypothesis that each metastasis originates from a single tumour cell is generally supported, recent studies using mouse models of cancer demonstrated the existence of polyclonal seeding from and interclonal cooperation between multiple subclones. Here we sought definitive evidence for the existence of polyclonal seeding in human malignancy and to establish the clonal relationship among different metastases in the context of androgen-deprived metastatic prostate cancer. Using whole-genome sequencing, we characterized multiple metastases arising from prostate tumours in ten patients. Integrated analyses of subclonal architecture revealed the patterns of metastatic spread in unprecedented detail. Metastasis-to-metastasis spread was found to be common, either through de novo monoclonal seeding of daughter metastases or, in five cases, through the transfer of multiple tumour clones between metastatic sites. Lesions affecting tumour suppressor genes usually occur as single events, whereas mutations in genes involved in androgen receptor signalling commonly involve multiple, convergent events in different metastases. Our results elucidate in detail the complex patterns of metastatic spread and further our understanding of the development of resistance to androgen-deprivation therapy in prostate cancer.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Prostate cancer research center (PCRC), Wellcome Trust Sanger Institute, Cancer Research UK, Genome Analysis Centre, Tampere University Hospital, Institute of Biosciences and Medical Technology, Johns Hopkins School of Medicine, Avoneaux Medical Institute, University of Liverpool, Institute of Cancer Research London, University of Cambridge, Cancer Research UK, Royal Marsden NHS Foundation Trust

Contributors: Gundem, G., Van Loo, P., Kremeyer, B., Alexandrov, L. B., Tubio, J. M., Papaemmanuil, E., Brewer, D. S., Kallio, H. M., Högnäs, G., Annala, M., Kivinummi, K., Goody, V., Latimer, C., O'Meara, S., Dawson, K. J., Isaacs, W., Emmert-Buck, M. R., Nykter, M., Foster, C., Kote-Jarai, Z., Easton, D., Whitaker, H. C., Neal, D. E., Cooper, C. S., Eeles, R. A., Visakorpi, T., Campbell, P. J., McDermott, U., Wedge, D. C., Bova, G. S.

Number of pages: 5

Pages: 353-357

Publication date: 15 Apr 2015

Peer-reviewed: Yes

Publication information

Journal: Nature

Volume: 520

Issue number: 7547

ISSN (Print): 0028-0836

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Original language: English

ASJC Scopus subject areas: Medicine(all), General

DOIs:

10.1038/nature14347

URLs:

<http://www.scopus.com/inward/record.url?scp=84928405167&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84928405167

Research output: Contribution to journal › Article › Scientific › peer-review

Membrane omega-3 fatty acids modulate the oligomerisation kinetics of adenosine A_{2A} and dopamine D₂ receptors
Membrane levels of docosahexaenoic acid (DHA), an essential omega-3 polyunsaturated fatty acid (ω -3 PUFA), are decreased in common neuropsychiatric disorders. DHA modulates key cell membrane properties like fluidity, thereby affecting the behaviour of transmembrane proteins like G protein-coupled receptors (GPCRs). These receptors, which have special relevance for major neuropsychiatric disorders have recently been shown to form dimers or higher order oligomers, and evidence suggests that DHA levels affect GPCR function by modulating oligomerisation. In this study, we assessed the effect of membrane DHA content on the formation of a class of protein complexes with particular relevance for brain disease: adenosine A_{2A} and dopamine D₂ receptor oligomers. Using extensive multiscale computer modelling, we find a marked propensity of DHA for interaction with both A_{2A} and D₂ receptors, which leads to an increased rate of receptor oligomerisation. Bioluminescence resonance energy transfer (BRET) experiments performed on living cells suggest that this DHA effect on the oligomerisation of A_{2A} and D₂ receptors is purely kinetic. This work reveals for the first time that membrane ω -3 PUFAs play a key role in GPCR oligomerisation kinetics, which may have important implications for neuropsychiatric conditions like schizophrenia or Parkinson's disease.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Computational Physics, Universitat Pompeu Fabra, Universitat Autònoma de Barcelona, Spain, Universiteit Gent

Contributors: Guixà-González, R., Javanainen, M., Gómez-Soler, M., Cordobilla, B., Domingo, J. C., Sanz, F., Pastor, M., Ciruela, F., Martínez-Seara, H., Selent, J.

Publication date: 22 Jan 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 19839

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Membrane omega-3 fatty acids modulate the oligomerisation kinetics of adenosine A_{2A} and dopamine D₂ receptors

DOIs:

10.1038/srep19839

URLs:

<http://urn.fi/URN:NBN:fi:ty-201604123806>

Source: Scopus

Source ID: 84955489920

Research output: Contribution to journal › Article › Scientific › peer-review

First passage time distribution in heterogeneity controlled kinetics: Going beyond the mean first passage time

The first passage is a generic concept for quantifying when a random quantity such as the position of a diffusing molecule or the value of a stock crosses a preset threshold (target) for the first time. The last decade saw an enlightening series of new results focusing mostly on the so-called mean and global first passage time (MFPT and GFPT, respectively) of such processes. Here we push the understanding of first passage processes one step further. For a simple heterogeneous system we derive rigorously the complete distribution of first passage times (FPTs). Our results demonstrate that the typical FPT significantly differs from the MFPT, which corresponds to the long time behaviour of the FPT distribution. Conversely, the short time behaviour is shown to correspond to trajectories connecting directly from the initial value to the target. Remarkably, we reveal a previously overlooked third characteristic time scale of the first passage dynamics mirroring brief excursion away from the target.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Computational Physics, National Institute of Chemistry Ljubljana, Institute for Physics and Astronomy, University of Potsdam

Contributors: Godec, A., Metzler, R.

Publication date: 8 Feb 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 20349

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

First passage time distribution in heterogeneity controlled kinetics - going beyond the mean first passage time

DOIs:

10.1038/srep20349

URLs:

<http://urn.fi/URN:NBN:fi:ty-201604123807>

Source: Scopus

Source ID: 84957603857

Research output: Contribution to journal › Article › Scientific › peer-review

Highly ductile amorphous oxide at room temperature and high strain rate

Oxide glasses are an integral part of the modern world, but their usefulness can be limited by their characteristic brittleness at room temperature. We show that amorphous aluminum oxide can permanently deform without fracture at room temperature and high strain rate by a viscous creep mechanism. These thin-films can reach flow stress at room temperature and can flow plastically up to a total elongation of 100%, provided that the material is dense and free of geometrical flaws. Our study demonstrates a much higher ductility for an amorphous oxide at low temperature than previous observations. This discovery may facilitate the realization of damage-tolerant glass materials that contribute in new ways, with the potential to improve the mechanical resistance and reliability of applications such as electronic devices and batteries.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, Physics, Research group: Nanophotonics, Italian Institute of Technology, Erich Schmid Institute of Materials Science, Bruker, Norwegian Univ. of Sci. and Technol., University of Lyon

Contributors: Frankberg, E. J., Kalikka, J., Ferré, F. G., Joly-Pottuz, L., Salminen, T., Hintikka, J., Hokka, M., Koneti, S., Douillard, T., Le Saint, B., Kreiml, P., Cordill, M. J., Epicier, T., Stauffer, D., Vanazzi, M., Roiban, L., Akola, J., Fonzo, F. D., Levänen, E., Masenelli-Varlot, K.

Number of pages: 6

Pages: 864-869

Publication date: 15 Nov 2019

Peer-reviewed: Yes

Publication information

Journal: Science

Volume: 366

Issue number: 6467

ISSN (Print): 0036-8075

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Scopus rating (2019): CiteScore 45.3 SJR 13.11 SNIP 7.521

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ASJC Scopus subject areas: General

DOIs:

10.1126/science.aav1254

Source: Scopus

Source ID: 85075053772

Research output: Contribution to journal › Article › Scientific › peer-review

Azobenzene-based sinusoidal surface topography drives focal adhesion confinement and guides collective migration of epithelial cells

Surface topography is a key parameter in regulating the morphology and behavior of single cells. At multicellular level, coordinated cell displacements drive many biological events such as embryonic morphogenesis. However, the effect of

surface topography on collective migration of epithelium has not been studied in detail. Mastering the connection between surface features and collective cellular behaviour is highly important for novel approaches in tissue engineering and repair. Herein, we used photopatterned microtopographies on azobenzene-containing materials and showed that smooth topographical cues with proper period and orientation can efficiently orchestrate cell alignment in growing epithelium. Furthermore, the experimental system allowed us to investigate how the orientation of the topographical features can alter the speed of wound closure in vitro. Our findings indicate that the extracellular microenvironment topography coordinates their focal adhesion distribution and alignment. These topographic cues are able to guide the collective migration of multicellular systems, even when cell–cell junctions are disrupted.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Materials Science and Environmental Engineering, BioMediTech, Research group: Biophysics of the eye, Research group: Chemistry & Advanced Materials, Italian Institute of Technology, Chan Zuckerberg Biohub, Lawrence Berkeley National Laboratory, University of California, Berkeley

Contributors: Fedele, C., Mäntylä, E., Belardi, B., Hamkins-Indik, T., Cavalli, S., Netti, P. A., Fletcher, D. A., Nymark, S., Priimagi, A., Ihalainen, T. O.

Number of pages: 15

Publication date: 2020

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 10

Issue number: 1

Article number: 15329

ISSN (Print): 2045-2322

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Azobenzene-based sinusoidal surface 2020

DOIs:

10.1038/s41598-020-71567-w

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202009287145>

Bibliographical note

INT=bmte,"Mäntylä, Elina"

Source: Scopus

Source ID: 85091199646

Research output: Contribution to journal > Article > Scientific > peer-review

Sensitivity enhancement of flexible gas sensors via conversion of inkjet-printed silver electrodes into porous gold counterparts

This work describes a facile, mild and general wet chemical method to change the material and the geometry of inkjet-printed interdigitated electrodes (IDEs) thus drastically enhancing the sensitivity of chemiresistive sensors. A novel layer-by-layer chemical method was developed and used to uniformly deposit semiconducting single-wall carbon nanotube (SWCNT)-based sensing elements on a Kapton[®] substrate. Flexible chemiresistive sensors were then fabricated by inkjet-printing fine-featured silver IDEs on top of the sensing elements. A mild and facile two-step process was employed to convert the inkjet-printed dense silver IDEs into their highly porous gold counterparts under ambient conditions without losing the IDE-substrate adhesion. A proof-of-concept gas sensor equipped with the resulting porous gold IDEs featured a sensitivity to diethyl ethylphosphonate (DEEP, a simulant of the nerve agent sarin) of at least 5 times higher than a similar sensor equipped with the original dense silver IDEs, which suggested that the electrode material and/or the Schottky contacts between the electrodes and the SWCNTs might have played an important role in the gas sensing process.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Wireless Identification and Sensing Systems Research Group, Georgia Institute of Technology, Georgia Institute of Technology, School of Electrical and Computer Engineering

Contributors: Fang, Y., Akbari, M., Sydänheimo, L., Ukkonen, L., Tentzeris, M. M.

Publication date: 1 Dec 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 8988

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-017-09174-5

DOIs:

10.1038/s41598-017-09174-5

URLs:

<http://urn.fi/URN:NBN:fi:tty-201709041865>

Source: Scopus

Source ID: 85027882802

Research output: Contribution to journal > Article > Scientific > peer-review

Upstream Transcription Factor 1 (USF1) allelic variants regulate lipoprotein metabolism in women and USF1 expression in atherosclerotic plaque

Upstream transcription factor 1 (USF1) allelic variants significantly influence future risk of cardiovascular disease and overall mortality in females. We investigated sex-specific effects of USF1 gene allelic variants on serum indices of lipoprotein metabolism, early markers of asymptomatic atherosclerosis and their changes during six years of follow-up. In addition, we investigated the cis-regulatory role of these USF1 variants in artery wall tissues in Caucasians. In the Cardiovascular Risk in Young Finns Study, 1,608 participants (56% women, aged 31.9 ± 4.9) with lipids and cIMT data were included. For functional study, whole genome mRNA expression profiling was performed in 91 histologically classified atherosclerotic samples. In females, serum total, LDL cholesterol and apoB levels increased gradually according to USF1 rs2516839 genotypes TT <CT <CC and rs1556259 AA <AG <GG as well as according to USF1 H3 (GCCCCG) copy number 0 <1 <2. Furthermore, the carriers of minor alleles of rs2516839 (C) and rs1556259 (G) of USF1 gene had decreased USF1 expression in atherosclerotic plaques ($P = 0.028$ and 0.08 , respectively) as compared to non-carriers. The genetic variation in USF1 influence USF1 transcript expression in advanced atherosclerosis and regulates levels and metabolism of circulating apoB and apoB-containing lipoprotein particles in sex-dependent manner, but is not a major determinant of early markers of atherosclerosis.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Optoelectronics Research Centre, Integrated Technologies for Tissue Engineering Research (ITTE), Tampere University Hospital, School of Management (JKK), Turun Yliopisto/Turun Biomateriaalikeskus, National Public Health Institute, Department of Clinical Chemistry, Itä-Suomen yliopisto, German Research Center for Environmental Health, University Central Hospital Kuopio, University of Bristol

Contributors: Fan, Y. M., Hernesniemi, J., Oksala, N., Levula, M., Raitoharju, E., Collings, A., Hutri-Kähönen, N., Juonala, M., Marniemi, J., Lyytikäinen, L. P., Seppälä, I., Mennander, A., Tarkka, M., Kangas, A. J., Soininen, P., Salenius, J. P., Klopp, N., Illig, T., Laitinen, T., Ala-Korpela, M., Laaksonen, R., Viikari, J., Kähönen, M., Raitakari, O. T., Lehtimäki, T.

Publication date: 11 Apr 2014

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 4

Article number: 4650

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2014): CiteScore 4.2 SJR 2.163 SNIP 1.58

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep04650

URLs:

<http://www.scopus.com/inward/record.url?scp=84898621322&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84898621322

Lower bound for the spatial extent of localized modes in photonic-crystal waveguides with small random imperfections

Light localization due to random imperfections in periodic media is paramount in photonics research. The group index is known to be a key parameter for localization near photonic band edges, since small group velocities reinforce light interaction with imperfections. Here, we show that the size of the smallest localized mode that is formed at the band edge of a one-dimensional periodic medium is driven instead by the effective photon mass, i.e. the flatness of the dispersion curve. Our theoretical prediction is supported by numerical simulations, which reveal that photonic-crystal waveguides can exhibit surprisingly small localized modes, much smaller than those observed in Bragg stacks thanks to their larger effective photon mass. This possibility is demonstrated experimentally with a photonic-crystal waveguide fabricated without any intentional disorder, for which near-field measurements allow us to distinctly observe a wavelength-scale localized mode despite the smallness ($\sim 1/1000$ of a wavelength) of the fabrication imperfections.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: CNRS, Université de Bordeaux, ICMCB, Université de Bourgogne Franche-Comté, University of Ottawa, Canada, University of York, Université de Paris-Sud

Contributors: Faggiani, R., Baron, A., Zang, X., Lalouat, L., Schulz, S. A., O'Regan, B., Vynck, K., Cluzel, B., De Fornel, F., Krauss, T. F., Lalanne, P.

Publication date: 1 Jun 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 27037

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

DOIs:

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<http://www.scopus.com/inward/record.url?scp=84973300726&partnerID=8YFLogxK> (Link to publication in Scopus)

Bibliographical note

EXT="Zang, Xiaorun"

Source: Scopus

Source ID: 84973300726

Research output: Contribution to journal › Article › Scientific › peer-review

Subangstrom resolution x-ray structure details aquaporin-water interactions

Aquaporins are membrane channels that facilitate the flow of water across biological membranes. Two conserved regions are central for selective function: the dual asparagine-proline-alanine (NPA) aquaporin signature motif and the aromatic and arginine selectivity filter (SF). Here, we present the crystal structure of a yeast aquaporin at 0.88 angstrom resolution. We visualize the H-bond donor interactions of the NPA motif's asparagine residues to passing water molecules; observe a polarized water-water H-bond configuration within the channel; assign the tautomeric states of the SF histidine and arginine residues; and observe four SF water positions too closely spaced to be simultaneously occupied. Strongly correlated movements break the connectivity of SF waters to other water molecules within the channel and prevent proton transport via a Grothuss mechanism.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Computational Science X (CompX), University of Gothenburg, University of Cambridge, Department of Biochemistry, Univ Illinois, University of Illinois System, University of Illinois Urbana-Champaign, Frederick Seitz Mat Res Lab, Dept Mat Sci & Engn

Contributors: Eriksson, U. K., Fischer, G., Friemann, R., Enkavi, G., Tajkhorshid, E., Neutze, R.

Number of pages: 4

Pages: 1346-1349

Publication date: 2013

Peer-reviewed: Yes

Publication information

Journal: Science

Volume: 340

Issue number: 6138

ISSN (Print): 0036-8075

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Scopus rating (2013): CiteScore 46.9 SJR 12.41 SNIP 7.72

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1126/science.1234306

URLs:

<http://www.scopus.com/inward/record.url?scp=84878943513&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84878943513

Research output: Contribution to journal > Article > Scientific > peer-review

Effects of Sintering Temperature on Crystallization and Fabrication of Porous Bioactive Glass Scaffolds for Bone Regeneration

In this work the sintering ability of borosilicate (S53B50), borophosphate (P40B10) and phosphate (Sr) bioactive glasses was investigated. The glass powders were crushed and sintered in air at a heating rate of 10 °C/min for 2 hours at sintering temperatures between 480 °C-600 °C. The aim was to define the optimum sintering temperature prior to glass crystallization. The density of the samples was found to decrease when the temperature was increased up to 580 °C; probably due to the inhibition of the viscous flow of the particles during sintering thereby reducing the densification of the material. Such low porosity is not suitable in tissue engineering. To process highly porous scaffolds with porosity required for scaffold applicable to tissue engineering, the powders were further mixed with 60 vol.% and 70 vol.% of $\text{NH}_4(\text{HCO}_3)$ foaming agent. Meanwhile, the density of the samples sintered with $\text{NH}_4(\text{HCO}_3)$ was found to decrease with an increase in $\text{NH}_4(\text{HCO}_3)$ content. This indicates an increase in porosity of the samples. The glass compositions reached an open porosity of more than 60% at the addition of 70 vol.% $\text{NH}_4(\text{HCO}_3)$. In addition, SEM micrograph revealed large pores with good interconnection between the pores.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Biomaterials and Tissue Engineering Group, BioMediTech, Department of Mining and Metallurgical Engineering, University of Witwatersrand

Contributors: Erasmus, E. P., Johnson, O. T., Sigalas, I., Massera, J.

Publication date: 1 Dec 2017

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 7

Issue number: 1

Article number: 6046

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2017): CiteScore 4.8 SJR 1.533 SNIP 1.258

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

erasmus et al. 2017

DOIs:

10.1038/s41598-017-06337-2

URLs:

<http://urn.fi/URN:NBN:fi:tty-201708021642>

Source: Scopus

Source ID: 85025143008

Research output: Contribution to journal > Article > Scientific > peer-review

In vitro Evaluation of Porous borosilicate, borophosphate and phosphate Bioactive Glasses Scaffolds fabricated using Foaming Agent for Bone Regeneration

In this work, glasses within the borosilicate borophosphate and phosphate family were sintered into 3D porous scaffolds using 60 and 70 vol. % $\text{NH}_4(\text{HCO}_3)$ as a foaming agent. All scaffolds produced remained amorphous; apart from one third

of the glasses which crystallized. All produced scaffolds had porosity >50% and interconnected pores in the range of 250-570 μm ; as evidenced by μCT . The in-vitro dissolution of the scaffolds in SBF and changes in compression were assessed as a function of immersion time. The pH of the solution containing the borosilicate scaffolds increased due to the typical non-congruent dissolution of this glass family. Borophosphate and phosphate scaffolds induced a decrease in pH upon dissolution attributed to the congruent dissolution of those materials and the large release of phosphate within the media. As prepared, scaffolds showed compressive strength of 1.29 ± 0.21 , 1.56 ± 0.63 , 3.63 ± 0.69 MPa for the borosilicate, borophosphate and phosphate samples sintered with 60 vol. % $\text{NH}_4(\text{HCO}_3)$, respectively. Evidence of hydroxyapatite precipitation on the borosilicate glass scaffolds was shown by SEM/EDS, XRD and ICP-OES analysis. The borophosphate scaffolds remained stable upon dissolution. The phosphate scaffolds were fully crystallized, leading to very large release of phosphate in the media.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Faculty of Biomedical Sciences and Engineering, Research group: Biomaterials and Tissue Engineering Group, African Material Science and Engineering Network (A Carnegie-IAS RISE Network), University of the Witwatersrand School of Chemical and Metallurgical Engineering, University of Witwatersrand, Department of Mining and Metallurgical Engineering

Contributors: Erasmus, E. P., Sule, R., Johnson, O. T., Massera, J., Sigalas, I.

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 3699

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-018-22032-2

DOIs:

10.1038/s41598-018-22032-2

URLs:

<http://urn.fi/URN:NBN:fi:tty-201803141372>

Source: Scopus

Source ID: 85042635107

Research output: Contribution to journal > Article > Scientific > peer-review

A Bayesian analysis of the chromosome architecture of human disorders by integrating reductionist data

In this paper, we present a Bayesian approach to estimate a chromosome and a disorder network from the Online Mendelian Inheritance in Man (OMIM) database. In contrast to other approaches, we obtain statistic rather than deterministic networks enabling a parametric control in the uncertainty of the underlying disorder-disease gene associations contained in the OMIM, on which the networks are based. From a structural investigation of the chromosome network, we identify three chromosome subgroups that reflect architectural differences in chromosome-disorder associations that are predictively exploitable for a functional analysis of diseases.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Research Community on Data-to-Decision (D2D), Prostate cancer research center (PCRC), Computational Biology and Machine Learning Lab., Faculty of Medicine, Health and Life Sciences, Queen's University, Belfast, Northern Ireland, University of Arkansas for Medical Sciences, Institute for Bioinformatics and Translational Research

Contributors: Emmert-Streib, F., De Matos Simoes, R., Tripathi, S., Glazko, G. V., Dehmer, M.

Publication date: 2012

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 2

Article number: 513

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2012): CiteScore 1.1 SJR 1.531 SNIP 0.997

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep00513

URLs:

<http://www.scopus.com/inward/record.url?scp=84864149036&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84864149036

Research output: Contribution to journal › Article › Scientific › peer-review

Surface-Enhanced Impulsive Coherent Vibrational Spectroscopy

Surface-enhanced Raman spectroscopy (SERS) has attracted a lot of attention in molecular sensing because of the remarkable ability of plasmonic metal nanostructures to enhance the weak Raman scattering process. On the other hand, coherent vibrational spectroscopy triggered by impulsive excitation using ultrafast laser pulses provides complete information about the temporal evolution of molecular vibrations, allowing dynamical processes in molecular systems to be followed in "real time". Here, we combine these two concepts and demonstrate surface-enhanced impulsive vibrational spectroscopy. The vibrational modes of the ground and excited states of poly[2-methoxy-5-(2-ethylhexyloxy)-1,4-phenylenevinylene] (MEH-PPV), spin-coated on a substrate covered with monodisperse silver nanoparticles, are impulsively excited with a sub-10 fs pump pulse and characterized with a delayed broad-band probe pulse. The maximum enhancement in the spectrally and temporally resolved vibrational signatures averaged over the whole sample is about 4.6, while the real-time information about the instantaneous vibrational amplitude together with the initial vibrational phase is preserved. The phase is essential to determine the vibrational contributions from the ground and excited states.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, Research area: Aerosol Physics, Research area: Optics, Research group: Nonlinear Optics, Research group: Aerosol Synthesis, Shanghai Institute of Optics and Fine Mechanics Chinese Academy of Sciences, National Chiao-Tung University

Contributors: Du, J., Harra, J., Virkki, M., Mäkelä, J. M., Leng, Y., Kauranen, M., Kobayashi, T.

Publication date: 4 Nov 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 36471

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

srep36471

DOIs:

10.1038/srep36471

URLs:

<http://urn.fi/URN:NBN:fi:tyy-201612204882>

URLs:

<http://www.scopus.com/inward/record.url?scp=84994682182&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84994682182

Research output: Contribution to journal › Article › Scientific › peer-review

Mechanically driven strategies to improve electromechanical behaviour of printed stretchable electronic systems

Stretchable electronics promise to extend the application range of conventional electronics by enabling them to keep their electrical functionalities under system deformation. Within this framework, development of printable silver-polymer composite inks is making possible to realize several of the expected applications for stretchable electronics, which range from seamless sensors for human body measurement (e.g. health patches) to conformable injection moulded structural electronics. However, small rigid electric components are often incorporated in these devices to ensure functionality. Under mechanical loading, these rigid elements cause strain concentrations and a general deterioration of the system's

electrical performance. This work focuses on different strategies to improve electromechanical performance by investigating the deformation behaviour of soft electronic systems comprising rigid devices through Finite Element analyses. Based on the deformation behaviour of a simple stretchable device under tensile loading, three general strategies were proposed: local component encapsulation, direct component shielding, and strain dispersion. The FE behaviour achieved using these strategies was then compared with the experimental results obtained for each design, highlighting the reasons for their different resistance build-up. Furthermore, crack formation in the conductive tracks was analysed under loading to highlight its link with the evolution of the system electrical performance.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Electrical Engineering, Research group: Plastics and Elastomer Technology, Research group: Laboratory for Future Electronics, Materials Science and Environmental Engineering, Research group: Wireless Communications and Positioning

Contributors: Di Vito, D., Mosallaei, M., Khorramdel, B., Kanerva, M., Mäntysalo, M.

Number of pages: 11

Publication date: 2020

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 10

Issue number: 1

Article number: 12037

ISSN (Print): 2045-2322

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

Mechanically driven strategies 2020

DOIs:

10.1038/s41598-020-68871-w

URLs:

<http://urn.fi/URN:NBN:fi:tuni-202008256627>

Source: Scopus

Source ID: 85088313221

Research output: Contribution to journal > Article > Scientific > peer-review

Step down Vascular Calcification Analysis using State-of-the-Art Nanoanalysis Techniques

New insights into the architecture and formation mechanisms of calcific lesions down to the nanoscale open a better understanding of atherosclerosis and its pathogenesis. Scanning electron- and atomic force microscope based nano-analytical characterization techniques were adapted to the assessment of an ex-vivo calcified coronary artery. Human atherosclerotic tissue and bone tissue reside a typical chemistry of Magnesium and Sodium rich Calcium phosphates, identified as whitlockite and Calcium apatite, respectively. Despite the obvious similarities in both chemistry and crystallography, there are also clear differences between calcified vascular tissue and bone such as the highly oriented growth in bone, revealing meso-crystal character, as opposed to the anisotropic character of calcified vascular lesions. While the grain size in vascular calcified plaques is in the range of nanometers, the grain size in bone appears larger. Spherical calcific particles present in both the coronary artery wall and embedded in plaques reveal concentric layers with variations in both organic content and degree of hydration.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Materials Science, Philipps University, Universitätsklinikum Gießen und Marburg GmbH

Contributors: Curtze, S. C., Kratz, M., Steinert, M., Vogt, S.

Publication date: 16 Mar 2016

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 6

Article number: 23285

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2016): CiteScore 4.2 SJR 1.692 SNIP 1.364

Original language: English
ASJC Scopus subject areas: General
Electronic versions:

Step down Vascular Calcification Analysis using State-of-the-Art Nanoanalysis Techniques

DOIs:

[10.1038/srep23285](https://doi.org/10.1038/srep23285)

URLs:

<http://urn.fi/URN:NBN:fi:tty-201604123799>

Source: Scopus

Source ID: 84961828954

Research output: Contribution to journal > Article > Scientific > peer-review

Automatic classification of IgA endomysial antibody test for celiac disease: a new method deploying machine learning

Widespread use of endomysial autoantibody (EmA) test in diagnostics of celiac disease is limited due to its subjectivity and its requirement of an expert evaluator. The study aimed to determine whether machine learning can be applied to create a new observer-independent method of automatic assessment and classification of the EmA test for celiac disease. The study material comprised of 2597 high-quality IgA-class EmA images collected in 2017–2018. According to standard procedure, highly-experienced professional classified samples into the following four classes: I - positive, II - negative, III - IgA deficient, and IV - equivocal. Machine learning was deployed to create a classification model. The sensitivity and specificity of the model were 82.84% and 99.40%, respectively. The accuracy was 96.80%. The classification error was 3.20%. The area under the curve was 99.67%, 99.61%, 100%, and 99.89%, for I, II, III, and IV class, respectively. The mean assessment time per image was 16.11 seconds. This is the first study deploying machine learning for the automatic classification of IgA-class EmA test for celiac disease. The results indicate that using machine learning enables quick and precise EmA test analysis that can be further developed to simplify EmA analysis.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: BioMediTech, Research group: Computational Biophysics and Imaging Group, Tampere University, Tampere University Hospital

Contributors: Caetano dos Santos, F. L., Michalek, I. M., Laurila, K., Kaukinen, K., Hyttinen, J., Lindfors, K.

Publication date: 1 Dec 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 9217

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

[s41598-019-45679-x](https://doi.org/10.1038/s41598-019-45679-x)

DOIs:

[10.1038/s41598-019-45679-x](https://doi.org/10.1038/s41598-019-45679-x)

URLs:

<http://urn.fi/URN:NBN:fi:tty-201907081944>

Source: Scopus

Source ID: 85068094140

Research output: Contribution to journal > Article > Scientific > peer-review

Real sequence effects on the search dynamics of transcription factors on DNA

Recent experiments show that transcription factors (TFs) indeed use the facilitated diffusion mechanism to locate their target sequences on DNA in living bacteria cells: TFs alternate between sliding motion along DNA and relocation events through the cytoplasm. From simulations and theoretical analysis we study the TF-sliding motion for a large section of the DNA-sequence of a common *E. coli* strain, based on the two-state TF-model with a fast-sliding search state and a recognition state enabling target detection. For the probability to detect the target before dissociating from DNA the TF-search times self-consistently depend heavily on whether or not an auxiliary operator (an accessible sequence similar to the main operator) is present in the genome section. Importantly, within our model the extent to which the interconversion rates between search and recognition states depend on the underlying nucleotide sequence is varied. A moderate dependence maximises the capability to distinguish between the main operator and similar sequences. Moreover, these

auxiliary operators serve as starting points for DNA looping with the main operator, yielding a spectrum of target detection times spanning several orders of magnitude. Auxiliary operators are shown to act as funnels facilitating target detection by TFs.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Department of Physics, University of Potsdam, Technical University Munich, Chemistry and Pharmacy, University of Southern Denmark, Institute for Physics And Astronomy, MEMPHYS - Centre for Biomembrane Physics

Contributors: Bauer, M., Rasmussen, E. S., Lomholt, M. A., Metzler, R.

Publication date: 8 Jul 2015

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 5

Article number: 10072

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2015): CiteScore 4.2 SJR 2.034 SNIP 1.595

Original language: English

ASJC Scopus subject areas: General

DOIs:

10.1038/srep10072

URLs:

<http://www.scopus.com/inward/record.url?scp=84936946155&partnerID=8YFLogxK> (Link to publication in Scopus)

Source: Scopus

Source ID: 84936946155

Research output: Contribution to journal > Article > Scientific > peer-review

Multilayer Aggregation with Statistical Validation: Application to Investor Networks

Multilayer networks are attracting growing attention in many fields, including finance. In this paper, we develop a new tractable procedure for multilayer aggregation based on statistical validation, which we apply to investor networks. Moreover, we propose two other improvements to their analysis: transaction bootstrapping and investor categorization. The aggregation procedure can be used to integrate security-wise and time-wise information about investor trading networks, but it is not limited to finance. In fact, it can be used for different applications, such as gene, transportation, and social networks, where they are inferred or observable. Additionally, in the investor network inference, we use transaction bootstrapping for better statistical validation. Investor categorization allows for constant size networks and having more observations for each node, which is important in the inference especially for less liquid securities. Furthermore, we observe that the window size used for averaging has a substantial effect on the number of inferred relationships. We apply this procedure by analyzing a unique data set of Finnish shareholders during the period 2004-2009. We find that households in the capital have high centrality in investor networks, which, under the theory of information channels in investor networks suggests that they are well-informed investors.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Industrial and Information Management, Faculty of Biomedical Sciences and Engineering, Research group: Predictive Society and Data Analytics (PSDA), Predictive Medicine and Data Analytics Lab, Institute of Biosciences and Medical Technology

Contributors: Baltakys, K., Kanninen, J., Emmert-Streib, F.

Publication date: 1 Dec 2018

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 8

Issue number: 1

Article number: 8198

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2018): CiteScore 6.4 SJR 1.414 SNIP 1.274

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598_018_26575_2

DOIs:

10.1038/s41598-018-26575-2

URLs:

<http://urn.fi/URN:NBN:fi:tty-201806212011>

Source: Scopus

Source ID: 85047865397

Research output: Contribution to journal › Article › Scientific › peer-review

Aerosol gas exchange system (AGES) for nanoparticle sampling at elevated temperatures: Modeling and experimental characterization

An aerosol gas exchange system (AGES) for nanoparticle sampling at elevated temperatures was developed, modeled, and further characterized with laboratory tests with respect to gas exchange efficiency and particle losses. The model describing the gas exchange was first verified with oxygen and later studied with several inert gases having molecular masses between 18 and 135 u. The exchange rate of the lightest compounds exceeds 90% efficiency at the flow rates used. In order to reach similarly high removal efficiencies for larger molecules, the residence time in the AGES has to be increased. The removal of sticky gases was studied with gaseous sulfuric acid. Results agreed with the model where the boundary condition is zero concentration on the wall. The AGES exhibits very limited particle losses (<5%) for mono-disperse 6 nm particles. Furthermore, diffusional losses for particles down to 1.2 nm were measured utilizing polydisperse aerosol. The experimental findings are in good agreement with the model derived. As both, gas exchange rate and particle losses, rely on the physical effect of diffusion, an optimization for enhanced gas exchange efficiency will come at the cost of increased diffusional particle losses. The presented model can be used as a tool to redesign and optimize the AGES for a desired application. With an application targeted design, particle dilution can be avoided, which can lead to improved results in many fields of aerosol measurement.

General information

Publication status: Published

MoE publication type: A1 Journal article-refereed

Organisations: Physics, Research group: The Instrumentation, Emissions, and Atmospheric Aerosols Group, Research area: Aerosol Physics, Graz University of Technology

Contributors: Bainschab, M., Martikainen, S., Keskinen, J., Bergmann, A., Karjalainen, P.

Number of pages: 12

Publication date: 20 Nov 2019

Peer-reviewed: Yes

Publication information

Journal: Scientific Reports

Volume: 9

Issue number: 1

Article number: 17149

ISSN (Print): 2045-2322

Ratings:

Scopus rating (2019): CiteScore 7.2 SJR 1.341 SNIP 1.365

Original language: English

ASJC Scopus subject areas: General

Electronic versions:

s41598-019-53113-5

DOIs:

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URLs:

<http://urn.fi/URN:NBN:fi:tuni-201912136857>

Source: Scopus

Source ID: 85075415168

Research output: Contribution to journal › Article › Scientific › peer-review

On the linear programming bound for linear Lee codes

Based on an invariance-type property of the Lee-compositions of a linear Lee code, additional equality constraints can be introduced to the linear programming problem of linear Lee codes. In this paper, we formulate this property in terms of an action of the multiplicative group of the field (Formula presented.) on the set of Lee-compositions. We show some useful properties of certain sums of Lee-numbers, which are the eigenvalues of the Lee association scheme, appearing in the linear programming problem of linear Lee codes. Using the additional equality constraints, we formulate the linear programming problem of linear Lee codes in a very compact form, leading to a fast execution, which allows to efficiently compute the bounds for large parameter values of the linear codes.

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Department of Signal Processing, Research group: Signal Interpretation and Compression-SIC
Contributors: Astola, H., Tabus, I.
Number of pages: 13
Pages: 1-13
Publication date: 1 Mar 2016
Peer-reviewed: Yes

Publication information

Journal: SpringerPlus
Volume: 5
Issue number: 1
Article number: 246
ISSN (Print): 2193-1801
Ratings:
Scopus rating (2016): CiteScore 1.4 SJR 0.447 SNIP 0.812
Original language: English
ASJC Scopus subject areas: General
Keywords: Lee codes, Lee-compositions, Lee-numbers, Linear codes, Linear programming bound
Electronic versions:
On the linear programming bound for linear Lee codes
DOIs:
10.1186/s40064-016-1863-8
URLs:
<http://urn.fi/URN:NBN:fi:tty-201604123798>
Source: Scopus
Source ID: 84959296573
Research output: Contribution to journal › Article › Scientific › peer-review

DroneRF dataset: A dataset of drones for RF-based detection, classification and identification

Modern technology has pushed us into the information age, making it easier to generate and record vast quantities of new data. Datasets can help in analyzing the situation to give a better understanding, and more importantly, decision making. Consequently, datasets, and uses to which they can be put, have become increasingly valuable commodities. This article describes the DroneRF dataset: a radio frequency (RF) based dataset of drones functioning in different modes, including off, on and connected, hovering, flying, and video recording. The dataset contains recordings of RF activities, composed of 227 recorded segments collected from 3 different drones, as well as recordings of background RF activities with no drones. The data has been collected by RF receivers that intercepts the drone's communications with the flight control module. The receivers are connected to two laptops, via PCIe cables, that runs a program responsible for fetching, processing and storing the sensed RF data in a database. An example of how this dataset can be interpreted and used can be found in the related research article "RF-based drone detection and identification using deep learning approaches: an initiative towards a large open source drone database" (Al-Sa'd et al., 2019).

General information

Publication status: Published
MoE publication type: A1 Journal article-refereed
Organisations: Computing Sciences, Qatar University
Contributors: Allahham, M. S., Al-Sa'd, M. F., Al-Ali, A., Mohamed, A., Khattab, T., Erbad, A.
Publication date: 1 Oct 2019
Peer-reviewed: Yes

Publication information

Journal: Data in Brief
Volume: 26
Article number: 104313
ISSN (Print): 2352-3409
Ratings:
Scopus rating (2019): CiteScore 1.5 SJR 0.105
Original language: English
ASJC Scopus subject areas: General
Keywords: Anti-drone systems, Classification, Drone identification, UAV detection
DOIs:
10.1016/j.dib.2019.104313

Source: Scopus
Source ID: 85071552598
Research output: Contribution to journal › Article › Scientific › peer-review

Speeding up crystallization

General information

Publication status: Published
MoE publication type: A2 Review article in a scientific journal
Organisations: Physics, Norwegian University of Science and Technology, Forschungszentrum Jülich (FZJ)
Contributors: Akola, J., Jones, R. O.
Number of pages: 1
Pages: 1386
Publication date: 15 Dec 2017
Peer-reviewed: Yes

Publication information

Journal: Science
Volume: 358
Issue number: 6369
ISSN (Print): 0036-8075
Ratings:
Scopus rating (2017): CiteScore 49.4 SJR 14.142 SNIP 7.366
Original language: English
ASJC Scopus subject areas: General
DOIs:
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Source: Scopus
Source ID: 85038641346
Research output: Contribution to journal › Review Article › Scientific › peer-review

Facile strain analysis of largely bending films by a surface-labelled grating method

Mechanical properties of flexible films, for example surface strain of largely bending films, are key to design of stretchable electronic devices, wearable biointegrated devices, and soft microactuators/robots. However, existing methods are mainly based on strain-gauge measurements that require miniaturized array sensors, lead wires, and complicated calibrations. Here we introduce a facile method, based on surface-labelled gratings, for two-dimensional evaluation of surface strains in largely bending films. With this technique, we demonstrate that soft-matter mechanics can be distinct from the mechanics of hard materials. In particular, liquid-crystalline elastomers may undergo unconventional bending in three dimensions, in which both the inner and outer surfaces of the bending film are compressed. We also show that this method can be applied to amorphous elastomeric films, which highlights the general importance of this new mechanical evaluation tool in designing soft-matter-based electronic/photonic as well as biointegrated materials.

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Contributors: Akamatsu, N., Tashiro, W., Saito, K., Mamiya, J. I., Kinoshita, M., Ikeda, T., Takeya, J., Fujikawa, S., Priimagi, A., Shishido, A.
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Automatic Posture and Movement Tracking of Infants with Wearable Movement Sensors

Infants' spontaneous and voluntary movements mirror developmental integrity of brain networks since they require coordinated activation of multiple sites in the central nervous system. Accordingly, early detection of infants with atypical motor development holds promise for recognizing those infants who are at risk for a wide range of neurodevelopmental disorders (e.g., cerebral palsy, autism spectrum disorders). Previously, novel wearable technology has shown promise for offering efficient, scalable and automated methods for movement assessment in adults. Here, we describe the development of an infant wearable, a multi-sensor smart jumpsuit that allows mobile accelerometer and gyroscope data collection during movements. Using this suit, we first recorded play sessions of 22 typically developing infants of approximately 7 months of age. These data were manually annotated for infant posture and movement based on video recordings of the sessions, and using a novel annotation scheme specifically designed to assess the overall movement pattern of infants in the given age group. A machine learning algorithm, based on deep convolutional neural networks (CNNs) was then trained for automatic detection of posture and movement classes using the data and annotations. Our experiments show that the setup can be used for quantitative tracking of infant movement activities with a human equivalent accuracy, i.e., it meets the human inter-rater agreement levels in infant posture and movement classification. We also quantify the ambiguity of human observers in analyzing infant movements, and propose a method for utilizing this uncertainty for performance improvements in training of the automated classifier. Comparison of different sensor configurations also shows that four-limb recording leads to the best performance in posture and movement classification.

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Chromatin organization regulates viral egress dynamics

Various types of DNA viruses are known to elicit the formation of a large nuclear viral replication compartment and marginalization of the cell chromatin. We used three-dimensional soft x-ray tomography, confocal and electron microscopy, combined with numerical modelling of capsid diffusion to analyse the molecular organization of chromatin in herpes simplex virus 1 infection and its effect on the transport of progeny viral capsids to the nuclear envelope. Our data showed that the formation of the viral replication compartment at late infection resulted in the enrichment of heterochromatin in the nuclear periphery accompanied by the compaction of chromatin. Random walk modelling of herpes simplex virus 1-sized particles in a three-dimensional soft x-ray tomography reconstruction of an infected cell nucleus demonstrated that the peripheral, compacted chromatin restricts viral capsid diffusion, but due to interchromatin channels

capsids are able to reach the nuclear envelope, the site of their nuclear egress.

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Contributors: Aho, V., Myllys, M., Ruokolainen, V., Hakanen, S., Mäntylä, E., Virtanen, J., Hukkanen, V., Kühn, T., Timonen, J., Mattila, K., Larabell, C. A., Vihinen-Ranta, M.

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