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Unified and Standardized Mass Spectrometry Data Processing in Python Using spectrum_utils

2023 | Wissenschaftlicher Artikel
Journal of proteome research, 22, 2, S. 625-631
Bittremieux, Wout; Levitsky, Lev; Pilz, Matteo; Sachsenberg, Timo; Huber, Florian; Wang, Mingxun; Dorrestein, Pieter C.

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Towards automated video-based assessment of dystonia in dyskinetic cerebral palsy: A novel approach using markerless motion tracking and machine

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learning

2023 | Wissenschaftlicher Artikel
Frontiers in Robotics and AI, 10, Article-Nr. 1108114
Haberfehlner, Helga; van de Ven, Shankara S.; van der Burg, Sven A.; Huber, Florian; Georgievska, Sonja; Aleo, Ignazio; Harlaar, Jaap; Bonouvrié, Laura A.; van der Krogt, Marjolein M.; Buizer, Annemieke I.

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Comparison of Cosine, Modified Cosine, and Neutral Loss Based Spectrum Alignment For Discovery of Structurally Related Molecules

2022 | Wissenschaftlicher Artikel
Journal of the American Society for Mass Spectrometry, 33, 9, S. 1733-1744
Bittremieux, Wout; Schmid, Robin; Huber, Florian; van der Hooft, Justin J. J.; Wang, Mingxun; Dorrestein, Pieter C.

Published:	2022
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Digital Object Identifier:	10.1021/jasms.2c00153

A community resource for paired genomic and metabolomic data mining CC BY

2021 | Wissenschaftlicher Artikel
Nature Chemical Biology, 17, 4, S. 363-368
Schorn, Michelle A.; Verhoeven, Stefan; Ridder, Lars; Huber, Florian; Acharya, Deepa D.; Aksenov, Alexander A.; Aleti, Gajender; Moghaddam, Jamshid Amiri; Aron, Allegra T.; Aziz, Saefuddin; Bauermeister, Anelize; Bauman, Katherine D.; Baunach, Martin; Beemelmanns, Christine; Beman, J. Michael; Berlanga-Clavero, María Victoria; Blacutt, Alex A.; Bode, Helge B.; Boullie, Anne; Brejnrod, Asker; Bugni, Tim S.; Calteau, Alexandra; Cao, Liu; Carrión, Víctor J.; Castelo-Branco, Raquel; Chanana, Shaurya; Chase, Alexander B.; Chevrette, Marc G.; Costa-Lotufo, Leticia V.; Crawford, Jason M.; Currie, Cameron R.; Cuypers, Bart; Dang, Tam; de Rond, Tristan; Demko, Alyssa M.; Dittmann, Elke; Du, Chao; Drozd, Christopher; Dujardin, Jean-Claude; Dutton, Rachel J.; Edlund, Anna; Fewer, David P.; Garg, Neha; Gauglitz, Julia M.; Gentry, Emily C.; Gerwick, Lena; Glukhov, Evgenia; Gross, Harald; Gugger, Muriel; Guillén Matus, Dulce G.; Helfrich, Eric J. N.; Hempel, Benjamin-Florian; Hur, Jae-Seoun; Iorio, Marianna; Jensen, Paul R.; Kang, Kyo Bin; Kaysser, Leonard; Kelleher, Neil L.; Kim, Chung Sub; Kim, Ki Hyun; Koester, Irina; König, Gabriele M.; Leao, Tiago; Lee, Seoung Rak; Lee, Yi-Yuan; Li, Xuanji; Little, Jessica C.; Maloney, Katherine N.; Männle, Daniel; Martin H, Christian; McAvoy, Andrew C.; Metcalf, Willam W.; Mohimani, Hosein; Molina-Santiago, Carlos; Moore, Bradley S.; Mullowney, Michael W.; Muskat, Mitchell; Nothias, Louis-Félix; O'Neill, Ellis C.; Parkinson, Elizabeth I.; Petras, Daniel; Piel, Jörn; Pierce, Emily C.; Pires, Karine; Reher, Raphael; Romero,

Diego; Roper, M. Caroline; Rust, Michael; Saad, Hamada; Saenz, Carmen; Sanchez, Laura M.; Sørensen, Søren Johannes; Sosio, Margherita; Süssmuth, Roderich D.; Sweeney, Douglas; Tahlan, Kapil; Thomson, Regan J.; Tobias, Nicholas J.; Trindade-Silva, Amaro E.; van Wezel, Gilles P.; Wang, Mingxun; Weldon, Kelly C.; Zhang, Fan; Ziemert, Nadine; Duncan, Katherine R.; Crüsemann, Max; Rogers, Simon; Dorrestein, Pieter C.; Medema, Marnix H.; van der Hooft, Justin J. J.

Published: 2021-02-15

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3470

Digital Object Identifier: 10.1038/s41589-020-00724-z

Spec2Vec: Improved mass spectral similarity scoring through learning of structural relationships

2021 | Wissenschaftlicher Artikel

PLOS Computational Biology, 17, 2, Article-Nr. e1008724

Huber, Florian; Ridder, Lars; Verhoeven, Stefan; Spaaks, Jurriaan H.; Diblen, Faruk; Rogers, Simon; van der Hooft, Justin J. J.

Published: 2021

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3468

Digital Object Identifier: 10.1371/journal.pcbi.1008724

Abstract

Spectral similarity is used as a proxy for structural similarity in many tandem mass spectrometry (MS/MS) based metabolomics analyses such as library matching and molecular networking. Although weaknesses in the relationship between spectral similarity scores and the true structural similarities have been described, little development of alternative scores has been undertaken. Here, we introduce Spec2Vec, a novel spectral similarity score inspired by a natural language processing algorithm-Word2Vec. Spec2Vec learns fragmental relationships within a large set of spectral data to derive abstract spectral embeddings that can be used to assess spectral similarities. Using data derived from GNPS MS/MS libraries including spectra for nearly 13,000 unique molecules, we show how Spec2Vec scores correlate better with structural similarity than cosine-based scores. We demonstrate the advantages of Spec2Vec in library matching and molecular networking. Spec2Vec is computationally more scalable allowing structural analogue searches in large databases within seconds.

Advances in decomposing complex metabolite mixtures using substructure- and network-based computational metabolomics approaches

2021 | Wissenschaftlicher Artikel

Natural Product Reports, 38, 11, S. 1967-1993

Beniddir, Mehdi A.; Kang, Kyo Bin; Genta-Jouve, Grégory; Huber, Florian; Rogers, Simon; van der Hooft, Justin J. J.

Published: 2021

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3477

Digital Object Identifier: 10.1039/D1NP00023C

MS2DeepScore: a novel deep learning similarity measure to compare tandem mass spectra

2021 | Wissenschaftlicher Artikel

Journal of Cheminformatics, 13, 1, S. 84

Huber, Florian; van der Burg, Sven; van der Hooft, Justin J. J.; Ridder, Lars

Published: 2021

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3484

Digital Object Identifier: 10.1186/s13321-021-00558-4

Abstract

Mass spectrometry data is one of the key sources of information in many workflows in medicine and across the life sciences. Mass fragmentation spectra are generally considered to be characteristic signatures of the chemical compound they originate from, yet the chemical structure itself usually cannot be easily deduced from the spectrum. Often, spectral similarity measures are used as a proxy for structural similarity but this approach is strongly limited by a generally poor correlation between both metrics. Here, we propose MS2DeepScore: a novel Siamese neural network to predict the structural similarity between two chemical structures solely based on their MS/MS fragmentation spectra. Using a cleaned dataset of > 100,000 mass spectra of about 15,000 unique known compounds, we trained MS2DeepScore to predict structural similarity scores for spectrum pairs with high accuracy. In addition, sampling different model varieties through Monte-Carlo Dropout is used to further improve the predictions and assess the model's prediction uncertainty. On 3600 spectra of 500 unseen compounds, MS2DeepScore is able to identify highly-reliable structural matches and to predict Tanimoto scores for pairs of molecules based on their fragment spectra with a root mean squared error of about 0.15. Furthermore, the prediction uncertainty estimate can be used to select a subset of predictions with a root mean squared error of about 0.1. Furthermore, we demonstrate that MS2DeepScore outperforms classical spectral similarity measures in retrieving chemically related compound pairs from large mass spectral datasets, thereby illustrating its potential for spectral library matching. Finally, MS2DeepScore can also be used to create chemically meaningful mass spectral embeddings that could be used to cluster large numbers of spectra. Added to the recently introduced unsupervised Spec2Vec metric, we believe that machine learning-supported mass spectral similarity measures have great potential for a range of metabolomics data processing pipelines.

matchms - processing and similarity evaluation of mass spectrometry data

2020 | Wissenschaftlicher Artikel

Journal of Open Source Software, 5, 52, S. 2411

Huber, Florian; Verhoeven, Stefan; Meijer, Christiaan; Spreeuw, Hanno; Castilla, Efraín; Geng, Cunliang; van der Hooft, Justin J. J.; Rogers, Simon; Belloum, Adam; Diblen, Faruk; Spaaks, Jurriaan H.

Published: 2020

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3485

Digital Object Identifier: 10.21105/joss.02411

Actin networks voltage circuits

2020 | Wissenschaftlicher Artikel
Physical Review E, 101, 5-1, Article-Nr. 052314
Siccardi, Stefano; Adamatzky, Andrew; Tuszyński, Jack; Huber, Florian; Schnauß, Jörg

Published: 2020

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3488

Digital Object Identifier: 10.1103/PhysRevE.101.052314

Computing on actin bundles network

2019 | Wissenschaftlicher Artikel
Scientific Reports, 9, 1, Article-Nr. 15887
Adamatzky, Andrew; Huber, Florian; Schnauß, Jörg

Published: 2019

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3466

Digital Object Identifier: 10.1038/s41598-019-51354-y

Abstract

Actin filaments are conductive to ionic currents, mechanical and voltage solitons. These travelling localisations can be utilised to generate computing circuits from actin networks. The propagation of localisations on a single actin filament is experimentally unfeasible to control. Therefore, we consider excitation waves propagating on bundles of actin filaments. In computational experiments with a two-dimensional slice of an actin bundle network we show that by using an arbitrary arrangement of electrodes, it is possible to implement two-inputs-one-output circuits.

Actin droplet machine

2019 | Wissenschaftlicher Artikel
Royal Society Open Science, 6, 12, Article-Nr. 191135
Adamatzky, Andrew; Schnauß, Jörg; Huber, Florian

Published: 2019

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3467

Digital Object Identifier: 10.1098/rsos.191135

Abstract

The actin droplet machine is a computer model of a three-dimensional network of actin bundles developed in a droplet of a physiological solution, which implements mappings of sets of binary strings. The actin bundle network is conductive to travelling excitations, i.e. impulses. The machine is interfaced with an arbitrary selected set of k electrodes through which stimuli, binary strings of length k represented by impulses generated on the electrodes, are applied and responses are recorded. The responses are recorded in a form of impulses and then converted to binary strings. The machine's state is a binary string of length k: if there is an impulse recorded on the ith electrode, there is a '1' in the ith position of the string, and '0' otherwise. We present a design of the machine and analyse its state transition graphs. We envisage that actin droplet machines could form an elementary processor of future massive parallel computers made from biopolymers.

GGIR: A Research Community–Driven Open Source R Package for Generating Physical Activity and Sleep Outcomes From Multi-Day Raw Accelerometer Data

2019 | Wissenschaftlicher Artikel
Journal for the Measurement of Physical Behaviour, 2, 3, S. 188-196
Migueles, Jairo H.; Rowlands, Alex V.; Huber, Florian; Sabia, Séverine; van Hees, Vincent T.

Published:	2019
Weblink:	https://opus4.kobv.de/opus4-hs-duesseldorf/3469
Digital Object Identifier:	10.1123/jmpb.2018-0063

Cytoskeletal crosstalk: when three different personalities team up

2015 | Wissenschaftlicher Artikel
Current Opinion in Cell Biology, 32, S. 39-47
Huber, Florian; Boire, Adeline; López, Magdalena Preciado; Koenderink, Gijsje H.

Published:	2015
Weblink:	https://opus4.kobv.de/opus4-hs-duesseldorf/3478
Digital Object Identifier:	10.1016/j.ceb.2014.10.005

Formation of regularly spaced networks as a general feature of actin bundle condensation by entropic forces

2015 | Wissenschaftlicher Artikel
New Journal of Physics, 17, 4, Article-Nr. 043029
Huber, Florian; Strehle, Dan; Schnauß, Jörg; Käs, Josef

Published:	2015
Weblink:	https://opus4.kobv.de/opus4-hs-duesseldorf/3483
Digital Object Identifier:	10.1088/1367-2630/17/4/043029

In vitro reconstitution of dynamic microtubules interacting with actin filament networks

2014 | Wissenschaftlicher Artikel
Methods in Enzymology, 540, S. 301-320
Preciado López, Magdalena; Huber, Florian; Grigoriev, Ilya; Steinmetz, Michel O.; Akhmanova, Anna; Dogterom, Marileen; Koenderink, Gijsje H.

Published: 2014

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3486

Digital Object Identifier: 10.1016/B978-0-12-397924-7.00017-0

Actin-microtubule coordination at growing microtubule ends

2014 | Wissenschaftlicher Artikel
Nature Communications, 5, S. 4778
Preciado López, Magdalena; Huber, Florian; Grigoriev, Ilya; Steinmetz, Michel O.; Akhmanova, Anna; Koenderink, Gijsje H.; Dogterom, Marileen

Published: 2014

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3487

Digital Object Identifier: 10.1038/ncomms5778

Abstract

To power dynamic processes in cells, the actin and microtubule cytoskeletons organize into complex structures. Although it is known that cytoskeletal coordination is vital for cell function, the mechanisms by which cross-linking proteins coordinate actin and microtubule activities remain poorly understood. In particular, it is unknown how the distinct mechanical properties of different actin architectures modulate the outcome of actin-microtubule interactions. To address this question, we engineered the protein TipAct, which links growing microtubule ends via end-binding proteins to actin filaments. We show that growing microtubules can be captured and guided by stiff actin bundles, leading to global actin-microtubule alignment. Conversely, growing microtubule ends can transport, stretch and bundle individual actin filaments, thereby globally defining actin filament organization. Our results provide a physical basis to understand actin-microtubule cross-talk, and reveal that a simple cross-linker can enable a mechanical feedback between actin and microtubule organization that is relevant to diverse biological contexts.

Emergent complexity of the cytoskeleton: from single filaments to tissue

2013 | Wissenschaftlicher Artikel
Advances in Physics, 62, 1, S. 1-112
Huber, Florian; Schnauß, Jörg; Rönicke, S.; Rauch, P.; Müller, K.; Fütterer, C.; Käs, Josef

Published: 2013

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3481

Digital Object Identifier: 10.1080/00018732.2013.771509

Abstract

Despite their overwhelming complexity, living cells display a high degree of internal mechanical and functional organization which can largely be attributed to the intracellular biopolymer scaffold, the cytoskeleton. Being a very complex system far from thermodynamic equilibrium, the cytoskeleton's ability to organize is at the same time challenging and fascinating. The extensive amounts of frequently interacting cellular building blocks and their inherent multifunctionality permits highly adaptive behavior and obstructs a purely reductionist approach. Nevertheless (and despite the field's relative novelty), the physics approach has already proved to be extremely successful in revealing very fundamental concepts of cytoskeleton organization and behavior. This review aims at introducing the physics of the cytoskeleton ranging from single biopolymer filaments to multicellular organisms. Throughout this wide range of phenomena, the focus is set on the intertwined nature of the different physical scales (levels of complexity) that give rise to numerous emergent properties by means of self-organization or self-assembly.

Counterion-induced formation of regular actin bundle networks

2012 | Wissenschaftlicher Artikel

Soft Matter, 8, 4, S. 931-936

Huber, Florian; Strehle, Dan; Kaes, Josef

Published: 2012

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3482

Self-regulative organization of the cytoskeleton

2011 | Wissenschaftlicher Artikel

Cytoskeleton, 68, 5, S. 259-265

Huber, Florian; Käs, Josef

Published: 2011

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3479

Digital Object Identifier: 10.1002/cm.20509

Abstract

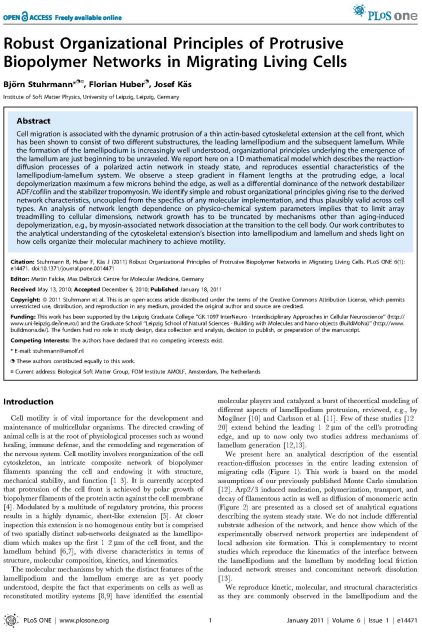
Despite its impressive complexity the cytoskeleton succeeds to persistently organize itself and thus the cells' interior. In contrast to classical man-made machines, much of the cellular organization originates from inherent self-assembly and self-organization allowing a high degree of autonomy for various functional units. Recent experimental and theoretical studies revealed numerous examples of cytoskeleton components that arrange and organize in a self-regulative way. In the present review we want to shortly summarize some of the principle mechanisms that are able to inherently trigger and regulate the cytoskeleton organization. Although taken individually most of these regulative principles are rather simple with intuitively predictable consequences, combinations of two or more of these mechanisms can quickly give rise to very complex, unexpected behavior and might even be able to explain the formation of different functional units out of a common pool of available building blocks.

Robust organizational principles of protrusive biopolymer networks in migrating living cells

2011 | Wissenschaftlicher Artikel

Plos One, 6, 1, Article-Nr. e14471

Stuhrmann, Björn; Huber, Florian; Käs, Josef



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Robust Organizational Principles of Protrusive Biopolymer Networks in Migrating Living Cells

Björn Stuhrmann*☯, Florian Huber☯, Josef Käs

Institute of Soft Matter Physics, University of Leipzig, Leipzig, Germany

Abstract

Cell migration is associated with the dynamic protrusion of a thin actin-based cytoskeletal extension at the cell front, which has been shown to consist of two different substructures, the leading lamellipodium and the subsequent lamellum. While the formation of the lamellipodium is increasingly well understood, organizational principles underlying the emergence of the lamellum are just beginning to be unraveled. We report here on a 1D mathematical model which describes the reaction-diffusion processes of a polarized actin network in steady state, and reproduces essential characteristics of the lamellipodium-lamellum system. We observe a steep gradient in filament lengths at the protruding edge, a local depolymerization maximum a few microns behind the edge, as well as a differential dominance of the network destabilizer ADF/cofilin and the stabilizer tropomyosin. We identify simple and robust organizational principles giving rise to the derived network characteristics, uncoupled from the specifics of any molecular implementation, and thus plausibly valid across cell types. An analysis of network length dependence on physico-chemical system parameters implies that to limit array treadmilling to cellular dimensions, network growth has to be truncated by mechanisms other than aging-induced depolymerization, e.g., by myosin-associated network dissociation at the transition to the cell body. Our work contributes to the analytical understanding of the cytoskeletal extension's bisection into lamellipodium and lamellum and sheds light on how cells organize their molecular machinery to achieve motility.

Citation: Stuhrmann B, Huber F, Käs J (2011) Robust Organizational Principles of Protrusive Biopolymer Networks in Migrating Living Cells. PLoS ONE 6(1): e14471. doi:10.1371/journal.pone.0014471

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Introduction

Cell motility is of vital importance for the development and maintenance of multicellular organisms. The directed crawling of animal cells is at the root of physiological processes such as wound healing, immune defense, and the remodeling and regeneration of the nervous system. Cell motility involves reorganization of the cell cytoskeleton, an intricate composite network of biopolymer filaments spanning the cell and endowing it with structure, mechanical stability, and function [1–3]. It is currently accepted that protrusion of the cell front is achieved by polar growth of biopolymer filaments of the protein actin against the cell membrane [4]. Modulated by a multitude of regulatory proteins, this process results in a highly dynamic, sheet-like extension [5]. At closer inspection this extension is no homogenous entity but is comprised of two spatially distinct subnetworks designated as the lamellipodium which makes up the first 1–2 μm of the cell front, and the lamellum behind [6,7], with diverse characteristics in terms of structure, molecular composition, kinetics, and kinematics.

The molecular mechanisms by which the distinct features of the lamellipodium and the lamellum emerge are as yet poorly understood, despite the fact that experiments on cells as well as reconstituted motility systems [8,9] have identified the essential molecular players and catalyzed a burst of theoretical modeling of different aspects of lamellipodium protrusion, reviewed, e.g., by Mogilner [10] and Carlsson et al. [11]. Few of these studies [12–20] extend behind the leading 1–2 μm of the cell's protruding edge, and up to now only two studies address mechanisms of lamellum generation [12,13].

We present here an analytical description of the essential reaction-diffusion processes in the entire leading extension of migrating cells (Figure 1). This work is based on the model assumptions of our previously published Monte Carlo simulation [12]. Arp2/3 induced nucleation, polymerization, transport, and decay of filamentous actin as well as diffusion of monomeric actin (Figure 2) are presented as a closed set of analytical equations describing the system steady state. We do not include differential substrate adhesion of the network, and hence show which of the experimentally observed network properties are independent of local adhesion site formation. This is complementary to recent studies which reproduce the kinematics of the interface between the lamellipodium and the lamellum by modeling local friction induced network stresses and concomitant network dissolution [13].

We reproduce kinetic, molecular, and structural characteristics as they are commonly observed in the lamellipodium and the

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Abstract

Cell migration is associated with the dynamic protrusion of a thin actin-based cytoskeletal extension at the cell front, which has been shown to consist of two different substructures, the leading lamellipodium and the subsequent lamellum. While the formation of the lamellipodium is increasingly well understood, organizational principles underlying the emergence of the lamellum are just beginning to be unraveled. We report here on a 1D mathematical model which describes the reaction-diffusion processes of a polarized actin network in steady state, and reproduces essential characteristics of the lamellipodium-lamellum system. We observe a steep gradient in filament lengths at the protruding edge, a local depolymerization maximum a few microns behind the edge, as well as a differential dominance of the network destabilizer ADF/cofilin and the stabilizer tropomyosin. We identify simple and robust organizational principles giving rise to the derived network characteristics, uncoupled from the specifics of any molecular implementation, and thus plausibly valid across cell types. An analysis of network length dependence on physico-chemical system parameters implies that to limit array treadmilling to cellular dimensions, network growth has to be truncated by mechanisms other than aging-induced depolymerization, e.g., by myosin-associated network dissociation at the transition to the cell body. Our work contributes to the analytical understanding of the cytoskeletal extension's bisection into lamellipodium and lamellum and sheds light on how cells organize their molecular machinery to achieve motility.

The cytoskeleton: An active polymer-based scaffold

2009 | Wissenschaftlicher Artikel

Biophysical Reviews and Letters, 04, S. 179-208

Smith, David; Gentry, Brian; Stuhrmann, Björn; Huber, Florian; Strehle, D. A.N.; Brunner, Claudia; Koch, Daniel; Steinbeck, Matthias; Betz, Timo; Käs, Josef A.

Published: 2009

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3489

Digital Object Identifier: 10.1142/S1793048009000983

Growing actin networks form lamellipodium and lamellum by self-assembly

2008 | Wissenschaftlicher Artikel

Biophysical Journal, 95, 12, S. 5508-5523

Huber, Florian; Käs, Josef; Stuhrmann, Björn

Published: 2008

Weblink: https://opus4.kobv.de/opus4-hs-duesseldorf/3480

Digital Object Identifier: 10.1529/biophysj.108.134817

Abstract

Many different cell types are able to migrate by formation of a thin actin-based cytoskeletal extension. Recently, it became evident that this extension consists of two distinct substructures, designated lamellipodium and lamellum, which differ significantly in their kinetic and kinematic properties as well as their biochemical composition. We developed a stochastic two-dimensional computer simulation that includes chemical reaction kinetics, G-actin diffusion, and filament transport to investigate the formation of growing actin networks in migrating cells. Model parameters were chosen based on experimental data or theoretical considerations. In this work, we demonstrate the system's ability to form two distinct networks by self-organization. We found a characteristic transition in mean filament length as well as a distinct maximum in depolymerization flux, both within the first 1-2 microm. The separation into two distinct substructures was found to be extremely robust with respect to initial conditions and variation of model parameters. We quantitatively investigated the complex interplay between ADF/cofilin and tropomyosin and propose a plausible mechanism that leads to spatial separation of, respectively, ADF/cofilin- or tropomyosin-dominated compartments. Tropomyosin was found to play an important role in stabilizing the lamellar actin network. Furthermore, the influence of filament severing and annealing on the network properties is explored, and simulation data are compared to existing experimental data.

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