Single Particle Tracking Based Reaction Progress Kinetic

Single molecule tools have begun to revolutionize the molecular sciences, from biophysics to chemistry to cell biology. They hold the promise to be able to directly observe previously unseen molecular heterogeneities, quantitatively dissect complex reaction kinetics, ultimately miniaturize enzyme assays, image components of spatially distributed samples, probe the mechanical properties of single molecules in their native environment, and "just look at the thing" as anticipated by the visionary Richard Feynman already half a century ago. Single Molecule Tools, Part B: Super-Resolution, Particle Tracking, Multiparameter, and Force Based Methods captures a snapshot of this vibrant, rapidly expanding field, presenting articles from pioneers in the field intended to guide both the newcomer and the expert through the intricacies of getting single molecule tools. Includes time-tested core methods and new innovations applicable to any researcher employing single molecule tools Methods included are useful to both established researchers and newcomers to the field Relevant background and reference information given for procedures can be used as a guide to developing protocols in a number of disciplines

This keenly awaited first overview of the field represents a complete guide to the structure and function of the most important mammalian cell membrane organelles. Filling a huge gap in the primary literature, this book is the first to cover the subject in detail. Following an introduction by Kai Simons, the discoverer of lipid rafts and the most prominent scientist in the field, chapters include: Historical background Distinct structures and functions Structural basis Signaling Viral entry and virion budding Cholesterol transport Caveolins Lipid shells Cell polarity and intracellular trafficking Cancer cells Of prime importance to molecular and cell biologists, biochemists, membrane scientists, cancer researchers, and virologists.

This new Springer volume, which comes complete with a free DVD, is a comprehensive and detailed overview of the synapse with emphasis on the glutamatergic synapse. Most chapters relate the synapse’s functional aspects to its molecular mechanisms. This approach shows which mechanisms are characterized on both the functional and structural level and can thus be considered firmly established. It’s an important text for neuroscientists and disease-oriented clinicians in neurology.

This book deals with randomly moving objects and their spreading. The objects considered are particles like atoms and molecules, but also living beings such as humans, animals, plants, bacteria and even abstract entities like ideas, rumors, information, innovations and linguistic features. The book explores and communicates the laws behind these movements and reports about astonishing similarities and very specific features typical of the given object under considerations. Leading scientists in disciplines as diverse as archeology, epidemics, linguistics and sociology, in collaboration with their colleagues from engineering, natural sciences and mathematics, introduce the phenomena of spreading as relevant for their fields. An introductory chapter on “Spreading Fundamentals” provides a common basis for all these considerations, with a minimum of mathematics, selected and presented for enjoying rather than frustrating the reader.

This book addresses nearly all aspects of the state of the art in LES & DNS of turbulent flows, ranging from flows in biological systems and the environment to external aerodynamics, domestic and centralized energy production, combustion, propulsion as well as applications of industrial interest. Following the advances in increased computational power and efficiency, several contributions are devoted to LES & DNS of challenging applications, mainly in the area of turbomachinery, including flame modeling, combustion processes and aeroacoustics. The book includes work presented at the tenth Workshop on 'Direct and Large-Eddy Simulation' (DLES-10), which was hosted in Cyprus by the University of Cyprus, from May 27 to 29, 2015. The goal of the workshop was to establish a state of the art in DNS, LES and related techniques for the computation and modeling of turbulent and transitional flows. The book is of interest to scientists and engineers, both in the early stages of their career and at a more senior level.

This book constitutes the thoroughly refereed proceedings of the 6th International Workshop on Hybrid Systems Biology, HSB 2019, held in Prague, Czech Republic, in April 2019. The 8 full papers presented in this book together with 1 short paper and 3 invited papers were carefully reviewed and selected from 13 submissions. They cover topics such as: modeling and analysis of metabolic, signaling, and genetic regulatory networks in living cells; models of tissues, organs, physiological models; models and methods coping with incomplete, uncertain and heterogeneous information including learning for biological systems, parametric synthesis and inference; stochastic and hybrid models in biology; hierarchical systems for multi-scale, multi-domain analysis; abstraction, approximation, discretization, and model reduction techniques; modeling, analysis and design for synthetic biology, cyber-biological systems and biomedical studies (e.g. therapies, teleoperation); game-theoretical frameworks and population models in biology (e.g. mixed-effects and Bayesian modeling); biological applications of quantitative and formal analysis techniques (e.g. reachability computation, model checking, abstract interpretation, bifurcation theory, stability and sensitivity analysis); efficient techniques for combined and heterogeneous (stochastic/deterministic, spatial/non-spatial) simulations for biological models; modeling languages and logics for biological systems with related analysis and simulation tools; and control architectures of biological systems including biology-in-the-loop systems and bio-robotics.

Genomics has gathered broad public attention since Lamarck put forward his top-down hypothesis of 'motivated change' in 1809 in his famous book "Philosophie Zoologique" and even more so since Darwin published his famous bottom-up theory of natural selection in "The Origin of Species" in 1859. The public awareness culminated in the much anticipated race to decipher the sequence of the human genome in 2002. Over all those years, it has become apparent that genomic DNA is compacted into chromatin with a dedicated 3D higher-order organization and dynamics, and that on each structural level epigenetic modifications exist. The book "Chromatin and Epigenetics" addresses current issues in the fields of epigenetics and chromatin ranging from more theoretical overviews in the first four chapters to much more detailed methodologies and insights into diagnostics and treatments in the following chapters. The chapters illustrate in their depth and breadth that genetic information is stored on all structural and dynamical levels within the nucleus with corresponding modifications of functional relevance. Thus, only an integrative systems approach allows to understand, treat, and manipulate the holistic interplay of genotype and phenotype creating functional genomes. The book chapters therefore contribute to this general perspective, not only opening opportunities for a true universal view on genetic information but also being key for a general understanding of genomes, their function, as well as life and evolution in general.

This handbook describes experimental techniques to monitor and manipulate individual biomolecules, including fluorescence detection, atomic force microscopy, and optical and magnetic trapping. It includes single-molecule studies of physical properties of biomolecules such as folding, polymer physics of protein and DNA, enzymology and biochemistry, single molecules in the

membrane, and single-molecule techniques in living cells.

This book compiles the accomplishments of the recent research project on photochemistry “Photosynergetics”, supported by the Ministry of Education, Culture, Sports, Science and Technology of Japan, aiming to develop and elucidate new methods and molecules leading to advanced utilization of photo-energies. Topics include photochemical responses induced by multiple excitation, multiphoton absorption, strong modulation of electronic states, developments of new photofunctional molecules, mesoscopic actuations induced by photoexcitation, and novel photoresponses in molecules and molecular assemblies. The authors stress that these approaches based on the synergetic interaction among many photons and many molecules enable the expansion of the accessibility to specific electronic states. As well, they explain how the development of reaction sequences and molecules/molecular assemblies ensure “additivity” and “integration” without loss of the photon energy, leading to new photoresponsive assemblies in meso- and macroscopic scales.

Introduces the detailed basis and recent development of single molecule/particle nanocatalysis based on single molecule techniques This unique book introduces and summarizes the recent development of single molecule/particle nanocatalysis to provide both comprehensive coverage of fundamentals for different methods now in widespread use and the extensive applications in different catalytic systems. Chapters are mainly based on different detection methods, including single molecule fluorescence microscopy, surface plasmon resonance spectroscopy, X-ray microscopy, and surface enhanced Raman spectroscopy. The book also includes numerous basic principles of different methods and application examples and features illustrations that help clarify presentations. Single Particle Nanocatalysis: Fundamentals and Applications starts with the history and development of single molecule techniques for nanocatalysis. It then shows readers how single molecule fluorescence microscopy (SMFM) reveals catalytic kinetics and dynamics of individual nanocatalysts. Next, it examines traditional SMFM-based single molecule nanocatalysis without super-resolution (SR) imaging, before moving on to the topic of SMFM-based SR imaging in single molecule nanocatalysis. Following chapters cover scanning electrochemical microscopy for single particle nanocatalysis; surface plasmon resonance spectroscopy for single particle nanocatalysis/reactions; X-ray-based microscopy of single-particle nanocatalysis; and surface-enhanced Raman spectroscopy for single particle nanocatalysis. The book finishes by introducing some less-practiced techniques for single particle nanocatalysis/electrochemistry. -Presents a systematical and complete introduction to the subject of single particle nanocatalysis?covering all of its fundamentals and applications -Helps readers fully understand the basis, role, and recent development of single molecule nanocatalysis -Teaches researchers how to gain new knowledge to successfully conduct their own studies within this rapidly increasing new area of research Single Particle Nanocatalysis: Fundamentals and Applications is an excellent reference book for experts in this area as well as for general researchers who want to learn how to study nanocatalysis at single molecule/particle level.

This book encompasses the exciting developments and challenges in the fast-moving and rapidly expanding research field of single-molecule kinetic analysis of cell signaling that promises to be one of the most significant and exciting areas of biological research for the foreseeable future. Cell signaling is carried out by complicated reaction networks of macromolecules, and single-molecule analyses has already demonstrated its power to unravel complex reaction dynamics in purified systems. To date, most of the published research in the field of single-molecule processes in cells, focus on the dynamic properties (translational movements of the centre of mass) of biological molecules. However, we hope that this book presents as many kinetic analyses of cell signaling as possible. Although single-molecule kinetic analysis of cellular systems is a relatively young field when compared with the analysis of single-molecule movements in cells, this type of analysis is highly important because it directly relates to the molecular functions that control cellular behavior and in the future, single-molecule kinetic analysis will be largely directed towards cellular systems. Thus, we hope that this book will be of interest to all those working in the fields of molecular and cell biology, as well as biophysics and biochemistry.

This thesis offers a unique guide to the development and application of ultrasensitive optical microscopy based on light scattering. Divided into eight chapters, it covers an impressive range of scientific fields, from basic optical physics to molecular biology and synthetic organic chemistry. Especially the detailed information provided on how to design, build and implement an interferometric scattering microscope, as well as the descriptions of all instrumentation, hardware interfacing and image processing necessary to achieve the highest levels of performance, will be of interest to researchers now entering the field.

A particulate two-phase flow CFD model was developed based on the FDNS code which is a pressure based predictor plus multi-corrector Navier-Stokes flow solver. Turbulence models with compressibility correction and the wall function models were employed as submodels. A finite-rate chemistry model was used for reacting flow simulation. For particulate two-phase flow simulations, a Eulerian-Lagrangian solution method using an efficient implicit particle trajectory integration scheme was developed in this study. Effects of particle-gas reaction and particle size change to agglomeration or fragmentation were not considered in this investigation. At the onset of the present study, a two-dimensional version of FDNS which had been modified to treat Lagrangian tracking of particles (FDNS-2DEL) had already been written and was operational. The FDNS-2DEL code was too slow for practical use, mainly because it had not been written in a form amenable to vectorization on the Cray, nor was the full three-dimensional form of FDNS utilized. The specific objective of this study was to reorder to calculations into long single arrays for automatic vectorization on the Cray and to implement the full three-dimensional version of FDNS to produce the FDNS-3DEL code. Since the FDNS-2DEL code was slow, a very limited number of test cases had been run with it. This study was also intended to increase the number of cases simulated to verify and improve, as necessary, the particle tracking methodology coded in FDNS. Chen, Y. S. and Farmer, R. C. Unspecified Center SECA-TR-92-06 ...

Lipids are a broad group of naturally occurring molecules which includes fats, waxes, sterols, fat-soluble vitamins (such as vitamins A, D, E and K), monoglycerides, diglycerides, phospholipids, and others. The main biological functions of lipids include energy storage, as structural components of cell membranes, and as important signaling molecules. This volume of Methods in Cell Biology covers such areas as Membrane structure and dynamics, Imaging, and Lipid Protein Interactions. It will be an essential tool for researchers and students alike. Covers such areas as membrane structure and dynamics, imaging, and lipid protein interactions An essential tool for researchers and students alike International authors Renowned editors

This volume provides descriptions of the occurrence of the UPR, methods used to assess it, pharmacological tools and other methodological approaches to analyze its impact on cellular regulation. The authors explain how these methods are able to provide important biological insights. This volume provides descriptions of the occurrence of the UPR, methods used to assess it, pharmacological tools and other methodological approaches to analyze its impact on cellular regulation. The authors explain how these methods are able to provide important biological insights.

Authored by a top-level team of both academic and industrial researchers in the field, this is an up-to-date review of mesoporous zeolites. The leading experts cover novel preparation methods that allow for a purpose-oriented fine-tuning of zeolite properties, as well as the related materials, discussing the specific characterization methods and the applications in close relation to each individual preparation approach. The result is a self-contained treatment of the different classes of mesoporous zeolites. With its academic insights and practical relevance this is a comprehensive handbook for researchers in the field and related areas, as well as for developers from the chemical industry.

This Open Access textbook provides students and researchers in the life sciences with essential practical information on how to quantitatively analyze data images. It refrains from focusing on theory, and instead uses practical examples and step-by step protocols to familiarize readers with the most commonly used image processing and analysis platforms such as ImageJ, MatLab and Python. Besides gaining knowhow on algorithm usage, readers will learn how to create an analysis pipeline by scripting

language; these skills are important in order to document reproducible image analysis workflows. The textbook is chiefly intended for advanced undergraduates in the life sciences and biomedicine without a theoretical background in data analysis, as well as for postdocs, staff scientists and faculty members who need to perform regular quantitative analyses of microscopy images.

In this first comprehensive resource to cover the application of single molecule techniques to biological measurements, the pioneers in the field show how to both set up and interpret a single molecule experiment. Following an introduction to single molecule measurements and enzymology, the expert authors consider molecular motors and mechanical properties before moving on to the applications themselves. Detailed discussions of studies on protein enzymes, ribozymes and nucleic acids are also included.

Continuing Garrett and Grisham's innovative conceptual and organizing Essential Questions framework, BIOCHEMISTRY guides students through course concepts in a way that reveals the beauty and usefulness of biochemistry in the everyday world. Offering a balanced and streamlined presentation, this edition has been updated throughout with new material and revised presentations. For the first time, this book is integrated with OWL, a powerful online learning system for chemistry with book-specific end-of-chapter material that engages students and improves learning outcomes. Important Notice: Media content referenced within the product description or the product text may not be available in the ebook version.

Analytical methods are the essential enabling tools of the modern biosciences. This book presents a comprehensive introduction into these analytical methods, including their physical and chemical backgrounds, as well as a discussion of the strengths and weakness of each method. It covers all major techniques for the determination and experimental analysis of biological macromolecules, including proteins, carbohydrates, lipids and nucleic acids. The presentation includes frequent cross-references in order to highlight the many connections between different techniques. The book provides a birdï¿1?2s eye view of the entire subject and enables the reader to select the most appropriate method for any given bioanalytical challenge. This makes the book a handy resource for students and researchers in setting up and evaluating experimental research. The depth of the analysis and the comprehensive nature of the coverage mean that there is also a great deal of new material, even for experienced experimentalists. The following techniques are covered in detail: - Purification and determination of proteins - Measuring enzymatic activity - Microcalorimetry - Immunoassays, affinity chromatography and other immunological methods - Cross-linking, cleavage, and chemical modification of proteins - Light microscopy, electron microscopy and atomic force microscopy - Chromatographic and electrophoretic techniques - Protein sequence and composition analysis - Mass spectrometry methods - Measuring protein-protein interactions - Biosensors - NMR and EPR of biomolecules - Electron microscopy and X-ray structure analysis - Carbohydrate and lipid analysis - Analysis of posttranslational modifications - Isolation and determination of nucleic acids - DNA hybridization techniques - Polymerase chain reaction techniques - DNA sequence and epigenetic modification analysis - Analysis of protein-nucleic acid interactions - Analysis of sequence data - Proteomics, metabolomics, peptidomics and toponomics - Chemical biology

Written by the leading experts in the field, this book describes the development and current state of the art in single molecule spectroscopy. The application of this technique, which started 1989, in physics, chemistry and biosciences is displayed.

"Single-molecule fluorescence microscopy is crucial for molecular biology studies, and traditional single-molecule microscopy techniques such as total internal reflection fluorescence microscopy (TIRFM) and confocal microscopy have greatly advanced our knowledge of biomolecular interactions. However, these traditional techniques suffer from limitations in field of view, insufficient per-molecule observation times, the requirement for dilute solutions, or the need for molecule tethering. All these problems can be solved with Convex Lens-induced Confinement (CLiC) microscopy. CLiC microscopy is able to isolate and trap single molecules in fabricated nanotopographies such as nanogrooves and nanowells. This provides a useful platform for visualizing biomolecular reactions: the biomolecules can be confined within the features, allowing for a much longer observation time without particles escaping from the field of view. It is important to develop analysis tools for dynamics and reactions under nanoconfinement to extract kinetic binding rates and diffusion coefficients.Here, we develop a single-particle tracking (SPT) and correlation analysis toolkit for probing the lateral dynamics of single molecules confined in nanowells. Specifically, we establish the localization error of SPT and the statistical accuracy of SPT under confinement. We derive the correlation analysis toolkit suitable for the geometry induced by CLiC and a nanowell array, and calculate the bias in the correlation results. We characterize and compare the two analysis approaches with simulations as well as CLiC microscopy data of nanoparticles and small DNA oligonucleotides." --

Recent advances in single molecule science have presented a new branch of science: single molecule cellular biophysics, combining classical cell biology with cutting-edge single molecule biophysics. This textbook explains the essential elements of this new discipline, from the state-of-the-art single molecule techniques to real-world applications in unravelling the inner workings of the cell. Every effort has been made to ensure the text can be easily understood by students from both the physical and life sciences. Mathematical derivations are kept to a minimum whilst unnecessary biological terminology is avoided and text boxes provide readers from either background with additional information. 100 end-of-chapter exercises are divided into those aimed at physical sciences students, those aimed at life science students and those that can be tackled by students from both disciplines. The use of case studies and real research examples make this textbook indispensable for undergraduate students entering this exciting field.

Closing a gap in the literature, this handbook gathers all the information on single particle tracking and single molecule energy transfer. It covers all aspects of this hot and modern topic, from detecting virus entry to membrane diffusion, and from protein folding using spFRET to coupled dye systems, as well recent achievements in the field. Throughout, the first-class editors and top international authors present content of the highest quality, making this a must-have for physical chemists, spectroscopists, molecular physicists and biochemists.

Microscale Diagnostic Techniques highlights the most innovative and powerful developments in microscale diagnostics. It provides a resource for scientists and researchers interested in learning about the techniques themselves, including their capabilities and limitations. The fields of Micro- and Nanotechnology have emerged over the past decade as a major focus of modern scientific and engineering research and technology. Driven by advances in microfabrication, the investigation, manipulation and engineering of systems characterized by micrometer and, more recently, nanometer scales have become commonplace throughout all technical disciplines. With these developments, an entirely new collection of experimental techniques has been developed to explore and characterize such systems.

Fluorescent proteins are intimately connected to research in the life sciences. Tagging of gene products with fluorescent proteins

has revolutionized all areas of biosciences, ranging from fundamental biochemistry to clinical oncology, to environmental research. The discovery of the Green Fluorescent Protein, its first, seminal application and the ingenious development of a broad palette of fluorescence proteins of other colours, was consequently recognised with the Nobel Prize for Chemistry in 2008. Fluorescent Proteins II highlights the physicochemical and biophysical aspects of fluorescent protein technology beyond imaging. It is tailored to meet the needs of physicists, chemists and biologists who are interested in the fundamental properties of fluorescent proteins, while also focussing on specific applications. The implementations described are cutting-edge studies and exemplify how the physical and chemical properties of fluorescent proteins can stimulate novel findings in life sciences.

Single molecule tools have begun to revolutionize the molecular sciences, from biophysics to chemistry to cell biology. They hold the promise to be able to directly observe previously unseen molecular heterogeneities, quantitatively dissect complex reaction kinetics, ultimately miniaturize enzyme assays, image components of spatially distributed samples, probe the mechanical properties of single molecules in their native environment, and "just look at the thing" as anticipated by the visionary Richard Feynman already half a century ago. Single Molecule Tools, Part A: Fluorescence Based Approaches captures a snapshot of this vibrant, rapidly expanding field, presenting articles from pioneers in the field intended to guide both the newcomer and the expert through the intricacies of getting single molecule tools. Includes time-tested core methods and new innovations applicable to any researcher employing single molecule tools Methods included are useful to both established researchers and newcomers to the field Relevant background and reference information given for procedures can be used as a guide to developing protocols in a number of disciplines

This book covers multi-scale biomechanics for oncology, ranging from cells and tissues to whole organ. Topics covered include, but not limited to, biomaterials in mechano-oncology, non-invasive imaging techniques, mechanical models of cell migration, cancer cell mechanics, and platelet-based drug delivery for cancer applications. This is an ideal book for graduate students, biomedical engineers, and researchers in the field of mechanobiology and oncology. This book also: Describes how mechanical properties of cancer cells, the extracellular matrix, tumor microenvironment and immuno-editing, and fluid flow dynamics contribute to tumor progression and the metastatic process Provides the latest research on non-invasive imaging, including traction force microscopy and brillouin confocal microscopy Includes insight into NCIs' role in supporting biomechanics in oncology research Details how biomaterials in mechano-oncology can be used as a means to tune materials to study cancer

The critically acclaimed laboratory standard for more than forty years, Methods in Enzymology is one of the most highly respected publications in the field of biochemistry. Since 1955, each volume has been eagerly awaited, frequently consulted, and praised by researchers and reviewers alike. Now with more than 300 volumes (all of them still in print), the series contains much material still relevant today-truly an essential publication for researchers in all fields of life sciences.

One of the unusual phenomena observed of suspensions involving viscoelastic liquids, like polymer solutions and melts, is the tendency of solid particles to form chains and microstructures. Till now, there is very little physical understanding of chaining dynamics. Limited experimental results arise from the absence of appropriate quantification methods in chain dynamics. The first part of this dissertation introduces a new approach for quantifying the chain dynamics based on the evolution of singlets, doublets, triplets, and multiplets as an explicit way of defining chain formation. Capturing the microstructural formation in this way, reveals the average chaining length, and the distribution of structural length scales in the medium, and the time scales associated with their formation. Then a global String Factor (SF) is suggested based on considering the long range orientational correlations within the cluster to help better understanding the effect of different parameters on chaining. By using a highly shear thinning polymer solution the effect of particle size, shear rate, viscoelasticity of the fluid, and shear thinning properties of the liquid phase on microstructure formations are studied. Based on these calculation chaining time scales are estimated and chaining velocities were on the order of 0.1-10 & mu;m/s. Singlet depletion is modeled with a first order reaction mechanism, and reaction rate constants are derived. By using single-mode Giesekus model to fit the viscosity data, extensional properties of the fluid is predicted. Using the extensional properties and tying that to the negative wake as a possible mechanism for chain formation, a new criteria for chain formation is proposed and verified. The second part descrides an investigation into the effect of particle interaction in viscoelastic fluids on different non-intrusive velocity measurement techniques like Particle Image Velocimetry (PIV) and Micro-Particle Image Velocimetry (& mu;PIV), which are both based on cross-correlation. Similar effects are examined for Particle Tracking Velocimetry (PTV) in these fluids, which is based on tracking individual particles. The main assumption of all these velocity measurement techniques is that the tracer particles follow the flow faithfully and not interact with each other. Then the fluid velocity field can be extracted directly from the tracer particle velocity. PIV measurements over a wide range of particle volumetric concentrations (0.005- 0.2% v/v) did not expose any particle interaction effects in a square cross-section channel flow. Measurement errors are quantified in detail by finding the RMS fluctuations in velocity measurements. Micro-PIV measurements were performed in a rectangular micro-channel, for a wide range of flow rates, with a fixed tracer concentration (0.2%). Velocity fluctuations did not show any dependence on the flow rate and average shear rate. Also we showed that the uncertainty in velocity measurement is one order of magnitude larger than chaining velocity. PTV is also used for comparing the velocity of singlets versus clusters over time in a cone and plate geometry. Over the limited time in which a particle is traveling through the field of view, no meaningful differences between the velocities could be observed. A theoretical approach for finding the limits of cross-correlation techniques (PIV, & mu;PIV) is introduced and the minimum detectible velocity is estimated to be on the order of 1-10 & mu;m/s. Chaining velocity is shown to be less than the minimum detectable velocity. In the last chapter, by using viscoelastic properties of polymer solutions, a novel technique (Low-Voltage Near-Field Electrospinning) for depositing and writing nano-fibers on a 3D substrate has been introduced and demonstrated.

This book features reviews by leading experts on the methods and applications of modern forms of microscopy. The recent awards of Nobel Prizes awarded for super-resolution optical microscopy and cryo-electron microscopy have demonstrated the rich scientific opportunities for research in novel microscopies. Earlier Nobel Prizes for electron microscopy (the instrument itself and applications to biology), scanning probe microscopy and holography are a reminder of the central role of microscopy in modern science, from the study of nanostructures in materials science, physics and chemistry to structural biology. Separate chapters are devoted to confocal, fluorescent and related novel optical microscopies, coherent diffractive imaging, scanning probe microscopy, transmission electron microscopy in all its modes from aberration corrected and analytical to in-situ and time-resolved, low energy electron microscopy, photoelectron microscopy, cryo-electron microscopy in biology, and also ion microscopy. In addition to serving as an essential reference for researchers and teachers in the fields such as materials science, condensed matter physics,

solid-state chemistry, structural biology and the molecular sciences generally, the Springer Handbook of Microscopy is a unified, coherent and pedagogically attractive text for advanced students who need an authoritative yet accessible guide to the science and practice of microscopy.

Traditionally, fluid mixing and the related multiphase contacting processes have always been regarded as an empirical technology. Many aspects of mixing, dispersing and contacting were related to power draw, but understanding of the phenomena was limited or qualitative at the most. In particular during the last decade, however, plant operation targets have tightened and product specifications have become stricter. The public awareness as to safety and environmental hygiene has increased. The drive towards larger degrees of sustainability in the process industries has urged for lower amounts of solvents and for higher yields and higher selectivities in chemical reactors. All this has resulted in a market pull: the need for more detailed insights in flow phenomena and processes and for better verifiable design and operation methods. Developments in miniaturisation of sensors and circuits as well as in computer technology have rendered leaps possible in computer simulation and animation and in measuring and monitoring techniques. This volume encourages a leap forward in the field of mixing by the current, overwhelming wealth of sophisticated measuring and computational techniques. This leap may be made possible by modern instrumentation, signal and data analysis, field reconstruction algorithms, computational modelling techniques and numerical recipes.

Single Molecule Tools, Part B: Super-Resolution, Particle Tracking, Multiparameter, and Force Based MethodsAcademic Press

Flooding is a global phenomenon that claims numerous lives worldwide each year. Set up to promote research into this area of study, this book contains the proceedings of the 4th International Conference on Flood Recovery, Innovation and Response. When flooding occurs in populated areas, it can cause substantial damage to property as well as threatening human life. In addition, many more people must endure the homelessness, upset and disruption that are left in the wake of floods. The increased frequency of flooding in the last few years, coupled with climate change predictions and urban development, suggest that these statistics are set to worsen in the future. Apart from the physical damage to buildings, contents and loss of life, which are the most obvious impacts of floods upon households, other more indirect losses are often overlooked. These indirect and intangible impacts are generally associated with disruption to normal life as well as longer term health issues including stress related illness. Flooding represents a major barrier to the alleviation of poverty in many parts of the developing world, where vulnerable communities are often exposed to sudden and life threatening events. This book covers a wide range of technical and management topics related to flooding and its impacts on communities, property and people. These include: Flood Modelling; Risk Assessment; Flood Management; Considering ‘Blue-Green’ Approaches to Flood Risk Management; Property-level Flooding and Health Consequences; State-of-the-art Flooding-damage Survey and Assessment; Emergency Preparedness and Response; Adaptation to Flood Risk.

BetaSys uses the example of regulated exocytosis in pancreatic ?-cells, and its relevance to diabetes, to illustrate the major concepts of systems biology, its methods and applications.

Random walk particle tracking methods are a computationally efficient family of methods to solve reactive transport problems. While the number of particles in most realistic applications is in the order of 10?6 - 10?9, the number of reactive molecules even in diluted systems might be in the order of fractions of the Avogadro number. Thus, each particle actually represents a group of potentially reactive molecules. The use of a low number of particles may result not only in loss of accuracy, but also may lead to an improper reproduction of the mixing process, limited by diffusion. Recent works have used this effect as a proxy to model incomplete mixing in porous media. The main contribution of this thesis is to propose a reactive transport model using a Kernel Density Estimation (KDE) of the concentrations that allows getting the expected results for a well-mixed solution with a limited number of particles. The idea consists of treating each particle as a sample drawn from the pool of molecules that it represents; this way, the actual location of a tracked particle is seen as a sample drawn from the density function of the location of molecules represented by that given particle, rigorously represented by a kernel density function. The probability of reaction can be obtained by combining the kernels associated with two potentially reactive particles. We demonstrate that the observed deviation in the reaction vs time curves in numerical experiments reported in the literature could be attributed to the statistical method used to reconstruct concentrations (fixed particle support) from discrete particle distributions, and not to the occurrence of true incomplete mixing. We further explore the evolution of the kernel size with time, linking it to the diffusion process. Our results show that KDEs are powerful tools to improve computational efficiency and robustness in reactive transport simulations, and indicates that incomplete mixing in diluted systems should be modeled based on alternative mechanistic models and not on a limited number of particles. Motivated by this potential, we extend the KDE model to simulate nonlinear adsorption which is a relevant process in many fields, such as product manufacturing or pollution remediation in porous materials. We show that the proposed model is able to reproduce the results of the Langmuir and Freundlich isotherms and to combine the features of these two classical adsorption models. In the Langmuir model, it is enough to add a finite number of sorption sites of homogeneous sorption properties, and to set the process as the combination of the forward and the backward reactions, each one of them with a pre-specified reaction rate. To model the Freundlich isotherm instead, typical of low to intermediate range of solute concentrations, there is a need to assign a different equilibrium constant to each specified sorption site, provided they are all drawn from a truncated power-law distribution. Both nonlinear models can be combined in a single framework to obtain a typical observed behavior for a wide range of concentration values. This approach opens up a new way to predict and control an adsorption-based process using a particle-based method with a finite number of particles. Finally, by classifying the particles to mobile and immobile states and employing transition probabilities between these two states, we take into account the porosity of the diluted system in the KDE model. The state of a particle is an attribute that defines the domain at which the particle is present at a given time within the porous medium. The transition probabilities are controlled by two parameters which implicitly determine the porosity. Simulations results show a good agreement with the analytical solutions of complete and incomplete mixing solutions, independent of the number of particles.

Diffusion plays an important role for many processes at the microscopic level in cells. In this dissertation we present two model systems in which we monitor diffusion with high precision single particle tracking to gain insight into cellular functions. First we present an in vitro membrane fusion assay, in which fusion intermediates are described by the thermal motion of a membrane coated tracer particle. In the second part the diffusive motion of endogenous lipid droplets in the model organism Schizosaccharomyces pombe is utilized to probe the cytoplasmic behavior in response to glucose starvation.