

features. In particular, we developed an unsupervised segmentation-less projection method in which the whole intensity volume is expanded in four dimensional spherical harmonics (4DSH). To demonstrate our technique, we used projections to compare the spatial distributions of actin, Golgi apparatus and nucleus within cells of an MDCK epithelium regardless of tissue size and support. We found a clear dependence of the internal architecture of individual cells on tissue size and type of support. We conclude that when information on the general spatial distribution of cell and tissue components is needed, and when the tissue geometry permits it, projection methods in general, and the 4DSH representation in particular, eliminate the need for choosing representative image regions or performing cumbersome image segmentation.

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Light Scattering Detects Changes In Subcellular Structure And Organization With Connections To Cell Function

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By incorporating new models into our light scattering analysis techniques that better account for the ellipsoidal shape of cellular organelles, we can determine not only the average size, but also the average shape of an ensemble of cell nuclei in culture. This advance permitted new insight into the nucleus structure, and by providing an accurate depiction of its contribution to the light scattering signal, has also enabled an enhanced ability to analyze density correlations and therefore subcellular organization in biological cells. We will present verification of our methods and results of two new studies facilitated by these recent developments. In the first study, we used light scattering to detect statistically significant structural changes in breast cancer cells within one hour after treatment with apoptosis-inducing drugs. Two conclusions emerge: First, the ability of this technique to discern early onset of apoptosis makes it a promising tool for monitoring cancer treatments; and second, monitoring the organization of subcellular organelles could be a powerful method for studying the mechanisms of apoptosis, and perhaps other functional changes in cells. In the second study, we evaluated the deformation of stem cell nuclei as a response to engineered nanotopographical cues and the mechanical properties of their substrate. As verified by image analysis and comparison to control samples, the changes in nuclear shape due to materials' properties and nanotopography are highly significant. Additionally, these shape changes relate to modifications in stem cell adhesion and mobility, and provide a connection between environmental cues, nuclear deformation, and cellular behavior. Both studies solidified light scattering as a promising tool to assess structure in biological samples, and indicate the potential to link these structural changes to corresponding alterations in cell function.

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Thermal Noise as a Probe for Cell Adhesion

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In the adhesion area of cells on solid substrates, there is a narrow cleft filled with electrolyte. The sheet resistance of the cleft is crucial for the interfacing of cells with semiconductors and metals. It can be estimated by applying intracellular or extracellular ac voltages and recording the response of current, of extracellular voltage or of transmembrane voltage. A more elegant approach relies on the Fluctuation-Dissipation Theorem which implies that an electrical resistance is related with voltage fluctuations. It was previously demonstrated that the voltage fluctuations in the area of adhesion can be recorded with transistors and that the resistance of the cell-chip junction can be estimated from the noise spectrum [1].

To attain a more reliable interpretation of the voltage noise, we measured spatial maps of the noise spectrum in the adhesion area. We used a Multi-Transistor-Array with a homogeneous surface of titanium dioxide [2]. The bandwidth of recording was 3 MHz at a spatial resolution of 7.8 μm . As a test system we used snail neurons that were cultured on chips coated with polylysine. We found a good agreement between the twodimensional maps of the noise spectra with a theory of thermal noise in a planar core-coat conductor. Sheet resistances on the order of 100 MOhm were obtained. Apart from the effect of the sheet resistance, the noise characteristics revealed changes of the membrane conductance and membrane capacitance. Thus thermal noise recording is a novel probe for the electrical properties of cell adhesion with subcellular resolution, with high bandwidth and without perturbation of the system.

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1517-Pos Board B361

Robust Pore Size Analysis of Filamentous Networks from 3D Confocal Microscopy

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We describe a robust method for determining morphological properties of filamentous biopolymer networks, such as collagen or other connective tissue matrices, from confocal microscopy image stacks. Morphological properties including pore size distributions and percolation thresholds are important for transport processes, e.g. particle diffusion or cell migration through the extracellular matrix. The method is applied to fluorescently labeled fiber networks prepared from rat tail tendon and calf skin collagen, at concentrations of 1.2, 1.6 and 2.4 mg/ml. The collagen fibers form an entangled and branched network. The medial axes, or skeletons, representing the collagen fibers are extracted from the image stack by threshold intensity segmentation and distance-ordered homotopic thinning. The size of the fluid pores as defined by the radii of largest spheres that fit into the cavities between the collagen fibers is derived from Euclidean distance maps and maximal covering radius transforms of the fluid phase. The size of the largest sphere that can traverse the fluid phase between the collagen fibers across the entire probe, called the percolation threshold, was computed for both horizontal and vertical directions. We demonstrate that by representing the fibers as the medial axis the derived morphological network properties are both robust against changes of the value of the segmentation threshold intensity and robust to problems associated with the point-spread function of the imaging system. We also provide empirical support for a recent claim that the percolation threshold of a fiber network equals the fiber diameter for which the Euler index of the networks becomes zero.

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Confocal Imaging Of Extracellular pH With Fluorescein Derivatives

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Extracellular pH (pH_e) is an important regulator of membrane-proteins, such as those involved in solute transport and matrix structure. In experimentally superfused cells or tissues, it is often assumed that pH_e is spatially uniform and invariant. Gradients of pH_e , however, may occur physiologically e.g. close to cell membranes or in tissue-regions with poor capillary perfusion. Fluorescein-derivatives are low-cost dyes for recording pH ratiometrically in dual-excitation mode (458nm/488nm). Fluorescein-DHPE is a phospholipid-conjugated dye for measurement of surface-membrane pH_e . Freshly isolated rat ventricular myocytes, membrane-loaded with the dye for 5min, produce a pH_e -sensitive signal that can be imaged confocally or measured using whole-cell epifluorescence. In low buffer superfusates (0.5mM Hepes), the dye reports transient acidification of surface pH_e during superfusion of 15mM NH_4Cl , owing to influx of NH_3 driving the local deprotonation of extracellular NH_4^+ . On removal of NH_4Cl , surface pH_e alkalinises transiently. Activation of Na^+/H^+ exchange (by imposing an intracellular acid-load) acidifies surface pH_e . Fluorescein-sulfonic acid is a highly polar fluorescein-derivative with negligible membrane-permeability. It was used (30 μM in superfusate) to image pH_e confocally in spherical (100-300 μm radius) clusters (spheroids) of HCT116 cells. A pH_e gradient was observed, with low pH_e at the core (due to the long core-surface diffusion distance). Larger spheroids developed a more acidic core pH_e . Size-matched spheroids made from cells transfected with carbonic anhydrase 9, a membrane-tethered extracellular enzyme, produced steeper pH_e gradients. This is due to catalysis of cell-derived CO_2 hydration in the extracellular space. Fluorescein-derivatives may therefore yield novel insights into the regulation of pH_e .

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Biophysical Modeling

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Modeling of Protein Adsorption on a Metal Surface: Brownian Dynamics Simulations

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The ability of proteins to bind selectively to different kinds of solid surfaces is widely used in advanced technologies in medicine, pharmacy, nanodevices and bioengineering. However, experimental data on the interfacial behavior of proteins is limited and our knowledge of the driving forces for protein-solid surface binding is still very poor. The present study is aimed at building

a computational model for understanding and predicting the chemical and physical properties of protein-solid surface systems.

As a test example, adsorption of the BLIP (beta-lactamase inhibitor protein) protein fused with different homotriptides to the gold surface is explored. The computational algorithm is based on Brownian dynamics simulations of a protein in the presence of a metal surface with interactions described by electrostatic, Lennard-Jones (LJ), and desolvation energy terms. The interatomic LJ potential describes both the van der Waals and the chemical interaction between amino acids and the gold surface with parameters derived from ab initio calculations and experimental data. The desolvation term includes protein desolvation as well as surface water desorption effects. The results of the computer simulations are compared with the experimentally observed binding characteristics of the systems under consideration.

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Gold clusters as Spatial Probes of Residue Position on Protein in Small Angle X-ray Scattering

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We are developing a new method for using proteins labeled with one or two gold clusters in small angle X-ray scattering. Gold cluster labeling provides strong cluster-cluster (for double-label) and cluster-protein (for single and double-labels) interference. Analysis of the former provides the distance between gold clusters, while the analysis of the latter provides the distance and relative orientation between gold cluster and protein.

Here, we have investigated what structural information can be extracted from labeled protein. Simulated scattering curves of single or double-cluster labeled hypothetical template structures (PDB models modified with mono-maleimido undecagold) were generated by the Debye formula using effective-atomic-scattering factors in solution. The template scattering curve is compared to the simulated scattering curves of trial structures generated by exhaustive rigid body searches for a fixed protein with rotated and translated gold cluster(s). For both single and double-labeled rigid body modeling (RBM), inter-body distance information was predicted within 1-2 Å error. However, the prediction of gold cluster position(s) was inaccurate (20-40 Å error for double-label, 5-50 Å error for single-label) presumably because inter-body distance information dominates over the relative orientation of gold cluster and protein. To predict accurate gold cluster position(s), we corrected inter-body distance(s) of trial structure by moving gold cluster(s) along the vector from protein to cluster during RBM. Gold cluster position(s) were improved significantly by correcting to the simulated template distance (2-7 Å for double-label, 2-5 Å for single-label), although the accuracy was reduced when using distance(s) determined by RBM (5-70 Å double-label, 2-12 Å single-label). Combining single and double-labeled data is being pursued.

This technique is being developed for two main applications: (1) discrimination of threading structures, (2) protein-protein docking model prediction.

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Molecular Dynamics Study of Carbon Nanotubes Interacting with Humic Acid - Towards a Mechanistic Understanding of Nanomaterial Transport in the Environment

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A general concern with nanomaterials used in contemporary nanotechnology applications and consumer products is their potential discharge into the nature [1,2]. At present, there is still very little knowledge about the environmental and biological effects of nanomaterials, and the factors contributing to their transport, uptake and transformation in biological organisms. As one of the most important class of nanomaterials, carbon nanotubes (CNTs) pose a specifically important topic of study. Being essentially hydrophobic needle-like molecules, CNTs are not inherently water-soluble. Yet, it is known that CNTs can be solubilized by various types of amphiphilic molecules. In the case of CNTs discharged into the environment, such molecules capable of inducing solubilization are abundant in the ubiquitous natural organic matter (NOM) within soil

and natural water sources. We have used molecular dynamics simulations to study the binding of humic acid (HA) - a major constituent of NOM - with a single-walled carbon nanotube (SWNT). As a representative structure for HA we have used an oligomer consisting of 12 monomers of the so-called Temple-Northeastern-Birmingham (TNB) HA model [3]. We describe in detail the factors affecting the binding of the HA oligomer to the SWNT, and its subsequent solubilization. In addition, aggregation processes of solubilized SWNTs, leading to their eventual precipitation with HA in experiments, are elucidated. The computational modeling is complemented by spectroscopic measurements of the HA-SWNT modes of binding.

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1522-Pos Board B366

Analysis Of Side-chain Dynamics Of PhoB Dna Binding/transactivation Domain Using Molecular Dynamics Simulations

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PhoB is a transcription activator protein involved in the regulation of 39 genes constituting the *pho* regulon of bacteria. The DNA-binding/transactivation domain is a C-terminal functional domain of the PhoB for binding of the *pho* box, which is situated upstream of the *pho* regulon. The NMR structure of the DNA binding form of the PhoB DNA-binding/transactivation domain was solved by our group (PDB: 2z33) (1). In addition, backbone and side-chain dynamics of PhoB-DNA binding/transactivation domain were analyzed using the NMR relaxation spectroscopy (2).

In the present study, molecular dynamics (MD) simulations of the free-form and DNA-binding form of PhoB-DNA binding/transactivation domain were carried out, and resulting backbone and side-chain dynamics were compared with those of NMR relaxation experiments. The model-free order parameters for the backbone N-H bond (S_{NH}^2) and the methyl-averaging axis (S_{axis}^2) obtained from the MD simulations were in agreement with experimental values. It was found that S_{NH}^2 and S_{axis}^2 correlate well with the root-mean-square fluctuation (RMSF) of the backbone nitrogen atoms and the methyl carbon atoms obtained from the MD simulations, respectively, in contrast to weak correlations between the order parameters and crystal temperature factors. The S_{axis}^2 - RMSF plot showed the clear dependence of S_{axis}^2 on amino-acid species and the positions of the methyl groups in the side-chains, suggesting that dynamics of the methyl group in side chains are strongly affected by geometry of side chains in amino-acid species.

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Conformational Change of F₁-ATPase ϵ Subunit upon ATP Binding Studied by Molecular Dynamics Simulations and Small-angle X-ray Scattering

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The ϵ subunit of F₁-ATPase acts as an endogenous inhibitor of the ATPase activity in F₁-ATPase. Biochemical and structural studies have shown that the ϵ subunit from the thermophilic Bacillus strain PS3 (TF1) binds ATP specifically, and the ATP binding induces the conformational change of the C-terminal domain of the ϵ subunit from the extended form to the folded form that allows ATP hydrolysis in F₁ motor. The mechanism of how ATP binding induces the conformational change of the ϵ subunit remains unclear, because the atomic detail of the conformational ensemble of the ATP-free form is still not known.

In this study, to address the above question, we used molecular dynamics (MD) simulations and small-angle X-ray scattering (SAXS) experiments. Analysis of the SAXS data measured at SPring-8 has shown that the overall structural characteristics of the ATP-bound form in solution are consistent with the crystal structure, while the molecular shape determined for the ATP-free form shows a more expanded conformation. We performed MD simulations for both the ATP-bound and ATP-free forms to obtain conformational ensemble of these forms, and the validity of the calculated ensembles was checked by a comparison of simulation-derived SAXS profiles with the experimentally observed profiles.