

9:48

H7 4 Ray-splitting correction to the Weyl formula: Experiment versus theory.REINHOLD BLUMEL, *Wesleyan University, Middletown, CT 06459-0155*

Ray splitting is a phenomenon we are all familiar with: A light ray hitting a water surface at an angle is split into a transmitted and a reflected ray. Ray splitting is not restricted to light and water, but occurs generally in all wave systems in which the properties of the propagation medium change rapidly on the scale of a wave length. It was predicted by Prange et al. [Phys. Rev. E 53, 207 (1996)] that ray splitting produces universal corrections to the Weyl formula, i.e. the average density of states. Following a brief review of Weyl's theory and the theory of ray splitting, this talk presents recent results of a first experimental confirmation of the existence of ray-splitting corrections to the Weyl formula. The experiment, a quasi two-dimensional microwave cavity loaded with two dielectric bars, has been carried out by Corrie Vaa and Peter Koch at the State University of New York at Stony Brook [C. Vaa, P. M. Koch, and R. Blumel, Phys. Rev. Lett. 90, 194102 (2003)]. This research is supported by the NSF under Grant Numbers PHY-9732443, PHY-0099398 and PHY-9984075.

10:24

H7 5 The structure of chaotic eigenfunctions.ERIC HELLER, *Harvard University*

This abstract not available.



8:00

H8 1 Three state spatially symmetric Brownian ratchetBRIAN GEISLINGER, *University of Alabama at Birmingham*RYOICHI KAWAI, *University of Alabama at Birmingham*

We investigate a biologically inspired Brownian ratchet consisting of three spatially symmetric potentials, each with the same periodicity. Spatial symmetry of the system is broken only by the phase shift between the different potentials, as opposed to the classic Brownian ratchet whose symmetry is broken by the shape of the potential. By switching from one potential to another with certain transition rates, directed motion can be obtained. The properties of the resulting current is investigated by numerical simulation and analytical theory.

8:12

H8 2 Ratchet model for type IV pilus retractionMARTIN LINDEN, *Condensed Matter Theory, KTH, 106 91 Stockholm, Sweden*TOMI TUOHIMAA, *Biomedical and X-ray Physics, KTH, 106 91 Stockholm, Sweden*ANN-BETH JONSSON, *Microbiology and Tumor Biology Center, Karolinska Institute, Box 280, 17177 Stockholm, Sweden*MATS WALLIN, *Condensed Matter Theory, KTH, 106 91 Stockholm, Sweden*

Type IV pilus retraction is required for twitching motility in a wide range of bacteria, including *Neisseria gonorrhoeae*, *Myxococcus xanthus* and *Pseudomonas aeruginosa*. The mechanism of retraction is believed to be filament disassembly mediated by PilT, a member of the AAA family of motor proteins. Recent laser tweezer measurements of the force-velocity relation of PilT in *N. gonorrhoeae*, reveal that single PilT complexes generate forces of over 100 pN. We assume that PilT forms a cyclic ATPase surrounding the base of the pilus and formulate a model of retraction in terms of coupled flashing ratchets. We obtain a force-velocity relation by numerical simulation of the model which is in qualitative agreement with the experimental results.

8:24

H8 3 Dynamics of Molecular Motors on Heterogeneous TracksYARIV KAFRI, *Harvard University*DAVID K LUBENSKY, *Bell Laboratories*DAVID R NELSON, *Harvard University*

There are many biological functions that involve movement of motors along a filament or polymeric molecule. The motors use chemical energy to propel themselves along the track. The interpretation of single molecule experiments which study them is in many cases model based. These models typically ignore the effect of the heterogeneous track (such as DNA). Independent of the microscopic details, these descriptions lead to a motion described by a biased random walker. Using exact results and general arguments it will be shown that disorder leads to anomalous dynamics of motors. Most notably, experiments should exhibit a region where the displacement of the motor as a function of time grows sublinearly. The implications on the interpretation of experiments on RNA polymerase, DNA polymerase / exonuclease and others will be discussed.

8:36

H8 4 STRUCTURAL DETERMINATION OF BIOMOLECULES IN MICROFLUIDIC SYSTEMSJOHN C. BUTLER, *Department of Materials Science and Engineering*ETIENNE MENARD, *Department of Materials Science and Engineering & Department of Chemistry, University of Illinois at Urbana Champaign*GERARD C. L. WONG, *Department of Materials Science and Engineering, Department of Physics, Department of Bioengineering*

Supramolecular biological complexes are often too large to be crystallized for structural studies. Here, we explore the use of microfluidic arrays to order a model self-assembled cytoskeletal system. Filamentous actin (F-actin) is a negatively charged protein rod and is a key structural component in the eukaryotic cytoskeleton. In this context, F-actin can self-assemble with actin binding proteins (ABP) in a highly regulated manner to dynamically form structures for a wide range of biomechanical functions. In this work, we will systematically study the action of 3 types of actin binding proteins (α -actinin, fimbrin, cofilin) on the self-assembled structures of F-actin that have been aligned in microfluidic arrays.