

Beyond Einstein Physics for the 21st Century

CONFERENCE BOOK



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BB-8-TUE

Molecular Nature of the Laminar-Turbulent Transition

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For the past 150 years, it has been a tenet of the continuum model of hydrodynamics that the dimensionless critical Reynolds number is the sole discriminant of laminar-turbulent transition, irrespective of the hydrodynamic medium. So for the same apparatus, such as a pipe gas efflux apparatus, it is asserted that the critical Reynolds number, $Re_c = \rho v_c d/\eta$, where ρ is the density, v_c is the critical velocity, d is the diameter of a tube, and η is the dynamic viscosity, should be the same for all gases. This tenet is supported by (1) a re-scaling of the Navier-Stokes equation, and (2) experiments which have heretofore been accurate only to some 10-30%. New experiments using rapid pressure measurements with a sampling rate of every millisecond [1], and vacuum technology equipment [2] show that this scale invariance is not true for the laminar-turbulent transition, thus questioning the basic assumption of continuum theory that the precise molecular nature of the gas used in the experiment is irrelevant. We will display results which are moleculedependent, raising questions on the exclusive use the Navier-Stokes equation as the defining equation for the study of turbulence.

[1] S. Novopashin, A. Muriel., Phys. Letters A 335 (2005) 435

[2] L. Hinkle, A. Muriel, Phys. Letters A, to be published

BB-9-TUE

A Monte Carlo Approach to Investigate Light Scattering in Biological Suspensions

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So far there have been developed several models to investigate the steady-state light transport in multilayered tissues, some of the most wellknown being MCNP and MCML. The algorithm implemented in the MCML assumes that the target consists of successive layers, each one having well defined average reflection and transmission coefficients. These codes consider a package of photons to be moved layer by layer in the target, having parts of the it scattered at different angles, transmitted or absorbed accordingly with the random numbers generated for each decision. In biological suspensions like blood, natural or at different dilutions, light scattering is done by the scattering centers only. The novel Monte Carlo approach we propose, moves one photon at a time and checks the scattering centers to determine which one will scatter the photon (quasi - ballistic approximation). Light scattering anisotropy, multiple scattering and internal reflection are considered.

The simulations results are compared with effective phase function calculations and with the experimental results on diluted RBC suspensions at different hematocrit values and scattering angles.

[1] D. Walson, N. Hagen, & all, Elastic Light Scattering from Single Cells: Orientational Dynamics in Optical Trap, Biophysical Journal 87 (2004) pp. 1298-1306.

BB-10-TUE

Do Positrons Measure Molecular Diameters?

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In introduction of Brown-motion paper, Albert Einstein wrote that classical thermodynamics could yield "exact dimensions of atoms" (eine exakte Bestimmung der wahren Atomgröße möglich). Now, Röntgenray diffraction, viscosity studies, Van der Waals gas-state yield molecular radii with high precision, unfortunately, all different: for Ar the viscosity yields 1.83Å and van der Waals 1.24 Å; for He one expects a lower radius but these are 1.09Å and 1.33Å, respectively. Measurements of total cross sections for positron scattering on molecules in gas phase, date from 70-ties[1]. In the zero-energy limit cross sections rise and at a few eV range show the Ramsauer minimum¹ but wide and flat. New measurements[2] with good statistics show that up to the positronium formation threshold cross sections are constant, like for hard-sphere scattering. The radii obtained[1,2] are 0.34Å for He, 0.52Å(!) for H₂, 1.0Å for Ar, 1.6Å for CO₂, 1.9Å for SF₆. Inner atomic potential is repulsive for positrons: do they measure atomic cores?

[1] W.E.Kauppila et al., Phys.Rev. Lett. 36 (1976) 580

[2] G.Karwasz et al., Acta Phys. Pol., in print

BB-11-TUE

Experimental Investigation of the Subdiffusion in a Membrane System

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We study diffusion in a membrane system consisting of two cells separated by a horizontally located nuclear membrane. We have filled the upper cuvette of the membrane system with an aqueous solution of polyethylene glycol 2000 (in a gel form) while in the lower one there has been water gel (2% agarose gel). The diffusion can be characterised by a form of time evolution of the so-called near-membrane layer (NML), where the concentration of diffusing substance drops k times When the thickness of NML, grows in time as t^{γ} with $\gamma=0.5$ we deal with normal or gaussian diffusion, when. If $\gamma > 0.5$ there is a superdiffusive and when γ <0.5 subdiffusive behaviour. To observe the time evolution of NML we have employed the laser interferometric technique: the interference fringes pattern has provided quantitative measurement of the substance concentration C(x,t) at position x and

at time t. Recording the interferograms with a given time step, we have constructed the profile of polyethylene glycol concentration. Our results show that the thickness of NML grows in time t as t^{γ} , with $\gamma < 0.5$, manifesting a subdiffusive character of the process. The concentration profiles C(x,t) scales as $t^{\beta}F(x/t^{\gamma})$, where the exponents β , and γ are fixed.

BB-12-TUE

Role of Percolative Water Network in Aqueous Systems: from Phase Transitions to Biological Activity

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Percolation transitions in aqueous systems are related to various phase transitions, such as liquid-liquid phase transitions in aqueous mixtures, liquid-liquid phase transitions of supercooled water, and quasi-2D layering transition of water at hydrophilic surfaces. Our results suggest that in a thermodynamically stable mixture, the two components could not show a 3D percolation simultaneously. In completely miscible mixtures, there is a concentration interval where both components are below their 3D percolation thresholds. Otherwise, liquid-liquid demixing occurs. Using this finding, we identified the components of liquidliquid decomposition in supercooled water. The line of percolation transitions of water at a hydrophilic surface meets the coexistence curve of the layering transition at the critical point. The formation of a spanning water network at the surface of finite objects, such as protein molecules, also occurs via a 2D percolation transition. This percolation transition coincides with the onset of biological activity of proteins at low hydration. Besides, thermal breaking of the spanning network of hydration water in protein solutions could be related to rapid changes of structure and function of proteins.

BB-13-TUE

Numerical Study of Diffusion in Timedependent Potentials

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Diffusion in time-dependent potentials plays a central role in the phenomenon of stochastic resonance, in physics of Brownian motors and in the recent discussion concerning the energetics of diffusion processes. We investigate numerically the one-dimensional diffusion of a particle in a linear time-dependent potential. For this purpose we solve the Fokker-Planck equation (FPE) with the Finite-Element Method (FEM). The particle is moving in a domain with two reflecting boundaries. The external time-independent force is modulated by a harmonically oscillating force. From the solution of the