

Dear IUPS2009 participants:

During the period of the 36th IUSP2009 Congress in Kyoto, three tutorial programs will be held (please see below). These programs aim to facilitate the practical understanding of participants about special themes by combining guiding lectures and practice. To estimate the number of participants correctly, we would like to encourage you to make advanced registration for each tutorial, although on-site registration will also be accepted.

Please refer to the information below, and if you are interested in participating either of them, please contact us as soon as possible at the address below.

We would like to add that, if the number of applicants would exceed the maximum expected one, we may close the registration.

We are looking forward to meeting you in Kyoto soon.

Kindest Regards,

Contact address:

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[Please describe your name and affiliation and the tutorial(s) of your interest].

Deadline for advanced registration: July 21, 2009.

Tutorial 1: Physiome/VPH projects tools (CellML Tutorial)

Date & Time: July 29 (Wed.), 14:15-16:45

Place: Room K

Organizers: Peter Hunter, Poul Nielsen

Expected number of participants: max. 40.

Requirements: Participants are encouraged to bring their own PC with wireless LAN capability.

Outline: Both CellML and cmgui are core elements of the Virtual Physiological Human Toolkit.

CellML (<http://www.cellml.org/>) is an XML-based language for description of quantitative mathematical models. The primary goal of the CellML project is to provide a lingua franca for such models to facilitate their distribution and reuse by the research community. Cmgui

(<http://www.cmiss.org/cmgui>) is an application for visualizing complex multidimensional data, for example, the kinds of detailed functional models of human organ systems developed within the Physiome Project.

This is a combined tutorial that will consist of a one hour lecture style introduction, followed by 90 minutes of hands-on exposure to either CellML or cmgui, (according to the attendee's choice) supervised by senior members of both projects. The CellML tutorial will show attendees how to

build and simulate a well known model in the OpenCell software, while the cmgui tutorial will give an introduction to cmgui, demonstrating how to create a custom visualisations of 3D organ models and data. Attendees should bring their own computers if possible, but workstations will be provided.

Tutorial 2: Molecular Imaging and Physiological Research

Date & Time: August 1 (Sat) 14:15-16:45

Place: Room I

Organizers: Yasuyoshi Watanabe, Norihiro Sadato

Expected number of participants: max. 40.

Requirements: none

Outline: *In vivo* molecular imaging has become a key technology for drug development and pathophysiological science. We are mostly utilizing PET (Positron Emission Tomography) as a first-choice modality, because of its ultra-high sensitivity for molecules, adequate temporal and spatial resolution, and especially broad spectrum of target molecules. The present status for development of PET molecular probes, instrumentations including microPET, and the methods for quantitative analyses will be introduced in this tutorial with some examples. Molecular imaging could bring the high-quality information about key molecules as disease markers for diagnosis, direct follow-up, and demonstration of drug effect in living patients with symptoms. Molecular imaging is useful for drug development; especially, drug delivery system, pharmacokinetics and pharmacodynamics, dose finding information for individuals corresponding to SNP's, direct evidence for accumulation in non-target organs related to the adverse effects, and evidence for drug effects with surrogate markers. In the tutorial, several presentations from different technical aspects and also videos will be provided.

Tutorial 3: Bioinformatics for Physiology

Date & Time: July 29 (Wed.), 9:30-12:00.

Place: Room J

Organizers: Haruki Nakamura, Kenta Nakai

Expected number of participants: max. 40.

Requirements: participants are encouraged to bring their own PC with wireless LAN capability.

Outline: Bioinformatics now provides a powerful tool for understanding physiological phenomena from the multi-scale and multi-level view points, covering from genome, protein molecules, cells, to organs. In this tutorial, using representative softwares and databases with PCs linking to the Internet, several exercises for bioinformatics study will be given. The theme of this tutorial course will cover: Genome analysis, Protein expression, Protein sequence and structure analysis, and Protein-protein interactions and network. Several specialists in those fields will make brief introductory lectures at the beginning of the exercise courses.