

**Modeling Multiscale Cardiovascular and Respiratory System Dynamics**  
**August 23-27, 2010 N140 William H. Foege Building**  
**University of Washington, Seattle, WA 98195**  
**(Ultimate Draft Syllabus)**

	<i>830-1015 AM</i>	<i>1030-1215 AM</i>	<i>1315-1500 PM</i>	<i>1515-1730 PM</i>
Monday 8:30 AM	<p>Introductions: Bassingthwaighte Modeling overview</p> <p>Strategies, Objectives in Multi-scale Modeling</p> <p>Hands on: Login</p>	<p>Gary Raymond: Aspirin: discussion of hypotheses, modeling clearance by reaction</p> <p>Hands on: Begin with compartmental models, 2-comp exchanges <u>Publication Standards Coding for reproducibility</u></p>	<p>Butterworth: JSim structure and function --- -Work Time-----</p> <p>Download JSim? --Importing from CellML and SBML- ----</p> <p>Bassingthwaighte : Progress Curves: Xanthine Oxidase kinetics (Optimize)</p> <p>ODEs--Hands on:</p>	<p>Bassingthwaighte : Lecture: Blood Tissue Exchange</p> <p>Multiple Indicator Dilution Expt</p> <p>Crone Extraction Data</p> <p><b>Mass Balance</b></p> <p>-work Time on PDEs -</p> <p>5:30 PM</p>
Tuesday 8:30 AM	<p><u>Jiri Kofranek</u></p> <p>Electrophysiol in Modelica</p> <p>Introduction to large models: Quanatitative Human Physiology</p>	<p><u>Kofranek,</u> <u>Waniewski,</u> <u>Butterworth,</u> <u>Sauro</u></p> <p>1. Computing <b>Platforms:</b> Matlab, JSim, Modelica, PCEnv, etc</p> <p>2. <b>Archives:</b> <b>SBML, CellML</b> <b>JSim</b> and others, incl. platform dependent ones.</p>	<p><u>Joseph Anderson:</u></p> <p>Modeling Pulmonary Mechanics and Gas Exchange I: modeling with electrical analogs</p> <p><u>Jhony Caucha:</u> Modeling Forced Expiratory Velocity <b>Practical Application</b></p>	<p><u>Joseph Anderson:</u> Modeling Pulmonary Mechanics and Gas Exchange II. spatially distributed permeation. Spatial profiles in capillary. Diffusion.</p> <p><b>Model Verification Methods</b></p> <p>5:30 PM</p>
Wednesday 8:30 AM	<p><u>Hong Qian:</u> Stochastic and Deterministic Modeling. Where do they intersect? 1. <b>Stochastic chem</b> 2. Gillespie algorithm</p>	<p><u>Hong Qian:</u> Biochem Network Models and their analysis. Building biochem <b>networks.</b> Critical paths.</p>	<p><u>Eric Shea-Brown:</u></p> <p>When does feedback destroy the precision of neural spike times?</p> <p><b>Stochasticity</b> in neural information flow: Channels, APs, synaptic vesicles</p>	<p><u>Eric Shea-Brown</u> Electrophys, mono-scale cell models: Boltzmann channel Boltz =&gt; HHActionPot</p> <p><u>Bassingthwaighte</u> : Beeler-Reuter Action Potential</p> <p><b>Real <u>Multi- scale:</u> Rudy2010</b></p> <p>5:30 PM</p>

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Thursday 8:30 AM	<u>Herbert Sauro</u> : Quantitative Synthesis of real Genetic Networks Working with Jarnac and <b>SBML            and Biomodels            and CellML            databases</b>	<u>Herbert Sauro</u> : Quantitative Simulation Analysis of Metabolic Nets  <b>Validation:</b>	<u>Bart Jardine</u> : <u>Matlab Intro</u> <u>CircAdapt</u>  <u>Jacek Waniewski</u> : constructing a peritoneal dialysis model using Matlab --work with Matlab: --compartmental model --diffusion model <b>Model            Validation:</b>	<u>Waniewski</u> : (cont)  <u>Bassingthwaighte</u> :Lung Purine Uptake (Pearson) participants construct distributed multipath model from BTEX10 to BTEX20 to multipath. <b>Model            Validation            END BY 5:15 PM</b>  5:30 PM: drive to Pier 55 ferry to Blake Island, Tillicum Village salmon dinner
Friday 8:30 AM	<u>Jim Caldwell</u> : rMBF: Regional Myocardial Blood Flow using PET Imaging. <b>Test of            Model Validity</b> Optimization for rMBF ====Hands on ===	<u>Bassingthwaighte</u> Model stages for rMBF estimation from PET images  <u>Kevin Hsu</u> : Effect of Noise in the data <b>Parameter            Evaluation</b>	<u>Gary Raymond and            Max Neal</u> : Modular Modeling Example constructions with FORTRAN and SemGen <b>Standards for            Modules</b>	Wrap-up: Key strategies? Review Platt 1964. Mono- versus multi- scale. Reproducible science Integration Biology More sets of standards? <b>Code Sharing</b>  5:30 PM