



GeneGo User Group Meeting Agenda 2010 - Europe

Wednesday,  
May 12th

TIME	TOPIC	PRESENTER
8:30 am	Registration and Breakfast	
9 - 9:30am	GeneGo Vision and Strategy Science and Technology	Yuri Nikolsky
9:30 - 9:45 am	2009 Review	Julie Bryant
9:45 - 10:15 am	Hunting for correctors of Cystic Fibrosis	Chris Larminie <i>GlaxoSmithKline</i>
10:15 - 10:45 am	MetaDrug: from compounds structure to affected pathways	Eugene Myshkin
10:45 - 11 am	Break	
11 - 11:30 am	Pathway Analysis of Motor Neuronal Specification and Differentiation in developing vertebrate	Dr. David Chambers <i>King's College London</i>
11:30 - 12 pm	Upcoming enhancements to toxicity analysis in MetaCore and MetaDrug	Richard Brennan
12 - 1 pm	Training Group 1: Using MetaCore to answer questions such as: What are my gene lists telling me? What processes are they involved in?  <ol style="list-style-type: none"> <li>1. What is biologically going on with my experimental data?</li> <li>2. Potential target - what biological effect altered if hit upstream and downstream</li> <li>3. Search for known target-around topics to find information</li> <li>4. From my gene lists what is most important</li> <li>5. I want to find out information about my datasets such as: <ol style="list-style-type: none"> <li>a. Which genes are important in x disease</li> <li>b. Which genes are known targets</li> <li>c. Which genes can be easily assayed and used as biomarkers</li> </ol> </li> <li>6. What are the top pathways for my genes (having maps or network answers confuse people)</li> <li>7. What are my top genes and what are they interacting with?</li> </ol>	Eugene Myshkin
12 - 1 pm	Training Group 2: Tox Workflows <ul style="list-style-type: none"> <li>• What are drug risk factors?</li> <li>• What is the mechanism?</li> </ul>	Richard Brennan
1 - 2pm	Lunch	
2 - 2:30 pm	Lessons learned about ECM of fibroids using pathway analysis of gene expression data	Jörg Mueller <i>Bayer Schering Pharma AG</i>
2:30 - 3 pm	Integration of MetaCore in the Genomics Platform workflow	Celine Delucinge-Vivier Data Analyst <i>University of Geneva</i>
3 - 3:15 pm	Break	
3:15 - 3:45 pm	Working with experimental data sets	Matt Newman Vice President Business Development <i>OmicSoft</i>

3:45 - 4:15 pm	Identifying androgen-responsive genes in the human endometrium	Elaine Marshall <i>University of Edinburgh Centre for Reproductive Biology MRC Human Reproductive Sciences Unit</i>
4:15 - 5:30 pm	Training Group 1: OmicSoft Training Group 2: microRNA	Matt Newman Eugene Myshkin