



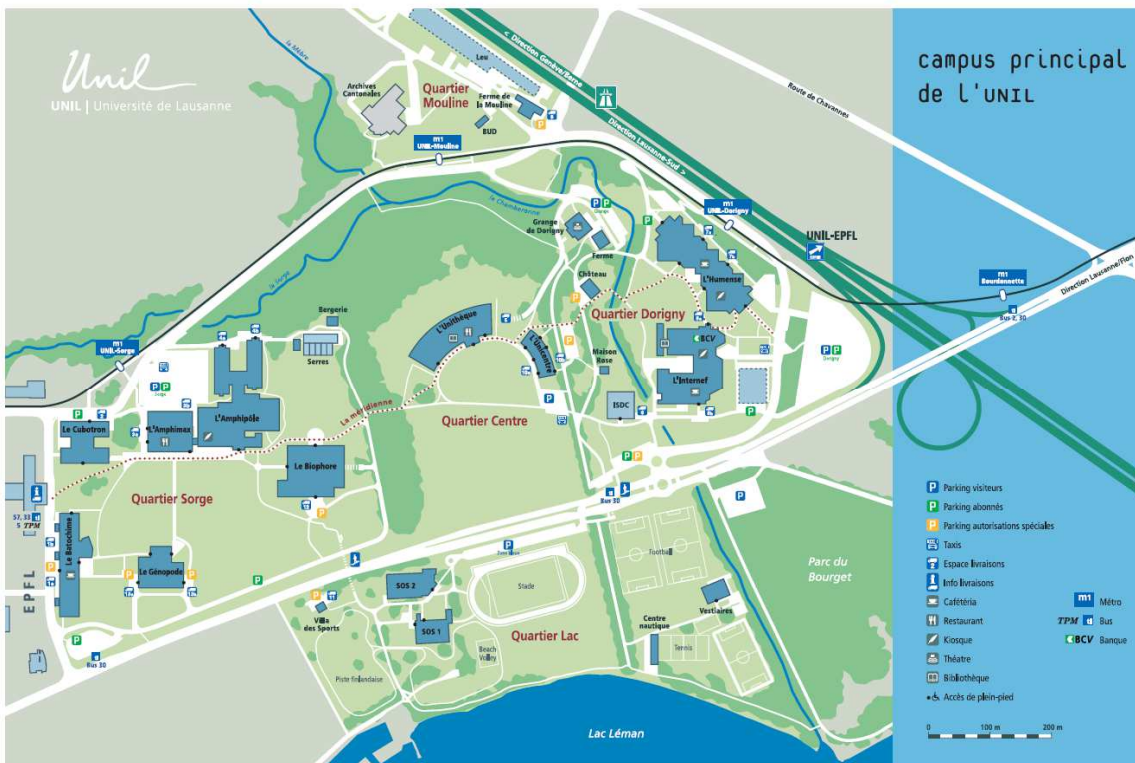
# Conference Agenda

Quest for Orthologs conference 2013

Session
Workshop
Round table discussion
Event

Quest for Orthologs conference 2013

UniL, Biophore



Wednesday, July 24, 2013








13:00 - 14:00	<b>Registration</b>
14:00 - 14:10	<b>Welcome</b> <i>Marc Robinson-Rechavi</i>
14:10 - 15:40	<i>Session I</i> <b>Orthology Prediction and Ortholog Databases I</b> <i>Chair: Ingo Ebersberger</i> <i>Auditorium</i>
14:10 - 14:40	<b>Toni Gabaldon</b> Challenges in phylogeny-based orthology prediction, and PhylomeDB/MetaPhOrs update
14:40 - 15:10	<b>Evgeny Zdobnov</b> OrthoDB: latest developments
15:10 - 15:40	<b>Adrian Altenhoff</b> Inferring Hierarchical Orthologous Groups From Orthologous Gene Pairs
15:40 - 16:10	<b>Break</b>
16:10 - 17:40	<i>Session II</i> <b>Orthology Prediction and Ortholog Databases II</b> <i>Chair: Matthieu Muffato</i> <i>Auditorium</i>
16:10 - 16:40	<b>Erik Sonnhammer</b> New InParanoid developments
16:40 - 17:10	<b>Fabian Schreiber</b> TreeFam is back with a new release, website, and interesting features
17:10 - 17:40	<b>Cecile Pereira</b> A meta approach for improving ortholog groups prediction
17:40 - 19:10	<b>Poster session and Dinner (18:00-19:00)</b>
19:10 - 20:40	<i>Session III</i> <b>Orthology Prediction and Ortholog Databases III</b> <i>Chair: Vincent Daubin</i> <i>Auditorium</i>
19:10 - 19:40	<b>Judith A Blake</b> The M:N Project at MGD: Beyond 1:1 Orthology Assertions
19:40 - 20:10	<b>Simon Penel</b> HOGENOM, a Database of Homologous Genes in Complete Genomes
20:10 - 20:40	<b>Ikuo Uchiyama</b> Enhancement of the Microbial Genome Database for Comparative Analysis (MBGD)

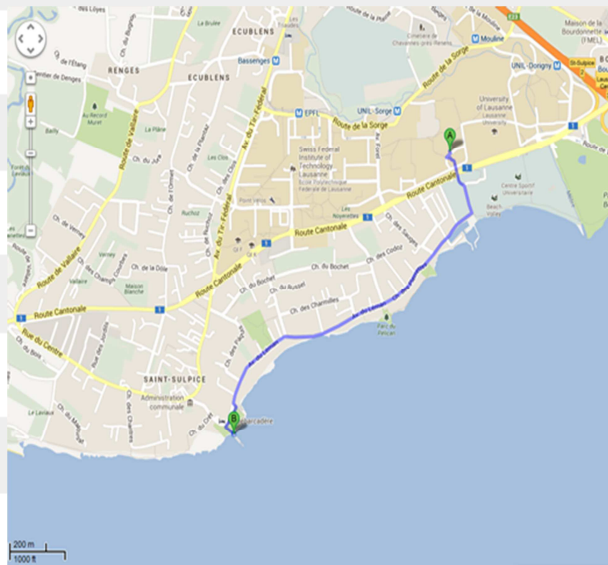
Thursday, July 25, 2013

9 : 0 0 - 1 0 : 3 0	<p style="text-align: right;"><i>Plenary Workshop I</i></p> <p style="text-align: center;"><b>Orthology Benchmarking</b> <i>Moderators: Brigitte Boeckmann, Christophe Dessimoz</i></p> <p style="text-align: right;"><i>Auditorium</i></p>
	<p><b>Christophe Dessimoz</b> Progress of the Quest for Orthologs benchmarking working group</p> <p><b>Adrian Altenhoff</b> The orthology benchmarking server</p> <p><b>Round table discussion</b> On the interpretation of benchmarking results</p>
1 0 : 3 0 - 1 1 : 0 0	Coffee
1 1 : 0 0 - 1 2 : 3 0	<p style="text-align: right;"><i>Plenary Workshop II</i></p> <p style="text-align: center;"><b>Reference Datasets</b> <i>Moderator: Maria Martin</i></p> <p style="text-align: right;"><i>Auditorium</i></p>
	<p><b>Alan Wilter Sousa da Silva</b> The Reference Proteomes: consensus protein data sets for the Quest of Orthologs Consortium (QfO)</p> <p><b>Paul D. Thomas</b> Time to reconsider xenologs?</p> <p><b>Christophe Dessimoz</b> Benchmarking orthology using simulated datasets</p> <p><b>Brigitte Boeckmann</b> A species tree for the QfO reference datasets</p>
1 2 : 3 0 - 1 4 : 0 0	Lunch, Conference photo
1 4 : 0 0 - 1 5 : 3 0	<p style="text-align: right;"><i>Session IV</i></p> <p style="text-align: center;"><b>Update on Orthology Prediction</b> <i>Chair: Adrian Altenhoff</i></p> <p style="text-align: right;"><i>Auditorium</i></p>
1 4 : 0 0 - 1 4 : 3 0	<p><b>Sebastien Moretti</b> Quality control of multiple sequence alignments</p>
1 4 : 3 0 - 1 5 : 0 0	<p><b>Ingo Ebersberger</b> Assessing the evolutionary traceability of proteins</p>
1 5 : 0 0 - 1 5 : 3 0	<p><b>Vincent Daubin</b> Phylogeny-aware approaches to the reconstruction of ancestral genomes</p>
1 6 : 0 0 - 1 6 : 3 0	Coffee

16:30 - 18:00	<i>Plenary Workshop III</i>
	<b>Assess Reality to Determine Next Steps</b> <i>Moderator: Paul Thomas</i>
	<i>Auditorium</i>
	<p><b>Brigitte Boeckmann</b> Orthology and the evolution of proteins</p> <p><b>Lucy Li</b> Scope and limits of domain-aware orthology inference</p> <p><b>Toni Gabaldon</b> Orthology prediction and confidence levels</p> <p><b>Ioannis Xenarios</b> Biocurations centralization or crowd sourcing - taking advantages of both approaches</p>
18:00 - 22:15	Event
18:00 - 18:45	Walk along the lake to Port St Sulpice (transport possible, contact organizers)
18:45 - 22:15	Cruise on a paddle wheel steamer and conference dinner
22:15	Arrival at Port - Lausanne-Ouchy

## BioPhore

1. Head **southeast** go 14 m  
total 14 m
-  2. Turn right toward **Ch. de la Roselière** go 30 m  
total 44 m
-  3. Turn left toward **Ch. de la Roselière**  
About 2 mins go 180 m  
total 230 m
-  4. Turn right toward **Ch. de la Roselière**  
About 1 min go 140 m  
total 350 m
-  5. Turn right onto **Ch. de la Roselière**  
About 2 mins go 140 m  
total 500 m
6. Continue onto **Ch. du Petit-Port**  
About 2 mins go 150 m  
total 650 m
7. Continue onto **Ch. des Pierrettes**  
About 5 mins go 350 m  
total 1.0 km
8. Continue onto **Av. du Léman**  
About 12 mins go 1.0 km  
total 2.0 km
-  9. Turn left go 24 m  
total 2.1 km
-  10. Turn right  
About 1 min go 110 m  
total 2.2 km
-  11. Turn left  
Destination will be on the left go 58 m  
total 2.2 km



## St-Sulpice VD

Friday, July 26, 2013

9 : 0 0 - 1 0 : 3 0	<p style="text-align: right;"><i>Plenary workshop IV</i></p> <p style="text-align: center;"><b>Function Assignment</b> <i>Moderator: Suzanna Lewis</i></p> <p style="text-align: right;"><i>Auditorium</i></p>	
	<p><b>Marc Robinson-Rechavi</b> Ongoing exploration of functional differences between human and mouse orthologs</p> <p><b>Nives Skunca</b> Quality of electronic GO annotations</p> <p><b>Jean-Francois Dufayard</b> From Fitch orthology to functional conservation in GreenPhylDB</p>	
1 0 : 3 0 - 1 1 : 0 0	Coffee	
1 1 : 0 0 - 1 2 : 3 0	<i>Parallel Workshops V</i>	
	<p style="text-align: right;"><i>V-a</i></p> <p style="text-align: center;"><b>Application of Orthology</b> <i>Moderator: Judith Blake</i> <i>Auditorium</i></p> <p><i>In prep.</i></p>	<p style="text-align: right;"><i>V-b</i></p> <p style="text-align: center;"><b>Standard formats</b> <i>Moderator: Marc Robinson-Rechavi</i> <i>Room 2107</i></p> <p><b>Erik Sonnhammer</b> Status of OrthoXML and SeqXML standards for orthology and sequence information</p> <p><b>Todd DeLuca</b> Enabling rapid data integration and discovery by providing Reference Proteomes orthologs in RDF.</p> <p><b>Jesualdo Tomás Fernández-Breis</b> Towards Orthology Linked Datasets</p> <p><b>Hirokazu Chiba</b> Construction of ortholog database using the semantic web technology</p>
1 2 : 3 0 - 1 4 : 0 0	Lunch	
1 4 : 0 0 - 1 4 : 3 0	<p style="text-align: right;"><b>Session V</b></p> <p><b>Report on parallel workshops</b> <i>Chair: Robert Waterhouse</i></p> <p style="text-align: right;"><i>Auditorium</i></p>	
1 4 : 3 0 - 1 5 : 3 0	<p style="text-align: right;"><i>Round table discussion</i></p> <p style="text-align: center;"><b>Achievements, Challenges, Outlook</b> <i>Moderators: Erik Sonnhammer, Toni Gabaldon</i></p> <p style="text-align: right;"><i>Auditorium</i></p>	
1 5 : 3 0 - 1 5 : 4 0	Closing	
1 5 : 4 0 - 1 6 : 0 0	Coffee	