

**Tentative program Integrative Bioinformatics Course,
Molecular and Computational Biology Research School – November 23-27, 2009**

	Monday (FL1)	Tuesday (FL1)	Wednesday (FL1)	Thursday (FL1)	Friday (FL1 ?)
0830		Introduction GSEA (KP)	Module 2: Gene Regulation (BL)	Module 3: Hyperbrowser (SG)	Module 4: Research presentations (IJ)
0900	Introduction (IJ)	GSEA practical	Continues	Continues	Course-grained quantitative modelling of a multicellular system: Revisiting vulval development in <i>C. elegans</i> . (JH)
1000	Students present	Identifier mapping introduction (MD)	Continues	Continues	TBA (MS)
1100	Continues	Meta analysis – introduction and practical (KP)	Continues	Continues	TBA (PP)
1200	Lunch	Lunch	Lunch	Lunch	Lunch
1230	Module 1: Integrative bioinformatics in context of microarray data analysis Introduction (KP); J-Express introduction (KP)	ProMeTra/ visualization Presentation (HN)	Continues	Continues	Discussion, summing up
1330	Differential expression (KP)	Systematic representation of KEGG pathways (MD)	Continues	Continues	
1430	Practical	ProMeTra practical	Continues	Technical issues	End of day
1600	End of day	End of day	End of day	End of day	

Presenters:

- Inge Jonassen, Computational Biology Unit, BCCS and Department of Informatics, UiB (IJ)
- Kjell Petersen, Computational Biology Unit, BCCS, UiB (KP)
- Michael Dondup, Computational Biology Unit, BCCS, UiB (MD)
- Heiko Neuweiger, CeBiTec, University of Bielefeld, Germany (HN)
- Boris Lenhard, Computational Biology Unit, BCCS, UiB (BL)
- Sveinung Gundersen (SG), Oslo University Hospital
- Mansoor Saqi, Rothamsted Research, Hertfordshire, UK (MS)
- Jaap Heringa, Vrije University, Amsterdam (JH)
- Pål Puntervoll, Computational Biology Unit, BCCS, UiB (PP)

Location: Fak laboratory 1 (FL1),