

“Bioinformatics and trees”

Hotel Ibis Mariahilf
Mariahilfer Gürtel 22-24
Vienna, Austria

March 11th – 12th 2015

Wednesday March 11th 2015

14.00 – 14.40

- **Ingo Ensminger**, University of Toronto (Canada): Using conifer transcriptome data - experimental design and data analysis strategies [40’]

14.40 - 15.00 Coffee break

15.00 – 16.25

- **David Torrents**, Barcelona Supercomputing Centre (Spain) : Supercomputing and Genomics [40’]
- **Marco Bink**, Wageningen University (The Netherlands): genotype imputation (and subsequent genomic prediction based on sequence data) [40’]

Thursday March 12th 2015

09.00 – 10.20

- **Inanc Birol**, University of British Columbia (Canada) : Assembly and analysis of the white spruce genome [40’]
- **Daniel Peterson**, Mississippi State University (USA) : Getting Bioinformatics through Its Awkward Adolescence. [40’]

10.20 – 10.45 Coffee break

10.45 – 12.10

- **Amin Madoui**, CEA-Genoscope (France): Heterozygous genome assembly by long read integration: application to the oak genome [40']
- **Arndt von Haeseler**, Center for Integrative Bioinformatics Vienna (Austria) : NextGenMap and the impact of highly polymorphic regions [40']

12.10 – 14.00 Lunch break

14.00 – 15.30

- **Nathaniel Street**, Umeå University (Sweden): Insights and challenges - the result of aspen by short read interaction [40']
- **Yves Van de Peer**, Ghent University (Belgium): Bioinformatics approaches to unveil ancient whole genome duplications in plants [40']