Summary of the Phylogenomics Workshop
1) Data

2) Orthology inference

3) Alignment & Trimming

4) Phylogenomic subsampling

5) Supermatrix vs individual genes

6) Model selection & Phylogenetic inference

7) Testing the robustness of your tree
1) Data

Source
Genomes
Transcriptomes
UCEs
RADseq
Metagenomics

Rosa Fernández (23rd January)
1) Data

Source

Genomes
Transcriptomes
UCEs
RADseq
Metagenomics

Exonic protein-coding sequences

Jacob L Steenwyk -> Gene trees challenge (single copy orthologs + orthoSNAP)
Jordi Paps (29th January)
Lisa Pokorny (31st January)

Rosa Fernández (23rd January)
1) Data

Source

Genomes
Transcriptomes
UCEs
RADseq
Metagenomics

Exonic protein-coding sequences
Introns
Other non-coding elements
Retroelements

Rosa Fernández (23rd January)
Toni Gabaldon (30th January)
Erin Molloy (26th January)
Lisa Pokorny (31st January)
1) Data

**Source**

Genomes  
Transcriptomes  
UCEs  
RADseq  
Metagenomics

Matt Christmas (26\textsuperscript{th} January)  
Aoife McLysaght (27\textsuperscript{th} January)

Erin Molloy (26\textsuperscript{th} January)  
Matt Christmas (26\textsuperscript{th} January)  
Lisa Pokorny (31\textsuperscript{st} January)

Gytis Dudas (30\textsuperscript{th} January)  
Ania Karnkowska (2\textsuperscript{nd} February)

Rosa Fernández (23\textsuperscript{rd} January)
1) Data

Taxon sampling

Marina Marcet-Houben (24th January)
Antonis Rokas (29th January)
Jordi Paps (29th January)

Rosa Fernández (23rd January)

Data quality

Rosa Fernández (23rd January)
Jordi Paps (29th January)
2) Orthology inference

Marina Marcet-Houben (24th January)

Pre-calculated orthologs

De novo inference

BLAST
Basic Local Alignment Search Tool

Best reciprocal hits

OrthoFinder 2
SwiftOrtho

Tree-based methods

Whole genome alignment

Syntenic information

Aoife McLysaght (27th January)

Matt Christmas (26th January)

Jacob L Steenwyk (24th January)

Lisa Pokorný (31st January)
3) **Alignment & Trimming**

**Alignment**

- DIALIGN [home]
- PASTA
- BAli---Phy
- MUMMALS
- MASS
- Ω
- W2
- ESPript 3.0
- PROBCONS
- PRANK
- MAFFT version 7

**Trimming**

- trimAl
- BMGE
- Gblocks
- PREQUAL

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Marina Marcet-Houben & Jacob L Steenwyk (23rd January)

Oleksiy M. Kozlov (27th January)
4) Phylogenomic subsampling

At the level of sites

Jacob L Steenwyk (23rd January)
Matt Christmas (26th January)
Antonis Rokas & Jacob L Steenwyk (29th January)

PhyKIT

At the level of genes

genesortR

Lisa Pokorny (31st January)

Oleksiy M. Kozlov (27th January)
5) Supermatrix vs individual genes

Gene tree ≠ species tree

Marina Marcet-Houben (24th January)

Lineage sorting

Gergely Szöllősi (1st February)

Toni Gabaldón (30th January)

Hybridization / Introgression

Concatenation partitioning + vs coalescence

PhyKIT

Jacob L Steenwyk & Karin Steffen (24th January)

Erin Molloy (25th-26th January)

Recombination

Aoife McLysaght (27th January)

Toni Gabaldón (30th January)

Duplication & Loss

Matt Christmas (26th January)

Selection

Toni Gabaldón (30th January)

Oleksiy M. Kozlov (25th January)
Model selection & phylogenetic inference

**Model selection**

- Olivier Gascuel (25th January)
- Jacob L Steenwyk & Karin Steffen (24th January)

**Phylogenetic inference**

- **Maximum Likelihood**
  - RAxML-NG
  - IQ-TREE
  - PhyML
  - FastTree

- **Coalescence**
  - Gene tree summary methods for unrooted trees
    - e.g. BUCKy, NuSet, USTAR, ASTRID, ASTRAL, ASTER, TREE-GRM, wQRM
  - Gene tree summary methods for rooted trees
    - e.g. MDC, STEM, MP-EST
  - Site-based methods
    - e.g. SNAPP, SVDQuartets, CASTER
  - Bayesian co-estimation methods (co-estimate gene trees & species tree)
    - e.g. *BEAST, StarBEAST2
  - Also see methods based on population allele frequencies
    - e.g. PoMo, implemented in RevBayes

- **Bayesian Inference**
  - PhyloBayes
  - BEAST
  - Gytis Dudas (30th January)
  - Edu Ocaña-Pallarès (30th January)
  - Erin Molloy (25th-26th January)
Testing the robustness of your tree

Tree visualization

Support

Olivier Gascuel (25th January)
Erin Molloy (25th-26th January)
Oleksiy M. Kozlov (25th January)
Antonis Rokas & Jacob L Steenwyk (29th January)

Phylogenetic bootstrap support
Ultrafast bootstrap
Transfer bootstrap expectation
GSF (Gene Support Frequency) // gene concordance factor (gCF)
Internode certainty
Tree certainty

... Incongruence

Michał Karlicki & Edu Ocaña-Pallarès (24th January)
Gytis Dudas (30th January)
4) Phylogenomic subsampling

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Repeat N times
8) Post-tree building analyses

Hélène Morlon (26th January)

Matt Christmas (26th January)

Matt Christmas (26th January)

Toni Gabaldon (30th January)

Antonis Rokas (31st January)

Lisa Pokorný (31st January)

Trait evolution

Comparative genomics

Population Genomics

Museomics

Biogeography