

WORKSHOP ON
PHYLOGENOMICS

data

orthology inference

alignment

trimming/masking

analyses

data

WORKSHOP ON GENOMICS

DATABASES (Ensembl, UNIPROT, SRA...)

Download

*DE
NOVO*

Raw reads

Sanitize

Filter

Assemble

Translate

Reduce
redundancy

Predict
genes

gene/protein
sequences

data



orthology inference



alignment



trimming/masking



analyses

- Best reciprocal hits
- Inparanoid
- OrthoMCL
- PorthoMCL
- OrthoFinder
- Tree based predictions

- Use pre-calculated orthology predictions
- Use an existing dataset

data



orthology inference



alignment



trimming/masking



analyses

- PASTA
- Bali-Phy
- MAFFT
- UPP
- Muscle

data



orthology inference



alignment



trimming/masking



analyses

- BMGE
- trimAl
- Gblocks
- Prequal

data



orthology inference



alignment



trimming/masking



analyses

analyses

1:1 orthologs

concatenation

- Manual
- Sequence Matrix
- CONCATENATOR
- catfasta2phymI
- FASconCAT-G
- Phyutility

data matrix

analyses

1:1 orthologs

orthologs and/or paralogs

data matrix

infer individual gene trees

PartitionFinder

partitioning

model selection

- RAxML-NG
- IQ-tree
- ModelTest

analyses

1:1 orthologs



infer multigene
trees

orthologs and/or paralogs



infer individual gene
trees

- RAxML
- IQ-tree
- PhyML
- FastTree
- PhyloBayes
- MCMCTree
- SVDQ

analyses

```
graph TD; analyses[analyses] --> networks[networks]; analyses --> multigene[Infer multigene trees]; analyses --> individual[infer individual gene trees]; networks --- introgression[Introgression/hybridization events]; networks --- tools[SplitsTree, Dendroscope, PhyloNet, ALE];
```

networks

Infer multigene trees

infer individual gene trees

Introgression/hybridization events

- SplitsTree
- Dendroscope
- PhyloNet
- ALE

analyses

1:1 orthologs



infer multigene trees

orthologs and/or paralogs



infer individual gene trees

ancestral state reconstruction

horizontal gene transfer detection

comparative genomics

gene trees/species tree reconciliation

evolutionary relationships

gene family evolution

...

gene duplication/loss

visualization

visualization

- Phylo.IO
- iTOL
- EVOLVIEW
- FigTree
- DensiTree
- TreeGraph2
- ETE3
- jsPhyloSVG
- DiscoVista
- Dendroscope
- SplitsTree
- R (many repositories)

Open Lab questions for further discussion in groups

What kind of **data** I need to answer a specific question?

I don't have **data**

There is not enough reference **data**

Contaminated **data**

...