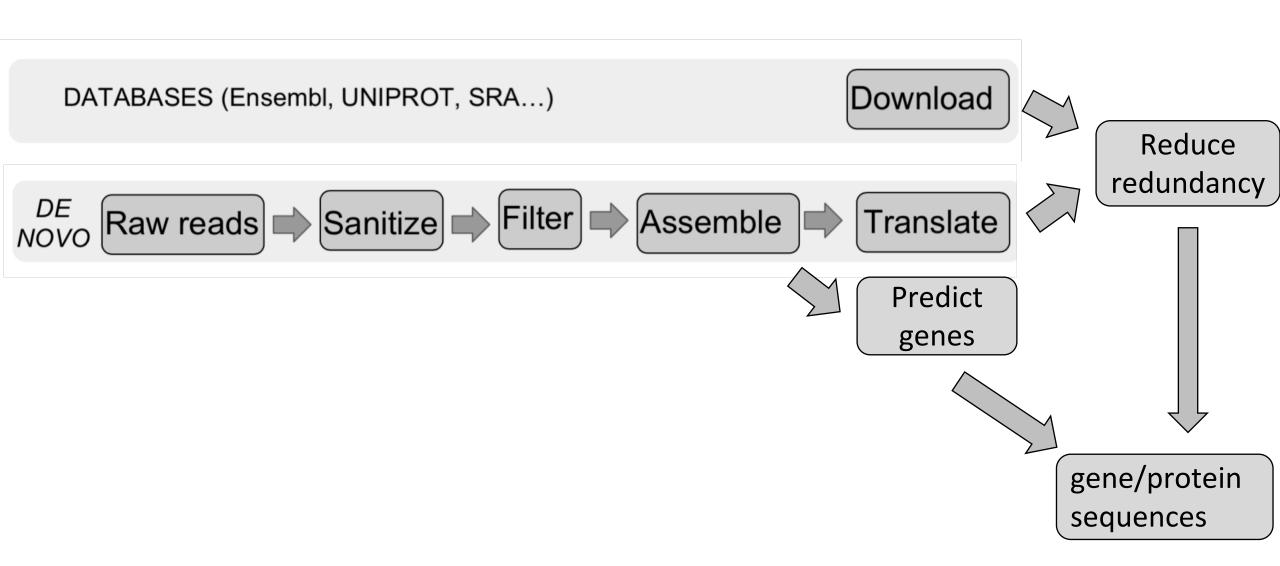


Anna Karnkowska thanks to Rosa Fernández

WORKSHOP ON GENOMICS





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



orthology inference



alignment



trimming/masking



analyses

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



orthology inference



alignment



trimming/masking



analyses

- BMGE
- trimAl
- Gblocks
- Prequal

data orthology inference alignment trimming/masking analyses

1:1 orthologs



concatenation

- Manual
- Sequence Matrix
- CONCATENATOR
- catfasta2phyml
- FASconCAT-G
- Phyutility



data matrix

1:1 orthologs

1

orthologs and/or paralogs

data matrix

infer individual gene trees



PartitionFinder

partitioning



model selection

- RAxML-NG
- IQ-tree
- ModelTest

1:1 orthologs



infer multigene trees



orthologs and/or paralogs

infer individual gene trees

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





networks

Infer multigene trees

infer individual gene trees

Introgression/hybridization events

- SplitsTree
- Dendroscope
- PhyloNet
- ALE

1:1 orthologs



orthologs and/or paralogs

infer multigene trees

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

. . .