## Interpreting/annotating gene phylogenies. Beyond intro bioinformatics.

- Species phylogeny
- <u>Timing duplications, outparalogs/inparalogs</u>
- <u>Whole genome duplications</u>
- <u>Duplications in FECA-2-LECA, endosymbiosis &</u> <u>HGT</u>

# Given problems with single gene trees where does the species tree comes from?

- Noisiness of gene trees necessitates use of species tree guided gene tree construction as e.g. TREEBEST as used by ENSEMBL
- Wait a second? If gene trees are often wrong, how do we know the species tree?
- Trees based on massive amounts of data: concatenated alignments, multi locus trees





## So why are gene trees often wrong?

- Too little data (too short alignments) for events that happened a long time ago, i.e. lack of resolution
- So how do we normally solve that for the *tree* of life, e.g. the *C. elegans / D. melanogaster* /human relations?

## Concatenating genes / multimarker and very strict data selection







### You can not always point to a tree while writing or talking so terminology: inparalogs & outparalogs

- Outparalogs duplicated **before** the speciation of the two species between which you define orthologs
- Inparalogs duplicated after the speciation of the two species between which you define orthologs
- orthologs, inparalogs and outparalogs are ±shorthand to discuss for a set of proteins how they are related / when they duplicated



#### inparalogs, outparalogs relative to speciation worm-human









#### Timing Duplications to FECA-2-LECA, e.g. tubulin "Candidatus Nitrosoarchaeum koreensis MY1" [339520150] artubulins Thaumarchaeota archaeon N4 [851357707] 81 "Candidatus Nitrosoarchaeum limnia SFB1" [329138201] dinarchaeote RP\_19 [KX764884] 100 Odinarchaeote LCB\_4 [OdinLCB4\_01330] silon tubulin 100 78 ryptic tubulin 100 Pol-B2 arCOG00329 Ita tubulin 100 bacterial tubulin B 100 cterial tubulin A gamma tubulin 41 100 alpha tubulin 63 100 beta tubulin 0.7







