**Phylogenetic trees**

* **Newick Format**
  + **(((A,B),C),(D,E)),F;**
  + **((B:0.2,(C:0.3,D:0.4)E:0.5)F:0.1)A;**
  + **(NP\_0095521:0.22,XP\_6415871:1.90,((AAN599741h:0.08,NP\_0010059:0.01):0.02704875,(NP\_0010273:0.06,(NP\_1755171:0.44,NP\_0012637:0.17):0.090):0.05):0.29);**

**Phylogenetic tree generators**

**All phylogenetics trees start with MSA.**

* **Simple Phylogeny (**[**https://www.ebi.ac.uk/jdispatcher/phylogeny/simple\_phylogeny**](https://www.ebi.ac.uk/jdispatcher/phylogeny/simple_phylogeny)**)**
  + **UPGMA and Neighbor-joining**
  + **Nicely integrated with EBI MSA tools**
  + **Not a lot of parameters (substitution model)**
  + **No boot strapping**
  + **DNA and Protein sequeunces**
* **PhyML (**[**https://toolkit.tuebingen.mpg.de/tools/phyml**](https://toolkit.tuebingen.mpg.de/tools/phyml)**)**
  + **Neighbor joining (Unrooted)**
  + **“Slower” but more accurate**
  + **Different substitution matrixes available**

**Phylogenetic tree viewers**

* **Treedyn (**[**http://www.phylogeny.fr/one\_task.cgi?task\_type=treedyn**](http://www.phylogeny.fr/one_task.cgi?task_type=treedyn)**)**
  + **Automatic rooting for Mid-point**
  + **Visualisation of unrooted trees possible**
  + **Tree editing possible (re-rooting)**
* **Itols (**[**https://itol.embl.de/**](https://itol.embl.de/)**)**