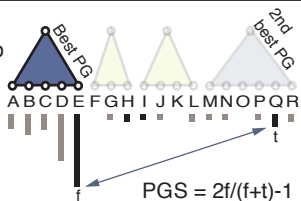


**Load the RASE database**

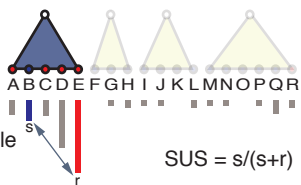


**Read next nanopore read**

**Predict strain and phylogroup**



**Predict susceptibility**



**Predict and report**

**Update weights**

**Match against the database**

**ProPhyle**

