# For every DNA read in a metagenomics sample
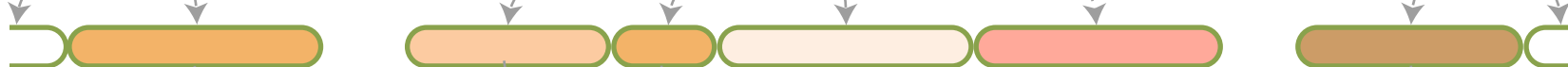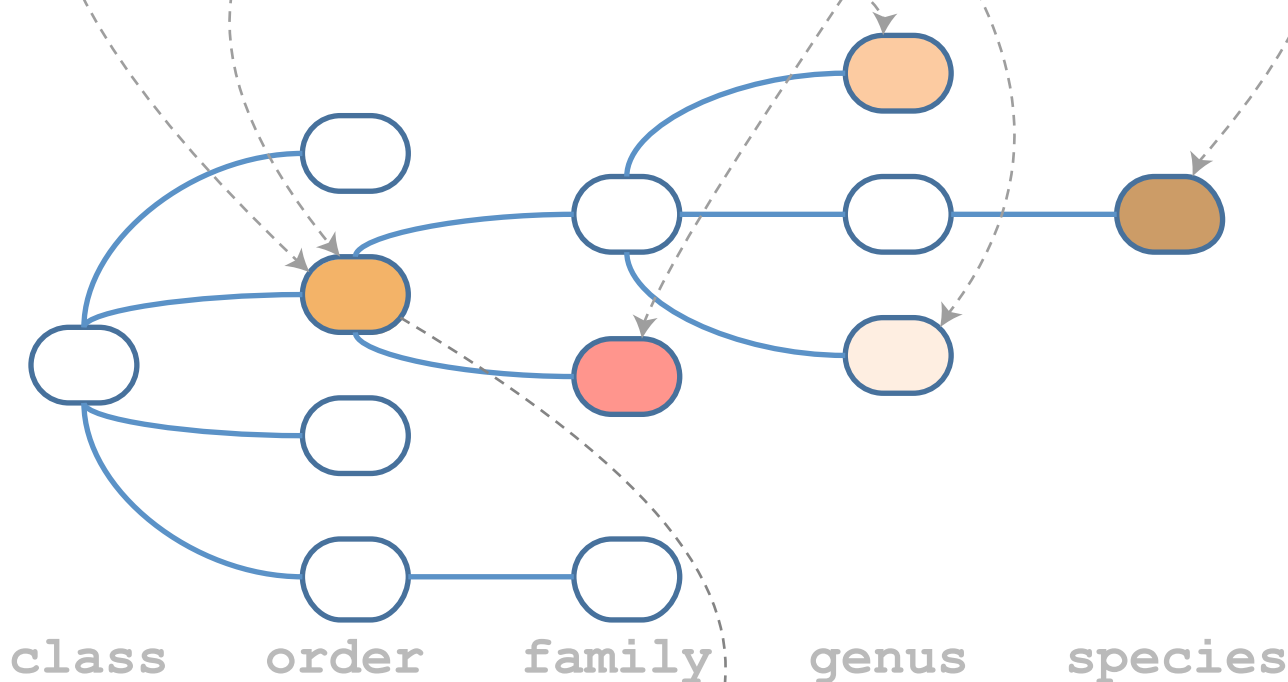


**Find genes with FragGeneScan and convert these into proteins**

**Split proteins into tryptic peptides**

**Calculate the taxonomic LCA for every peptide**

class    order    family    genus    species

**Aggregate resulting LCAs with novel LCA\* approach**

class    order    family    genus    species