Zeitplan GOBI:

02.04.2024 Abgabe und Schlusspräsentation

Schritte zum Arbeitsplan:

1: Pick gene for Drosophila (or from other insects) -> search genome (we picked yellow-E-3)
-> use Google Scholar, NCBI, Datasets in UNiprot (only reviewed)

- maybe look into: blood consumption, phytophagia (eat plants), parasitsm, Mykophagia,
pollynation), gustatory receptors, chemosensory receptors, opsisns, caterpillar venom?)

2: find orthology in other insect of the nearby clades (look at page 1 for insect evolution)
(gene duplication theory + tandem inversed duplication) -> use timetree.org!!

-(page 4: 1. find gene 2. look at boundaring genes 3. compare with other animals
4. compare ortholog to ortholog!!(in different lines) + look at exons)

-not all duplicates of proteins have same probability, use fracture, duplication not= same function

-do not look at names of proteins, often don't tell anything about similarity

-find multi-gene-families or unique genes

3: extract sequences and translate?

4: Use Uniprot to create homology

5: create phylogenetic tree + do comparative genomics:

6: use protein language models/function analysis

- Pick a gene in *Drosophila* (of protein)

- Find it in *Drosophila* genome

- Find its orthologs in the genomes of other insects

- Extract and translate the sequences

- Use UniProt to locate their more distinct homologues

- Do comparative genomics and phylogenetics study

- Do protein language model/structure/function analysis

- Present in a form of a scientific paper

- Defend as a 15m talk

Tools (not sure what it sould be used for:)

- compare genes within species: Genomicus (not for insects?)

- to find conservated regions in different organisms: Cinteny

- to visualize syntenic regions from ortholog genes, compute similarity: Synima

- visualize synteny: mySyntenyPortal

- calculate similarity +analyze + for proteins(?) -> Genespace