
Protein Prediction 2

Exercise
Team 6
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Previously

- Parse whole HPO database into HpoTree structure
- Create annotation map (sequence-id → list of terms)
- Extract full path for each annotation from tree
- *gethpo.py <uniprot-id>*
 - ✓ List of annotations
 - ✓ Path of each annotation

New

- Merge multiple paths into a tree
- Frequency counter for each term
- *gethpo.py* <uniprot-id>
 - ✓ List of annotations
 - ✓ Path of each annotation
 - ✓ Combined tree with term frequency

DEMO
