BioUSeR

Requirements

- Retrieve gene sequence
- Sequence similarity search given a protein sequence
- Predict gene structure
- Align protein sequences

Normalized Tasks

- Build phylogenetic trees
  - Input: sequence alignment
  - Output: phylogenetic tree
  - Method:
  - Species:
  - Disease:
  - Annotations
    - Build
    - Phylogenetic
    - Phylogenetic tree
  - Show ancestors Show descendants

Service

INB: www.bioinfo.uma.es:runCreateTreeFromClustalw

- Analyze domains given a protein sequence