

Evolutionary and Structural Analysis of Pathogen Proteins.

Final year UG project 2024-25
2024-11-03 (Week 7)

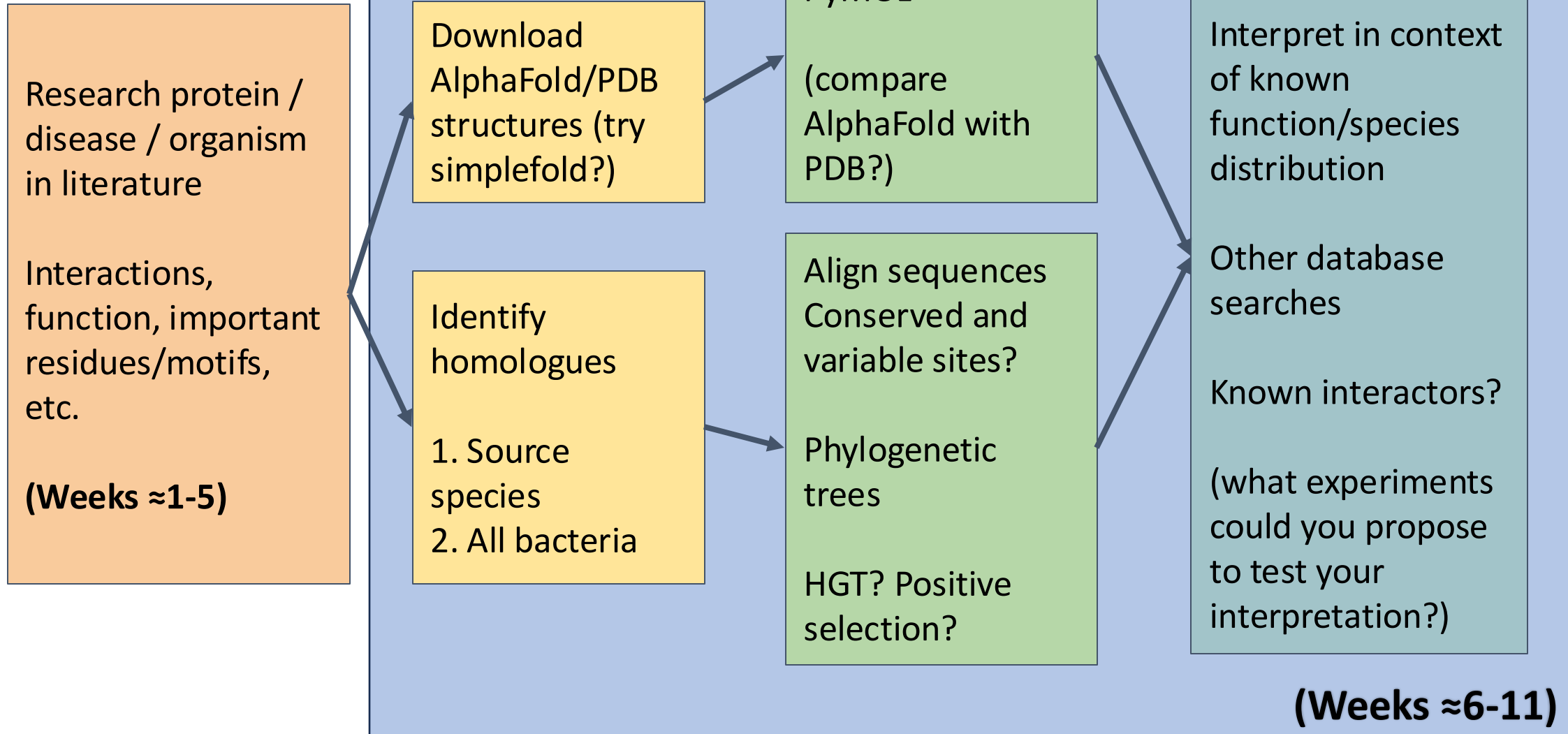
Candidate proteins – start points

Any changes needed?

Organism	Host	Gene/Protein	PHI accession	Student
<i>Escherichia coli</i>	<i>Homo sapiens</i>	<i>espY</i>	PHI:8647	LB
<i>Shigella flexneri</i>	<i>Homo sapiens</i>	<i>ipaI</i>	PHI:9253	LT
<i>Candida albicans</i>	<i>Mus musculus</i>	<i>sap6</i>	PHI:10193	IM
<i>Pseudomonas aeruginosa</i>	<i>Homo sapiens</i>	<i>tplE</i>	PHI:6646	AE
<i>Vibrio vulnificus</i>	<i>Mus musculus</i>	<i>vvhA</i>	PHI:6877	JT

<http://www.phi-base.org/>

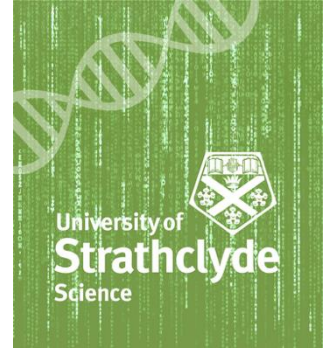
Workflow



Your questions/comments/issues

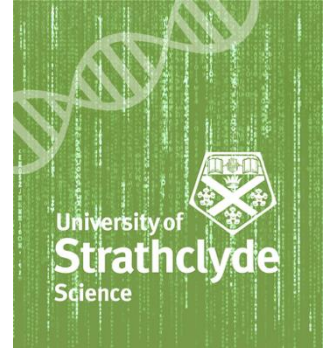
(What would you like to talk about?)

Points for discussion?



- What would you like to cover?
- **Keep investigating your protein**
- Make a tree for your sequences
 - How does the tree look?
 - Are organisms/species grouped together how you'd expect? Any surprises?
 - Is there evidence supporting gene duplication (two clades, with the same organisms repeated)?
 - Is there evidence supporting horizontal gene transfer (organism in the "wrong" clade)?
- Compare to sequence data
 - Do patterns of sequence variation map onto your tree?
- Galaxy workflow or scripting?
 - Have you created a workflow for your analysis: alignment? making a tree?
 - Have you noted/saved the tool versions/parameter settings for writing your thesis?

Thursday Seminar



- Kimberly Kline (University of Geneva)
- “Exploring microbe-host interactions in Enterococcal biofilms”
- 2pm, HW111-114
- (HW613 if you want to talk to her immediately after the seminar)
 - “Bacterial Adhesins in Host-Microbe Interactions” [https://www.cell.com/cell-host-microbe/fulltext/S1931-3128\(09\)00178-4](https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(09)00178-4)
 - “A tale of two pili: assembly and function of pili in bacteria” [https://www.cell.com/trends/microbiology/fulltext/S0966-842X\(10\)00040-5?code\u003dcell-site=](https://www.cell.com/trends/microbiology/fulltext/S0966-842X(10)00040-5?code\u003dcell-site=)
 - “Gram-Positive Uropathogens, Polymicrobial Urinary Tract Infection, and the Emerging Microbiota of the Urinary Tract” <https://doi.org/10.1128/9781555817404.ch19>

Next Week's Group Meeting
Monday 10th November 13:30 HW324

Useful Links

Useful tools (many others are available)

GalaxyEU: <https://usegalaxy.eu/>

- Sequence alignment (e.g. MAFFT), phylogenetics (e.g. RaxML), positive selection (e.g. codeML)

iTOL: <https://itol.embl.de/>

- Visualisation/annotation of phylogenetic trees

PyMOL: <https://pymol.org/2/> and/or ChimeraX: <https://www.cgl.ucsf.edu/chimerax/>

- Protein structure visualisation/annotation

Jalview: <http://www.jalview.org/>

- Visualisation of multiple sequence alignments

Useful sites/databases

PHI-base: <http://www.phi-base.org/>

- Proteins involved in host-pathogen interactions, with linked evidence

EMBL AlphaFold: <https://www.alphafold.ebi.ac.uk/>

- AlphaFold predictions for proteins from model organisms

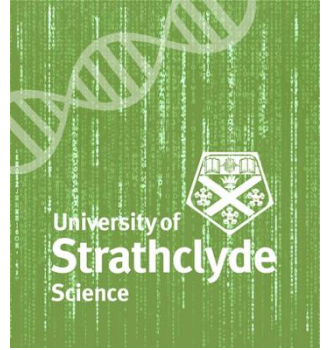
UniProt: <https://www.uniprot.org/>

- Protein sequence (including homologous sequences) and functional information with evidence

RCSB/PDB: <https://www.rcsb.org/>

- Repository of record for protein structures

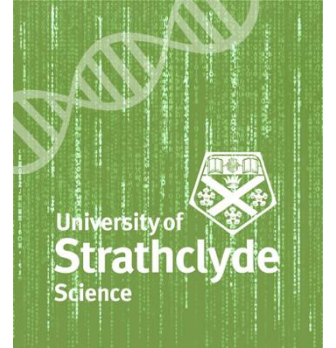
SIPBS CompBiol Sites



- BM432 Project Pages
 - <https://sipbs-compbiol.github.io/bm432-project/>
- An incomplete little book of bioinformatics
 - <https://sipbs-compbiol.github.io/little-bioinformatics-book/>

Project Management Tools

You may want tools to...



- Manage your time
 - E.g. Pomodoro technique (e.g. BeFocused, [Pomofocus](#), [Forest](#))
- Schedule work
 - Reminders (macOS, MS Office)
 - Calendar (macOS, MS Office), with email alerts
 - [Trello](#), [Asana](#), etc.
- Manage your project data and information effectively
 - [How to name files](#)
 - [Project management guidelines](#) (BM432, 2022-23 session; me and Dr Feeney)
 - [How to keep a lab notebook](#)
 - Keeping a computational biology lab notebook:
<https://doi.org/10.1371/journal.pcbi.1004385>
 - [Organising a lab book](#)