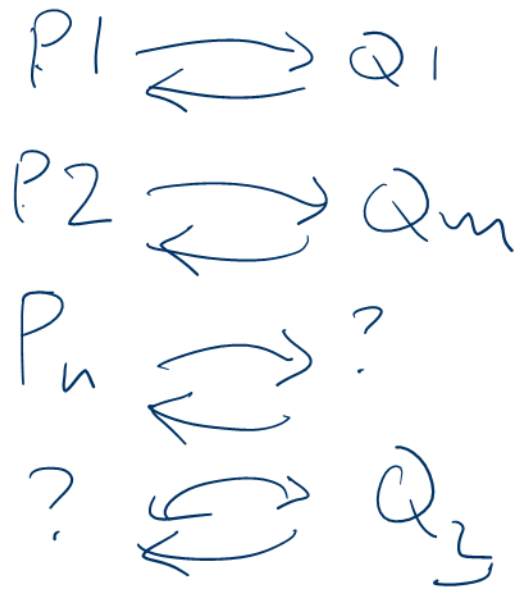
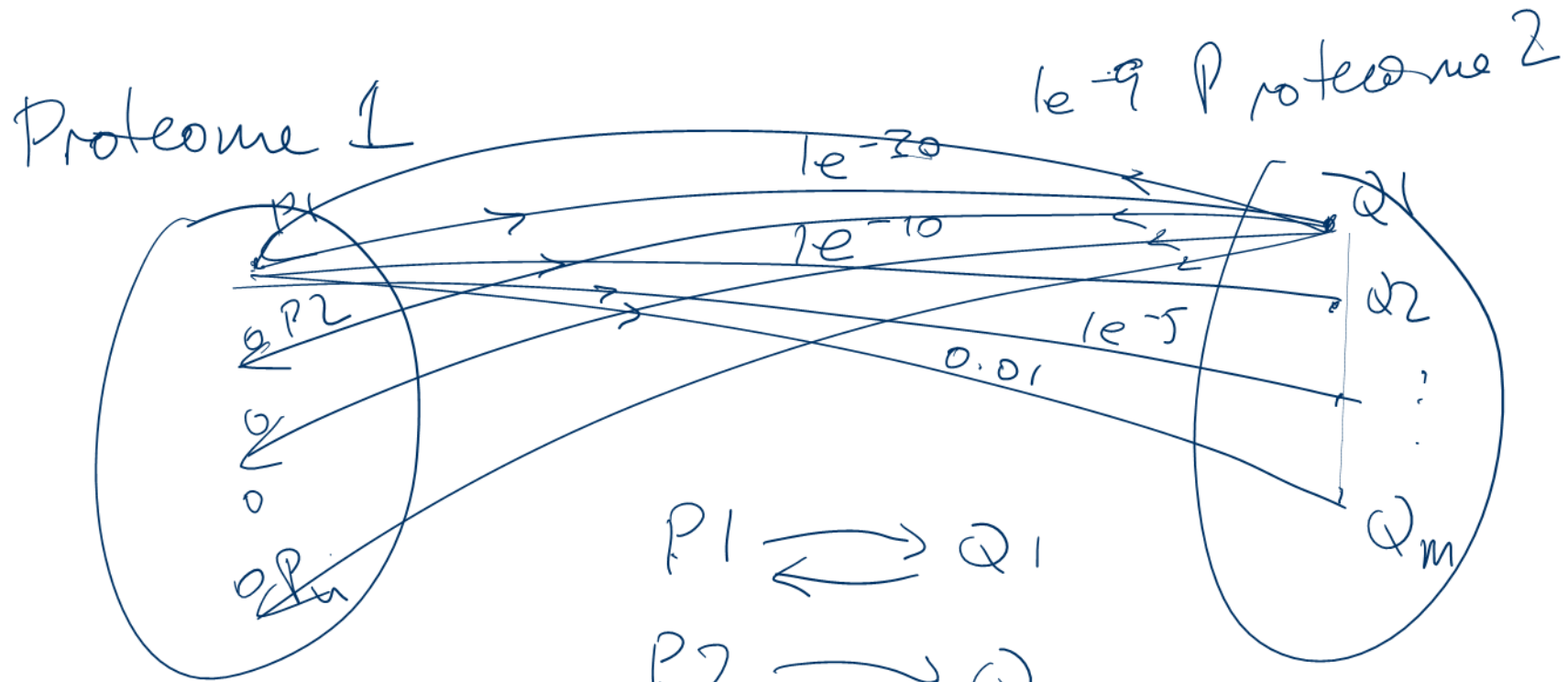


Class Project: Blast Database

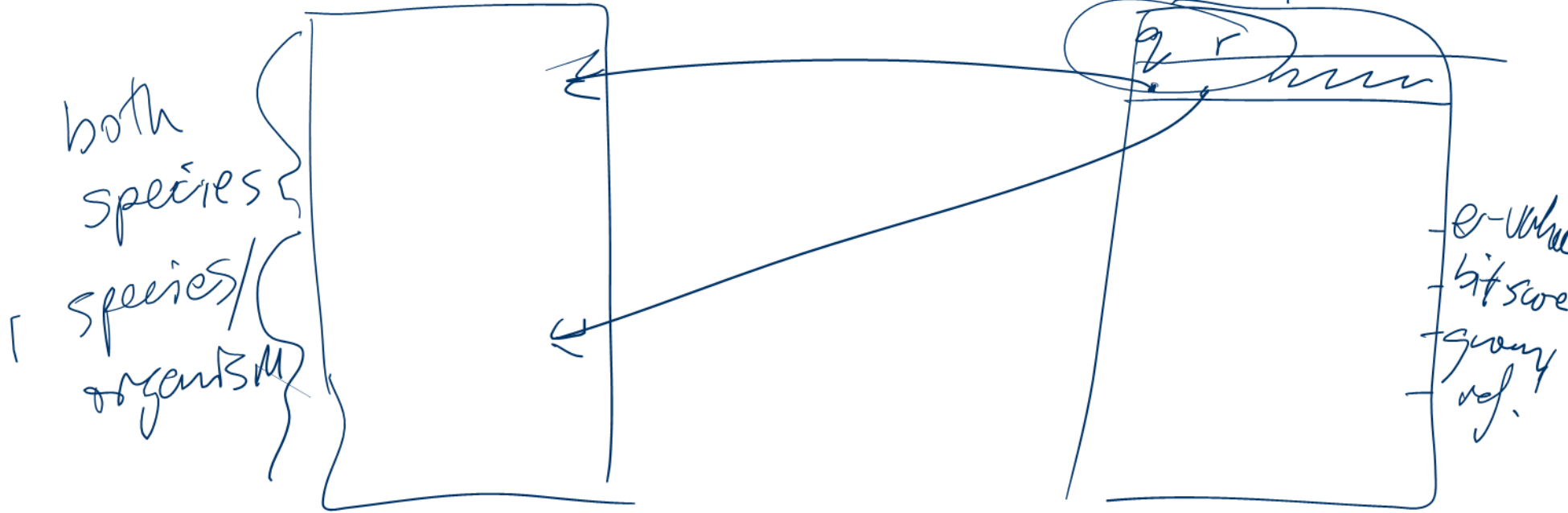


1. Write a program that computes all pairwise blast alignments for two species' proteomes and stores the alignments in a relational database.
2. Write a program that retrieves the blast alignment for two proteins (specified by their accessions) from the relational database.
3. Write a program that finds pairs of orthologous proteins that are mutually best hits in the species' proteomes.



Protein

Alignment

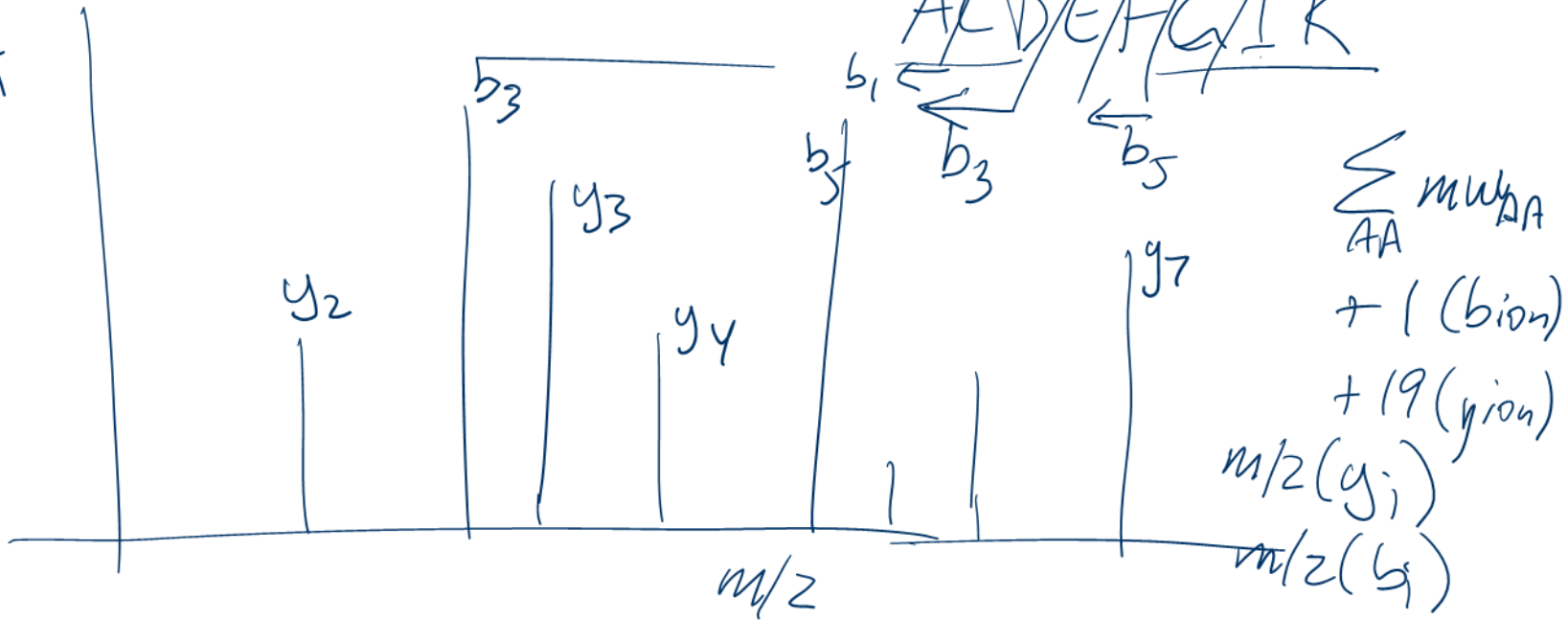


Class Project: MS/MS Viewer



- Write a program to display peptide fragmentation spectra from an mzXML file.
 - The program will take an mzXML file, a scan number, and a peptide sequence as input.
 - The peptide's b-ion and y-ion m/z values should be computed, and peaks matching these m/z values annotated with appropriate labels.
 - The output figure/plot should aid the user in determining whether or not the peptide is a good match to the spectrum.

int



Class Project: Protein Digest



- Write a simple web-server application using TurboGears to carry out an *in silico* enzymatic digest of a user-provided protein sequence.
 - Users should be able to specify min and max length, min and max molecular weight, # of missed cleavages, and specific enzyme.
 - Output should be a table of peptides, with their length, molecular weight, # of missed cleavages, and amino-acids to left and right of each peptide in the protein sequence.

ACDEFK/ACDEFR/PACDEFR/ACDEF

Trypsin: KR, except if followed by P
C-terminus to

- ACDEFK . A

K . ACDEFR PACDEFR . A

R . ACDEF . -

- ACDEFK ACDEFR PACDEFR . A 1

R . ACDEFR PACDEFR ACDEF . - 1

0 MW = $\sum_{AA} MW_{AA}$
+ 18

missed
cleavages

≤ 1

