MCB 5472 Assignment #7:
Multiple sequence alignment
March 5, 2014

Remember:

- Assignment #6 is due before next Wednesday's class
  - Worth 20 marks (not on assignment, sorry!)
- In addition to today's (short) assignment

Today

- Using the sequences on the website:
  - Create multiple sequence alignments using MUSCLE, MAFFT, and PRANK
  - Compare these to each other and the reference alignment also on the website

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- Based on 3D structural superimpositions that were manually adjusted to ensure proper alignment
- The data file on the website is "BB12043", containing 34 proteins sequences each having 20-40% sequence identity to each other
  - To discuss in 1 hour: what affect does this have?
  - NOTE: no benchmark is perfect, and one can certainly argue that there are flaws in this one!

Alignment commands

- MUSCLE:

```
>muscle –in [input_file] –out [output_file]
```

- MAFFT:

```
>mafft --auto [input_file] > [output_file]
```

- PRANK:

```
>prank –d=[input_file] –o=[output_file]
```

Sequence viewers

- MEGA6 (Windows, Mac): http://www.megasoftware.net/
- Jalview (all platforms): http://www.jalview.org/Web_Installers/install.htm
- Seaview (all platforms): http://doua.prabi.fr/software/seaview