Methods – General

To address the two broad questions of this thesis – the evolution of vision and the evolution of chemokine signalling – I used bioinformatic approaches. Although the exact methods used for each chapters are specific, they share some general communalities.

In this chapter, I will cover the main steps that were common for all results chapters, describing how the techniques/tools used work. However, further details of how these techniques/tools were used are described more precisely in each respective chapters.

Two broad categories of methods were used in this thesis: molecular phylogenetic analyses; and single-cell RNA sequencing analyses.

Molecular phylogenetic analyses

* Data mining
* Gene tree construction
* Etc

Single-cell analyses