Neat from scratch review 19/04/2022

**Genetics**

* A redundancy with storing NodeGenes and ConnectionGenes twice, once in node\_pool & conn\_pool and once in each Genome. This can be reduced to only storing these genes in their respectives pools in the Neat class, and storing references to their hashcodes in genomes, with their weights. This would need a new class, e.g. NodeGeneRef which holds a hashcode a weight and an ‘enabled’ bool.
* VecSet is a mess and needs to be minimalised.

**Population**

* Fields are a bit of a mess. Would like to separate data from functional fields.
* Champion should be a g\_id