

**Presentation title:** *De novo* assembly of next generation sequence data

**Date:** Monday 4 July 2011

**Abstract**

*De novo* assembly is the process of reconstructing a genomic DNA sequence using only a set of much shorter error-prone sequences (reads) sampled from the genome. A good metaphor is to take a newspaper, make fifty photocopies, shred them all, and then try to reconstruct the original newspaper - somewhat challenging. This presentation will discuss the principles of and approaches to *de novo* assembly of genomic and transcriptomic data from the current NGS platforms (Illumina, SOLiD, 454, IonTorrent). Practical Issues of computational and memory requirements, assembly terminology, naming and file formats, available software, and an example run-through of an assembly using the Velvet software will also be covered.