* Bionano4 solve is a list of command line tools that analyse output from proprietary optical mapping machines e.g. Saphyr and Irys developed by Bionano Genomics.
* Datasets for Bionano Access may be able to work for solve. Access is just GUI based but results visualisation might not work.
* Sample test data might be available from bionano access’s structural variation section since structural variation calling is part of the assembly pipeline.
* Source of bionano download: <https://bionanogenomics.com/support/software-downloads/>
* Most relevant tools are:
* Pipeline for de novo assembly
* RefAligner for alignment
* UTIL shell scripts to run de novo assembly scripts.
* cohortQC which produce MQR, a summary dataset of alignment to cmap reference.
* RefGenome containing human reference sequence in cmap files

Background scientific knowledge:

* **You have a wealth of information in BS2040 Bioinformatics Week2 Lecture 5 Eukaryotic genomes to comparative genomics. All you need is Week2 lecture 4 and lecture 5.**
* **The key is to find synteny (conserved genes) between fusarium decemcellulares and…**