Bioinformatics- Genomic Argentina (20 - 30 students)

Necessary resources:

* 1 laptop per student (MAC or Windows). Students with Windows should install the Putty program.
* Internet connection to work online as well as to download sequences.
* Access to Beocat? Tupac-Conicet? Required programs will be installed in the cluster used.
* Illumina reads to work with (genome to assembling).

Schedule

Day 1.

Introduction to NGS technologies. Introduction to Bioinformatics. Text editors usually employed in Bioinformatics. Unix: generalizations and utilities applied to Bioinformatics. R software: useful graphical functions in Bioinformatics.

Day 2.

Illumina technology: generation of DNA fragments to several analyses: a) Molecular markers SNPs and INDELs in population genomics. Galaxy Platform. Data processing: Fastq files, interpretation. Quality. Alignments with reference genomes and generation of BAM files. Software: HaplotypeCaller - GATK. IGViewer. Phylogenies.

Day 3.

Illumina technology: generation of DNA fragments to several analyses: b) Assembling of fungal genomes. Data processing: Fastq files, interpretation. Quality. SAM tools. Software: DiscovarDenovo. Calculation of coverage. IGViewer.

Day 4.

Case study:

1. Assembling of some fungal genome (our Fs/Ft?). Study of useful parameters of quality. Basic notions on genomic annotations.
2. Cluster de genes en hongos. Generation of data (NCBI downloading), alignments, cluster location in different species, alignments visualization.
3. Population genomics: PCA using SNPs generated with HaplotypeCaller.