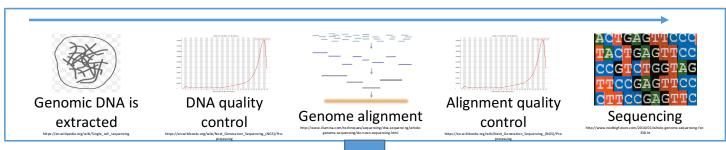
WHOLE GENOME RESEQUNCING REVEALS POPULATION HISTORY

Just as the Human Genome Project seeks to understand the physical and functional structure of the human genome, scientists are looking at the genomes of all types of organisms to get a better understanding of the evolutionary processes that made them who they are. How is this done?

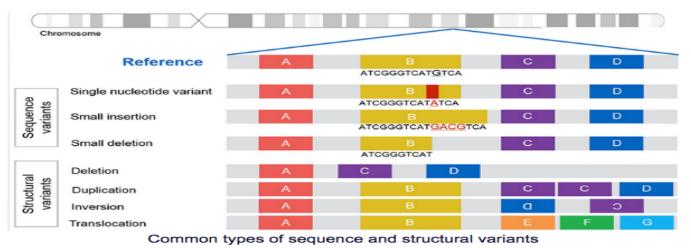
DNA Processing and Quality Control



Variant Identification



Variants of different types are identified by comparing the DNA from the samples to a reference genome.

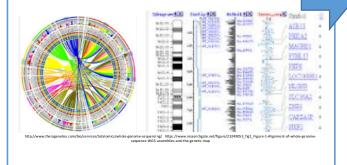


http://www.labspaces.net/blog/1627/When_Whole_Genome_Sequencing_Doesn___t_Give_Us_the_Whole_Genome

Population Genetics and Molecular Evolution

Whole genome variants between and among the reference genome and samples uncover patterns of genetic diversity.

All this data is run through bioinformatics approaches which can generate data such as genetic distance matrices, population estimates and functional predictions.



These patterns along with detailed historical data like climate changes or migration reveal the population history of a species, such as a small parasite *Schistacephalus mansoni*, shown here.

