# Hierarchical Genome Assembly Process

SMRT Analysis:

Features Hierarchical Genome Assembly Process (HGAP) to generate high-quality *de novo* assemblies of genomes, using Single Molecule, Real-Time (SMRT) Sequencing data. HGAP is:

- An easy-to-use assembler accessible via the SMRT Link graphical user interface that performs both *de novo* assembly and polishing of resulting contigs

- Best suited for genomes ≤3 Gb, with low heterozygosity or routine assemblies with established parameters

How it Works: HGAP and polishing are the essential components of assembling SMRT Sequencing data.
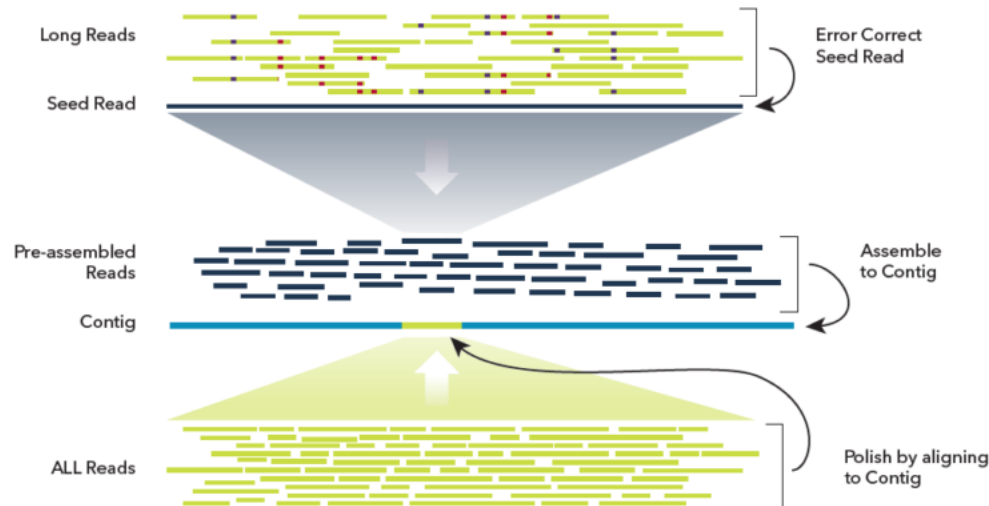
Original Publication: Chin, C.-S., et al. (2013) Nonhybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nature Methods, 10(6), 563–569.