

# **GENOME SEQUENCING TECHNOLOGY AND ALGORITHMS**

**Margret Antonson**

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Our intention is not to provide a comprehensive review of sequencing technology , assembly algorithms or downstream downstream analyses.

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After the initial assembly, contigs are typically joined to form longer stretches of sequence known as scaffolds. Computational reconstruction of a longer sequence from smaller sequence reads.

Even correctly assembled sequences can lead to best hits from distantly related species. If captive animals are available, such samples can often be utilized as a source of high-quality DNA, but note that genomic variation identified from such sources may not be representative of wild populations. Cloud Computing for Science [http:](http://) Despite the considerable challenge to annotate genes in newly sequenced species where preexisting gene models are mostly lacking, automated gene annotation has in principle become possible for individual research groups Yandell and Ence

Mardis From conservation genetics to conservation genomics. Reference-guided assembly of four diverse Arabidopsis thaliana genomes.