



Next Gen Sequencing for Strain Development

Commercializing Industrial Biotechnology Panel on Strain Development

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Strain Development with Next Gen Sequencing

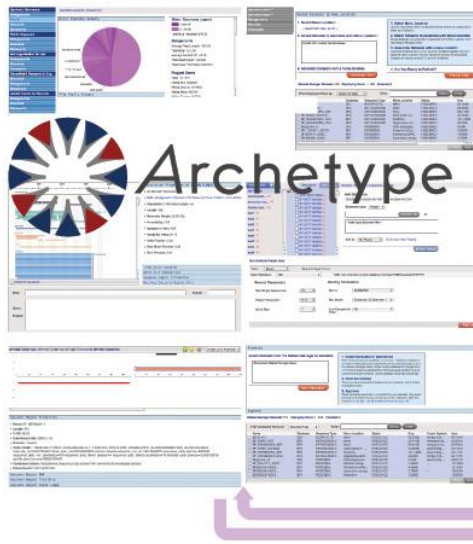
Advanced Technologies have accelerated the rate of Strain Development over the past three years.

- Next Gen Sequencing
- Transcriptomics et al.
- DNA synthesis
- A Platform that integrate the Analyses has been particularly useful.

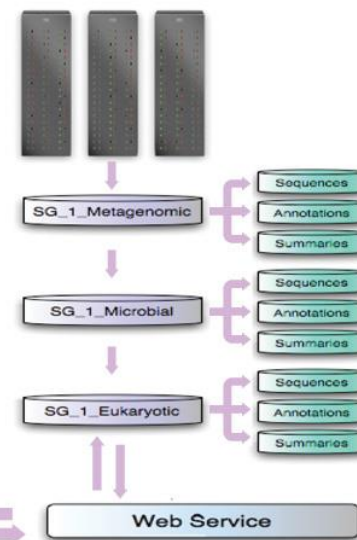
Synthetic Genomics Discovery & Design Software: Archetype®

- Powerful tertiary analysis tool that automatically annotates all sequence information and provides a web UI for scientists to mine information.
- Users can store, annotate and mine 1000s of genomic sequences of all different types (prokaryotic and eukaryotic genomes) using automated pipelines.
- Design software enables rapid synthesis of 1000s of genes or pathways.

Comprehensive User Interface



Scalable Data Model



Usage

- Metagenomes
- Microbial genomes
- Public genomes
- Eukaryotic genomes

Capabilities

- Automated gene annotation
- Comparative genomics
- cDNA annotation
- Pathway mining
- Automated 16s/18s analysis
- Gene assembly design

Next Gen Sequencing

In House Sequencing	
NextSeq/HiSeq/MiSeq	PacBio
Short Reads,	Long Reads, single molecule
Biocatalyst Discovery Transcriptomics (RNASeq) Resequencing (inserts, deletions, SNPs) Gapped Genomes	Metabolic Engineering Complete Genomes

- **Automated Annotation**
 - Gene calling with cDNA guidance.
 - Suggested compartmentalization.
 - Supported metabolic pathways
 - Contract optical maps
 - Manual curation as required.
- **Resequencing Alignments**

Transcriptomes

RNASeq: Map onto annotated genome sequence and/or Metabolic Model

- Supports gene calling
- Identify gene networks by inference
- Identify successful and unanticipated results of metabolic engineering.
- Automated pipeline from raw data
 - summary tables of expression estimates
 - differential expression

DNA Synthesis

- Automated design and ordering for Gibson Assembly.
 - Oligo optimization of efficient assembly
 - Codon optimization
- Very large genes & operons
 - Rapid turn around on most genes
 - Routine delivery of large constructs
 - Speed cycles with slow growing hosts.
 - Projects of 0.5 to 1.0 Mb.
- Assemble chromosome in yeast...
 - Transplantation to each host is an issue.