PURDUE UNIVERSITY Discovery Park

Bioinformatics Core

PURDUE UNIVERSITY Agricultural Research and Graduate Education

Vision

The vision of the Bioinformatics Core is to facilitate, amplify, and accelerate biological research and discovery through application of bioinformatics. It will do so by delivering high quality analysis in a timely and economical manner. It will be responsive to customer needs and evolve with advances in the field. It will actively engage in and seek out opportunities to advance the educational mission of the University.

Team

Jyothi Thimmapuram, Ph.D.
Bioinformatics Core Director
jyothit@purdue.edu

Shaojun Xie, Ph.D.
Assistant Core Director
xie186@purdue.edu

Ketaki Bhide, M.S.
Bioinformatics Data Analyst
bhide@purdue.edu

Contact:
bioinformatics@purdue.edu

Website:
www.bioinformatics.purdue.edu

Mailing list:
https://lists.purdue.edu/mailman/listinfo/bioinformatics-core

Wiki page:
https://wiki.itap.purdue.edu/display/BioCoreFacility/Home

Epigenetics

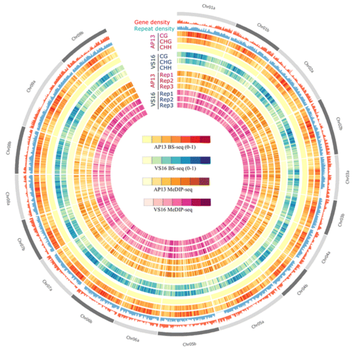
Histone modifications - identification of histone marks in the genome using ChIP-seq data

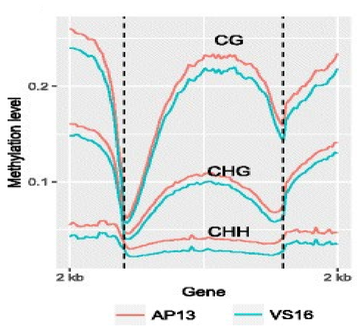
ChIP-seq – identification of genome-wide DNA binding regions for transcription factors and other proteins

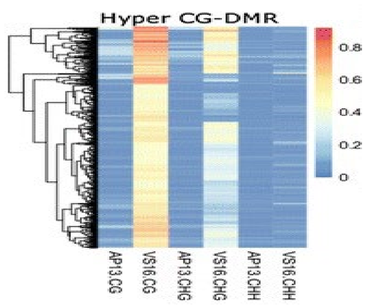
MNase-seq - identification of location of various regulatory regions in the genome.

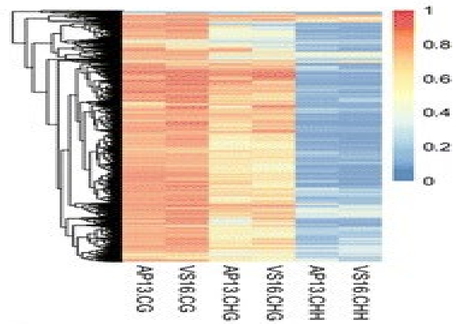
MeDIP-Seq - identification of methylated regions and differentially methylated regions (DMR) between samples.

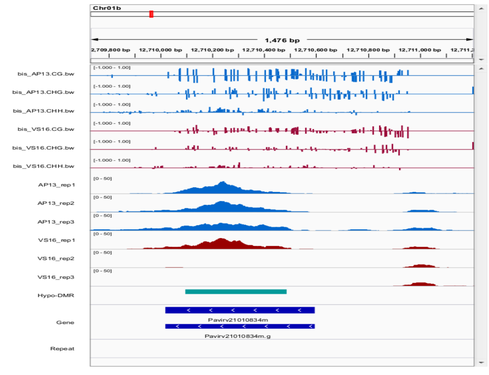
Bisulfite Sequencing- generation of single-base resolution of DNA methylome and identification of DMRs and integration of DMRs with transcriptome data.











Dworkin et al., 2017

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Transcriptome Analysis

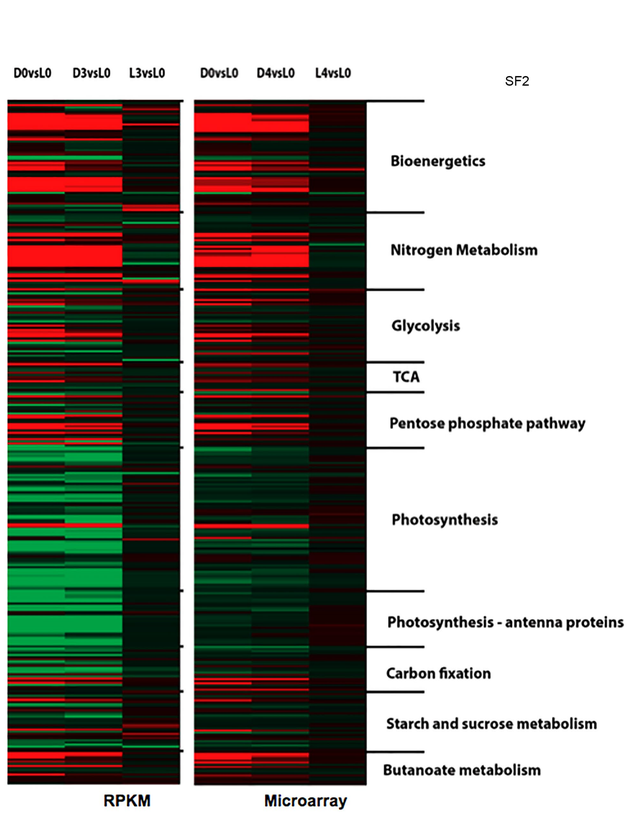
RNA-Seq - quantification of known genes and identification of statistically significant differentially expressed genes.

scRNA-Seq –identification and interpretation of sources of heterogeneity from single-cell transcriptomic measurements,

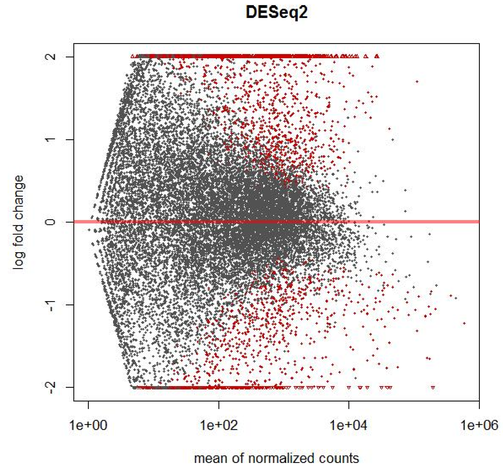
miRNA - identification of novel miRNAs, quantification of known/novel miRNAs and differentially expressed miRNAs.

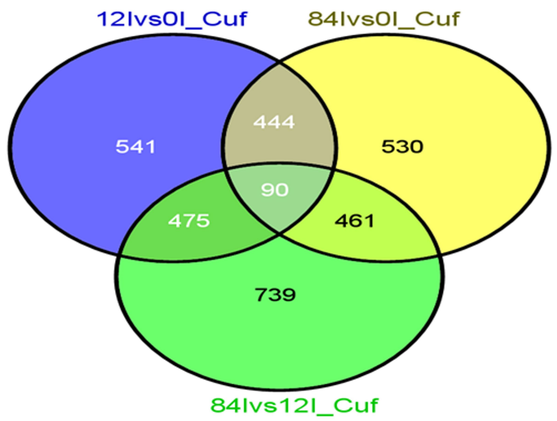
lncRNA - identification of novel ncRNAs, quantification of known/novel ncRNAs and differentially expressed ncRNAs .

Microarray - identification of statistically significant differentially expressed genes hybridized on microarray.

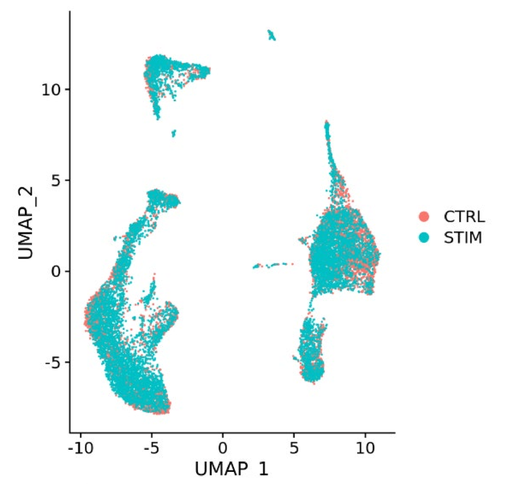


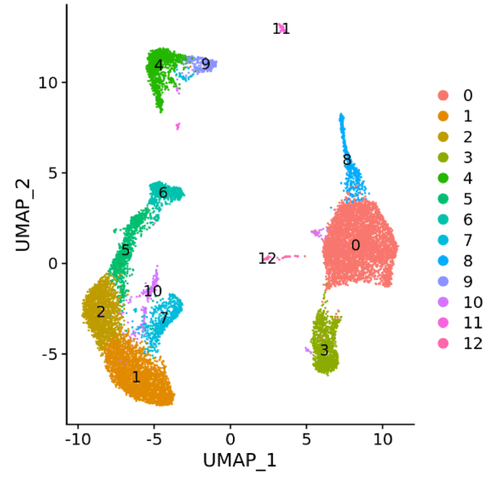
Welkie et al., 2014





Ayyappan et al., 2015

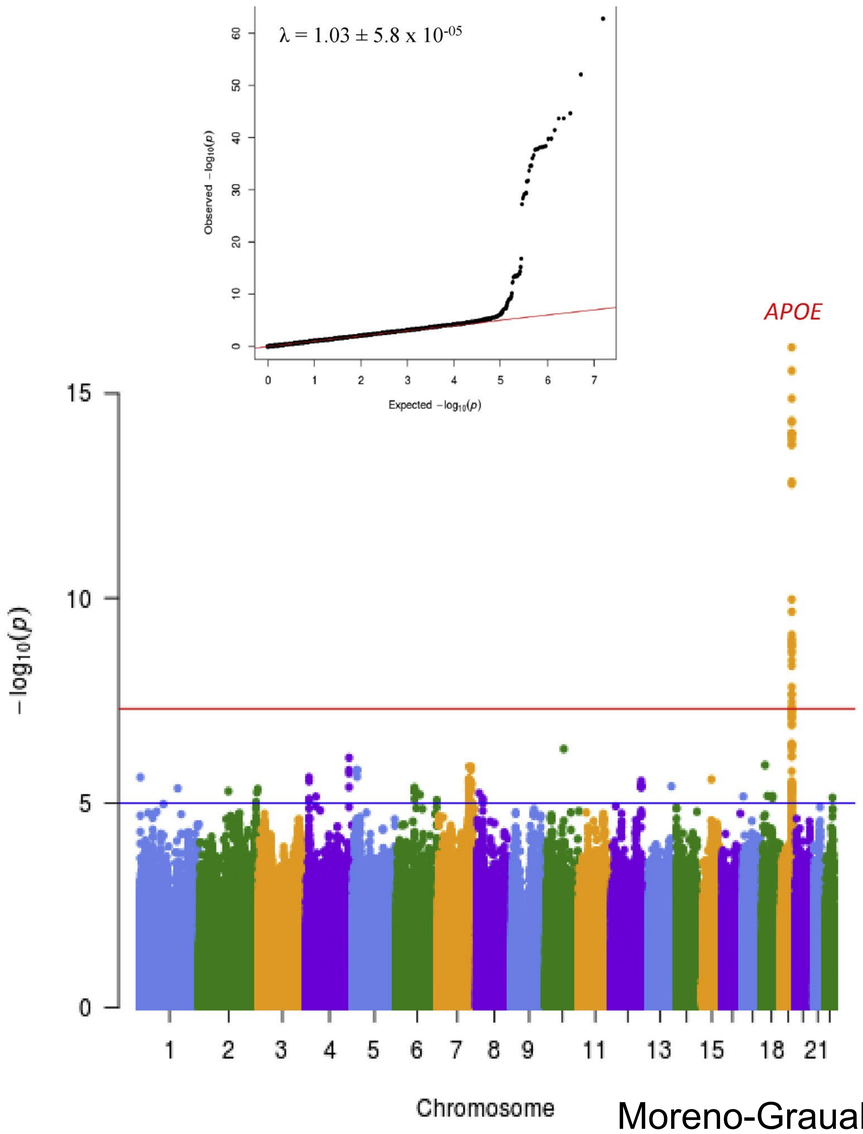




Fine Mapping and Gene Cloning in Human and Mouse

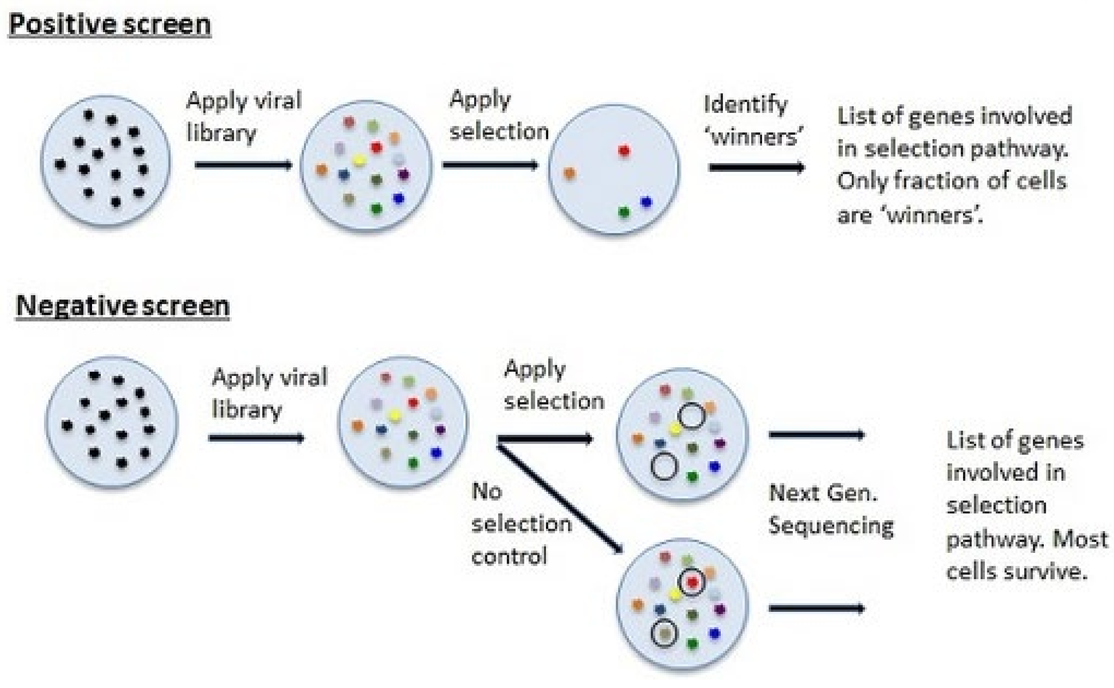
GWAS/QTL mapping – identification of functional regions/variants using genetic markers (e.g. SNPs identified from RAD-seq data)

Forward genetic screening using CRISPR-Cas9 – unbiased discovery and functional characterization of specific genetic elements associated with a phenotype of interest.



Moreno-Grauab, et al 2019: GR@ACE project

CRISPR-Cas9 screening



123,411 sgRNAs targeting 19,050 in humans

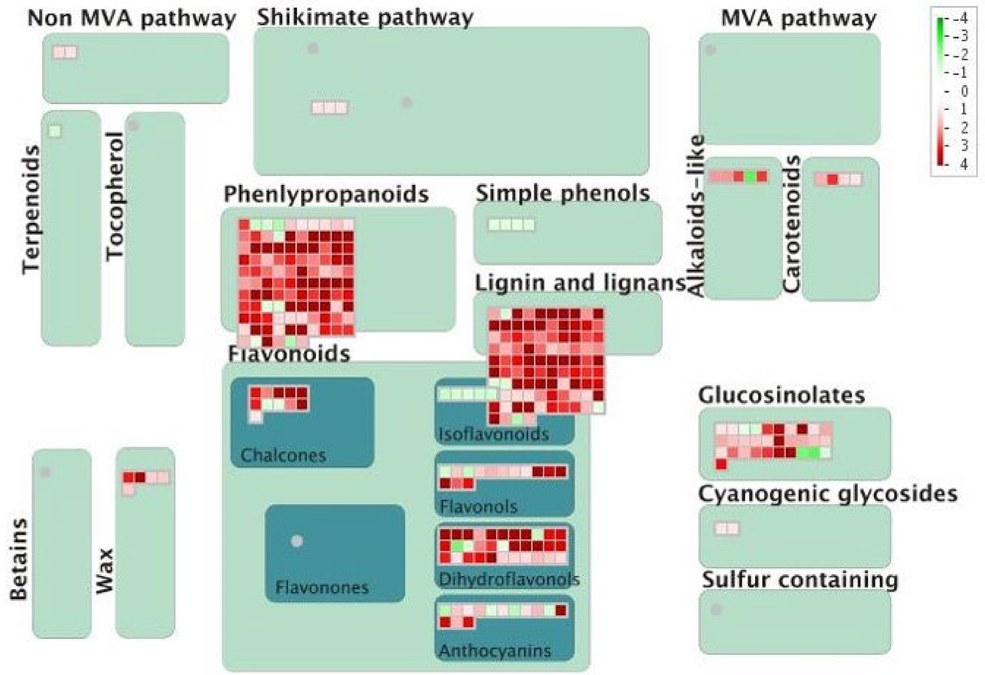
https://www.addgene.org/guides/pooled-libraries/

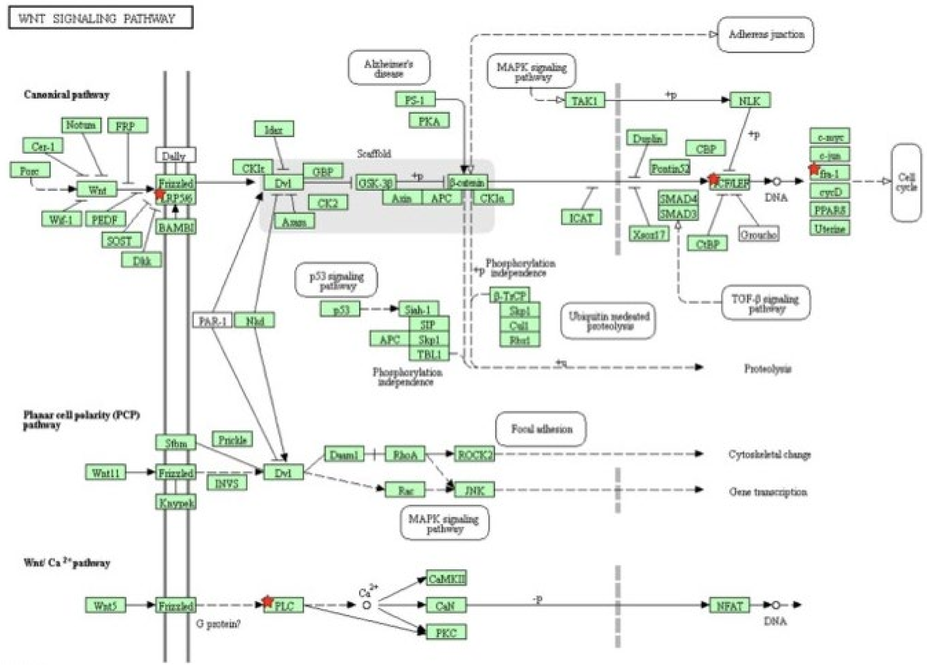
Functional Analysis for Omics Data

Pathway - classification and enrichment of pathways.

GO - classification and enrichment of GO (gene ontology).

GSEA – determination of whether a gene set shows statistically significant differences between two biological states (e.g. disease vs control)





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Genome Analysis

***de novo* assembly** - assembly of NGS DNA/RNA reads into ordered or unordered contigs and/or scaffolds.

Gene prediction and annotation - identification of coding regions in genome/transcriptome and annotation of predicted genes using homology based search using closely related genomes.

Structural Analysis - analyses of SNP, indel, CNV, SSR and repeat elements.

Comparative genomics - genomic features such as gene order, regulatory sequences are compared between different genomes.

Metagenomics

16S ribosomal RNA (rRNA), 18S rRNA and ITS - study of phylogeny and taxonomy of prokaryotes, eukaryotes and fungi respectively in microbial communities.

Metagenomics - investigate the presence of different microbes and their functions in microbial communities.

Metatranscriptomics - report the function and activity of expressed genes in a specific microbial environment.

Proteomics

Metabolomics

Integration of multi -omics