

The New Mexico IDeA Network for Biomedical
Research Excellence (INBRE) *Bioinformatics Core*
at NCGR presents

Virtual Bioinformatics Intensive

on Differential gene Expression (DE), Metagenomics and Visualization

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Agenda

- NCGR overview
 - Key Areas
 - Research
- Course Overview
- Student Information

National Center for Genome Resources

Genomic data science and education for a better world

As leaders in DNA sequence analysis, we partner with government, industry, and academia to drive biological discovery in all kingdoms of life.



Experts in experimental design, software, computation, data integration and training a skilled workforce.

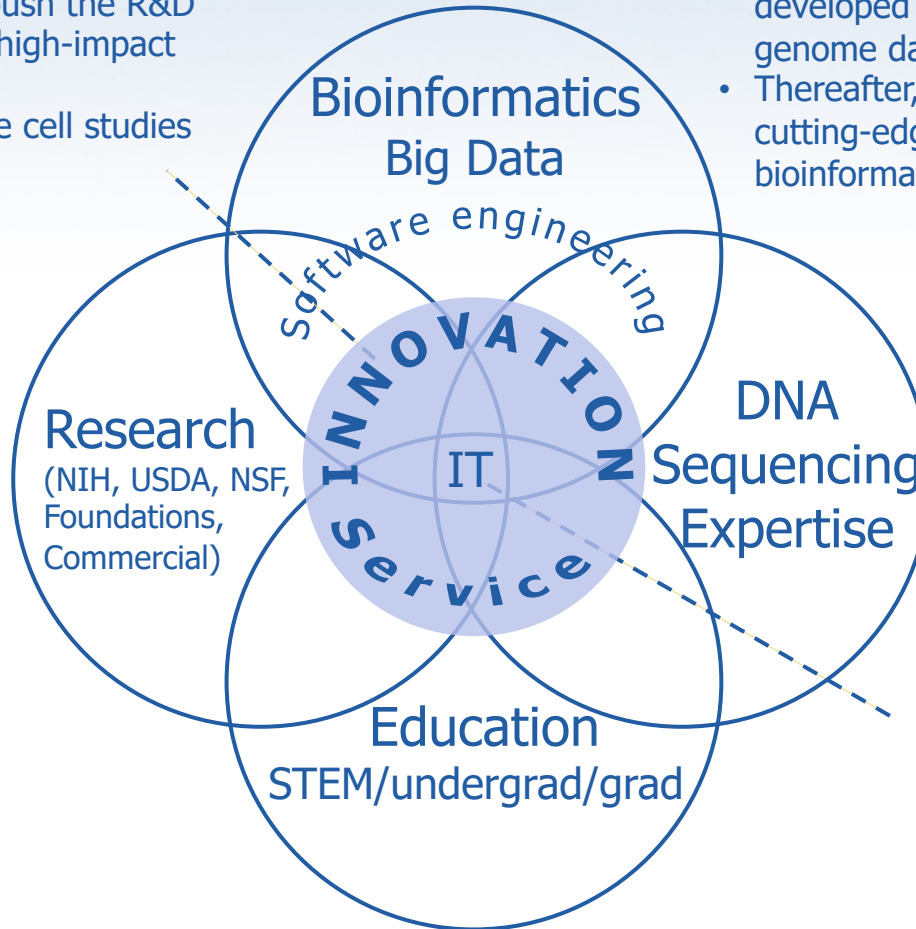
NCGR's Key Areas

Genomic exploration solutions

- Exploit technologies, push the R&D envelope, and deliver high-impact results
- Ground-breaking single cell studies

Research in all kingdoms of life

- Expertise through numerous sequencing and bioinformatics projects
- > 225 publications



Bioinformatics champions for > 20 yrs

- Human genome project pedigree: developed the first relational human genome database (spun out of LANL)
- Thereafter, developed a multitude of cutting-edge "omics" tools and bioinformatics resources

Nest generation sequencing pioneers

- 1st Illumina sequencing certified service provider in North America (2008)
- Early adopter of Pacific Biosciences sequencing technology
- Experimental design

Robust computational resources and petabyte-scale storage in a secure local infrastructure

Biotech Education. The center offers genomics/bioinformatics college seminars, workshops, internships, and pre K-12 basic science education including genomics and bioinformatics from grade three and up.

Research at NCGR

- All kingdoms of life
- Human health
- Plant science and nutrition



The University of Sheffield.



Bayer CropScience



National Institute of General Medical Sciences



IMP INTERNATIONAL MESOTHELIOMA PROGRAM



GLOBAL



National Center for Genome Resources

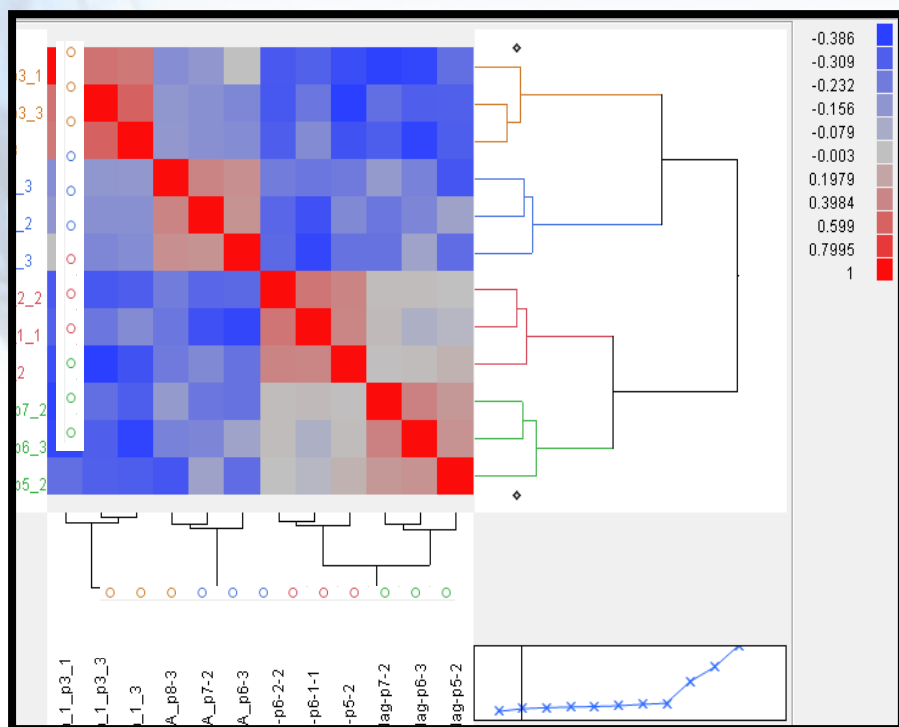


Course overview

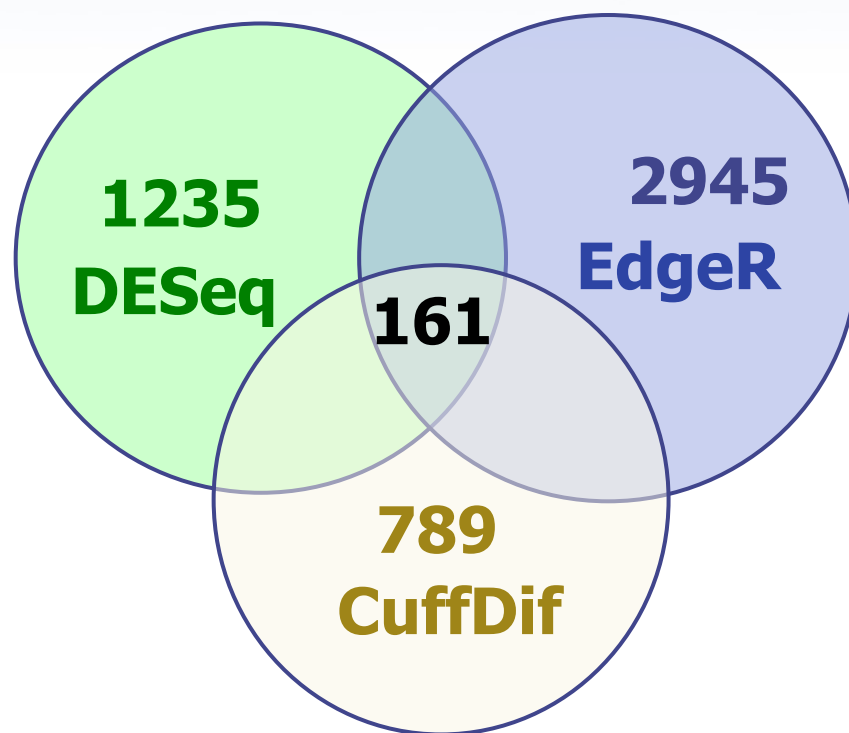
- ❑ Pre-reqs completion
- ❑ Computer systems set-up and coordination
- ❑ NCGR/NMINBRE/Course Introduction
- ❑ Participant Icebreaker
- ❑ System Orientation/Linux & Bash Basics
- ❑ Sequencing tech and lab protocols
- ❑ Differential gene Expression
- ❑ Pathway Analysis
- ❑ Visualization
- ❑ 16S Community Analysis
- ❑ Whole Genome Metagenomics
- ❑ Metatranscriptomics

Differential gene expression

Sequence-read counts of mRNA samples for expression profiling has supplanted probe array-based methods



Heatmap and Dendrogram



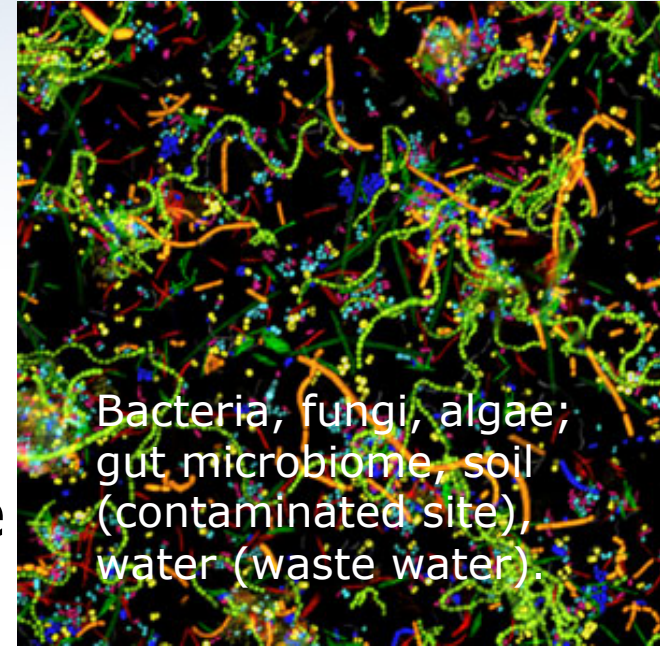
Pathway Analysis: find networks of gene interaction and function

Attaches known biological information, or functional annotation, to genomic elements.

Examples include expression, interaction, regulation, biological function, and biochemical function.

Microbial Community Analysis Meta-Genomics/Transcriptomics

- Investigate the variable regions of the small ribosomal subunit 16S gene: What species are there?
- Whole genome metagenomics: What are the genomes of these microbes?
- Metatranscriptomics: Whose active in the community?



Bacteria, fungi, algae;
gut microbiome, soil
(contaminated site),
water (waste water).

Credit: Alex Valm.

Composition, Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes.

Stacey M Lambeth, Trechelle Carson, Janae Lowe, Thiruvarangan Ramaraj, Jonathan W. Leff, Li Luo, Callum J Bell, Vallabh O Shah. *J Diabetes Obes* 2(3): 1-7. doi:10.15436/2376-0949.15.031. [PMID: 26756039](https://pubmed.ncbi.nlm.nih.gov/26756039/)

Student Information

- ❑ Workshop weebly website
 - Find course documents in the calendar
- ❑ Virtual environment tips
 - ❑ Enable video and audio
 - ❑ Mute audio until speaking
 - ❑ Be interactive and ask questions - we're here to help!
- ❑ Funding/Acknowledgements
 - ❑ IDeA Award from NIGMS (5P20GM103451)
 - ❑ NCGR staff who assisted
- ❑ Survey & Certificate of Completion

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Thank you!

Questions?

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