Snyder Bioinformatics Hub

Where biology meets algorithms

https://TheBioHub.ca/

UNIVERSITY OF CALGARY

Calvin, Phoebe and Joan Snyder Institute for Chronic Diseases

Welcome to the Bioinformatics Hub

The Bioinformatics Hub serves as the pivotal nexus for bioinformatics at the Snyder Institute for Chronic Diseases

Our Mission

To accelerate discovery by giving researchers easy access to advanced bioinformatics methods, shared resources, and collaborative infrastructure.

The Bioinformatics Hub sits at the intersection of biological science and computational analytics. **We promote transparency, openness, and reproducibility in all aspects of research.**

Our goal is to create a connected research community that moves beyond traditional boundaries and advances innovation in chronic disease research.

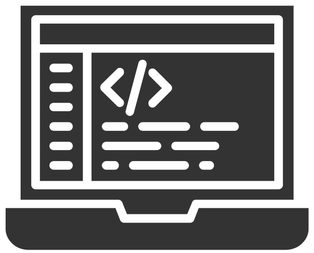
Our Vision

To ensure every researcher—regardless of discipline—has the tools, expertise, and support needed to succeed.

By building an inclusive and collaborative research ecosystem, **we aim to drive meaningful advances in the prevention, diagnosis, and treatment of chronic diseases**.

Our Services

End-to-end bioinformatics support—from study design to biological insight



Workflow Design

We create streamlined and reproducible bioinformatics workflows tailored to your research needs.

Method Development

We build and implement advanced computational methods to tackle complex biological questions.

Data Management

We design and maintain structured databases to ensure reliable, scalable, and accessible research data.

What We Deliver

01 Online, self-contained report with QC and analysis results, complete scripts, and embedded figures

02 Docker-containerized analysis environment with pinned dependencies, clear run instructions, and reproducible workflows

03 Pre- and post-processed datasets with QC outputs and metadata, so preprocessing steps don’t need repeating

04 Publication-quality figures with consistent styling and export formats, ready for manuscripts, posters, and presentations

Areas We Support

Comprehensive omics expertise across genomics, pharmacogenomics, transcriptomics, and microbiome

Genomics

- Analyze whole-genome and -exome sequencing data
- Detect and prioritize variants, including SNVs/INDELs/SVs
- Link genomics to clinical features through association
- Identify actionable mutations to support interpretation

Pharmacogenomics

- Analyze *in vitro* and *in vivo* pharmacogenomic profiles
- Quantify drug response patterns in dose–response assays
- Compare model systems before and after drug treatment
- Detect synergy signals in combination drug screens

Expression and Spatial

- Process bulk RNA-seq data from QC to gene-level counts
- Identify differential expression and functional pathways
- Cluster and annotate cell types from single-cell RNA-seq
- Analyze spatial profiles and support image segmentation

Microbiome

- Profile microbial communities from 16S rRNA data
- Resolve taxa and functions with shotgun metagenomics
- Improve strain-level calls using long-read metagenomics
- Link host traits to microbiome features and associations

Why Partner With Us

Collaborative expertise, reproducible analysis, and actionable insights—tailored to your research

Fast turnaround with clear milestones

We prioritize rapid, predictable delivery so you can make decisions quickly and keep projects moving, supported by clear timelines, defined milestones, and frequent check-ins

Rigorous QC with comprehensive diagnostics

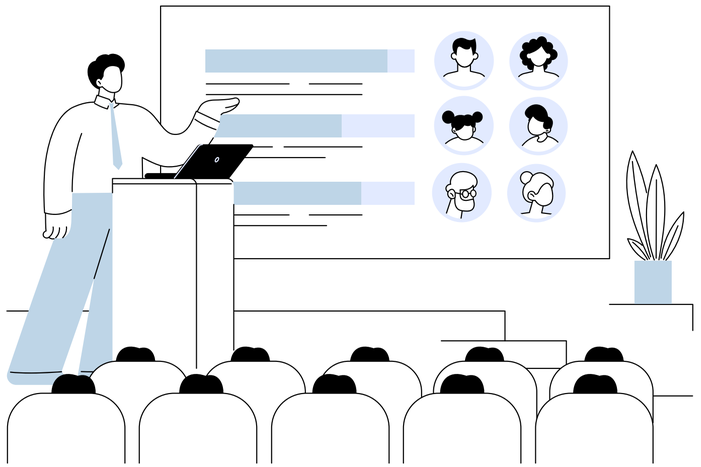
We apply thorough quality control at every stage of the workflow and provide a full suite of diagnostic plots and summary metrics, helping you catch issues early and interpret results with confidence

Reproducible by default with containerized workflows

Every analysis is delivered as a fully reproducible package, including a Docker-based environment, complete scripts for reruns and training, and an online, versioned report—so revisions are straightforward and you don’t need to manage backups or manual version control

Domain and methodological expertise with research-ready guidance

We bring deep experience across genomics, bulk and single-cell transcriptomics, spatial omics, pharmacogenomics, and medical informatics—combining sound statistical practice with biological context to recommend appropriate methods, avoid common pitfalls, and deliver results that stand up to review and publication.



Our Projects

From data to discovery—together

No method? No problem! We build what your project needs

When existing tools don't fit your data or research question, we don't force a workaround—we collaborate with you to create a solution. For long-read metagenomics, we faced a gap in robust relative abundance estimation and developed BASEN (github.com/Snyder-Institute/basen), a purpose-built approach for quantifying abundance from long-read data. The result is a workflow that meets the science first and is delivered with reproducible code and clear reporting.

Integrate across omics? No headaches! We connect the dots for you

When your story spans multiple datasets or modalities, we help you move beyond siloed analyses and toward a unified interpretation. That's why we built Spatial Omics Toolkit 2 (github.com/Snyder-Institute/sotk2), an in-house R package that enables cross-platform omics integration by comparing deconvolution-derived modules across datasets and linking shared biological programs through network-based community detection. The result is a practical way to identify consistent signals across bulk, single-cell, spatial, and protein-level data—so you can focus on biology, not tool limitations.

Have resources? Visualize it! Interactive gives you better insight

When you have a large, complex dataset, interactive exploration helps researchers and readers turn results into hypotheses and spot patterns that static figures can miss. P-values alone rarely tell the whole story—different thresholds can surface different results—so the key is understanding the trend as criteria change. We build Shiny apps that let users adjust cutoffs on the fly and immediately see how signals strengthen, weaken, or stay consistent across comparisons, giving clear insight into robust patterns versus threshold-sensitive findings. As an example, you can explore an interactive demo of Spatial Omics Toolkit 2 (shinyapps.ucalgary.ca/sotk2). The result is a practical, shareable interface that makes your data easier to interpret, validate, and communicate.

The Bioinformatics Hub was established in September 2025, and we are actively developing production-level QC/analysis reports and Shiny apps.
As publications become available and can be shared publicly, this page will be updated with real-world examples—please stay tuned.

Bring Us Your Data

We’ll help you turn it into insight—with fast turnaround, rigorous QC, and reproducible results.

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