The Harvard Chan Bioinformatics Core

Bioinformatics support for the Harvard community

James M. Billingsley

CFAR Executive Committee Meeting 1-22-21

Core Update
<table>
<thead>
<tr>
<th>Partners</th>
<th>Description</th>
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<tbody>
<tr>
<td>Harvard T.H. Chan School of Public Health</td>
<td>As part of the Department of Biostatistics at the Harvard T.H. Chan School of Public Health we work closely with our colleagues in the department and in the Program in Quantitative Genomics.</td>
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<td>NIEHS</td>
<td>The core is also a member of the Environmental Statistics and Bioinformatics Core at the HSPH-NIEHS Center for Environmental Health.</td>
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<td>Harvard Catalyst</td>
<td>The core serves as the Harvard Catalyst Bioinformatics Consulting group to support researchers within the general Harvard community and affiliated hospitals.</td>
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<td>HSCI</td>
<td>The core is a part of the Center for Stem Cell Bioinformatics which serves members of the Harvard Stem Cell Institute community.</td>
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<td>Harvard Medical School</td>
<td>Through funding from the Tools and Technology group we can offer help to researchers on the quad at Harvard Medical School.</td>
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<td>CFAR Harvard University Center for AIDS Research</td>
<td>The HBC support HIV researchers as part of the The Harvard University Center for AIDS Research Biostatistics and Bioinformatics Core</td>
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<td>Cure Alzheimer's Fund</td>
<td>We receive funding through the Cure Alzheimer’s Fund.</td>
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Bioinformatics Support

- Transcriptomics: RNA-seq, small RNA-seq, single cell RNA-Seq
- Epigenetics: ChIP-seq, genome-wide methylation, ATAC-Seq
- DNA Variation: WGS, exome-seq, Structural variants
- Functional enrichment analysis
- Experimental design
Grant and Manuscript Support

- Letters of Support
- Review manuscripts
- Standard Descriptions/Best Practices
- CFAR Developmental Grants
- Data submission GEO
CFAR members support for HIV-related projects

- Free grant support
- Exp. design, power analyses, budgets, biosketches
- Letters of support, manuscript review
- 10 free hours of analyses for Early Career Investigators
Effects of tesamorelin on hepatic transcriptomic signatures in HIV–associated NAFLD

Lindsay T Fourman, James M Billingsley, George Agyapong, Shannan J Ho Sui, Meghan N Feldpausch, Julia Purdy, Isabel Zheng, Chelsea S Pan, Kathleen E Corey, Martin Torriani, David E Kleiner, Colleen M Hadigan, Takara L Stanley, Raymond T Chung, Steven K Grinspoon

Growth Hormone Releasing Hormone Reduces Circulating Markers of Immune Activation in Parallel with Effects on Hepatic Immune Pathways in Individuals with HIV-Infection and Nonalcoholic Fatty Liver Disease

Takara L. Stanley, Lindsay T. Fourman, Lai Ping Wong, Ruslan Sadreyev, James M. Billingsley, Meghan N. Feldpausch, Isabel Zheng, Chelsea S. Pan, Autumn Boutin, Hang Lee, Kathleen E. Corey, Martin Torriani, David E. Kleiner, Raymond T. Chung, Colleen M. Hadigan, Steven K. Grinspoon

Publications

22 in 2020
9 scRNA-Seq, 5 Bulk RNA-Seq
Variant calling, ATAC-seq, methylation, metabolomics

Ongoing Research Associated with SARS-CoV-2 or HIV

- SARS-CoV-2 genomic assembly
- SARS-CoV-2 scRNA-Seq and bulk RNA-Seq in lung epithelial tissue and lung tissue organoids
- HIV low frequency variant calling optimization; drug resistance
- Integration of bulk RNA-Seq and ATAC-Seq; HIV post-treatment control
- A number of different bulk and scRNA-Seq experiments; HIV latency
- scRNA-Seq SIV-specific CD4+ cells in context of SIV vaccines in NHP