



HCGS

Hubbard Center for Genome Studies

January 2015
Issue 1



NEWSLETTER

Inside this Issue

- *Happenings @ HCGS*
- Staff Profiles
- Policies on Libraries/Samples
- Bioinformatics Corner
- Publications

Want to know more about what we do? Stop by our website for a visit: <http://hcgsh.unh.edu/>

Happenings at HCGS

Welcome to our first Monthly newsletter. The intention of this newsletter is to help communicate changes in services, new applications and to introduce our affiliates and colleagues to the HCGS staff. We are starting 2015 with some significant changes. The most notable change is the implementation of a new LIMS system for sample submission and tracking. This will be beta-tested with selected users in January. We are also very excited to be able to offer extended read lengths for the rapid run mode of the HiSeq 2500. An upgrade to 250bp paired-end reads is available for our instrument and will be offered starting in February. Finally, the HCGS is undergoing some minor structural renovations to create a HCGS office and consultation space on the 4th floor of Gregg Hall.



Staff Profiles

Jordan Ramsdell graduated from UNH with a Bachelor's degree in Genetics (Genomics) and now attends UNH for his Master's in Computer Science. He has worked in the HCGS for over two years, and is actively involved helping others at UNH as well as members of NH-INBRE with bioinformatics.



If you go far enough back, your genome connects you with bacteria, butterflies, and barracuda - the great chain of being linked together through DNA. ~ Spencer Wells

Bioinformatics



A major role of the HCGS is to support data analysis and security for data generated by the HCGS. Toward that goal the HCGS maintains platforms for secure storage (cobb.unh.edu) and shared platforms for bioinformatic analysis (e.g. pinky). It is our hope that all projects start with a consultation that defines the experimental design including anticipated needs for bioinformatics. Feseha Abebe-Akele and Jordan Ramsdell are available for support of your projects. Specifically instructions for gaining access to your data on

cobb can be found on our website at (<http://hcg.unh.edu/ServicesAndPricing/DataAccess.html>). If you have any trouble please contact Feseha .

The primary shared platform for bioinformatics analysis is pinky. To establish and account on pinky or to have software added please contact Feseha. Pinky is a shared instrument, very useful, but data storage is not secure.

Feseha's email is Feseha.Abebe-Akele@unh.edu.

Publications

Please acknowledge our NSF MRI Grant in your publications: NSF DBI-1229361.

HCGS Library Sample Storage Policy

All libraries generated at HCGS will be stored on site no longer than 3 months. If longer storage for libraries is desired, notification must be sent to HCGS no later than a month before the 3-month deadline. Libraries sent to HCGS (i.e. anything not generated at HCGS) will follow the same policy.

HCGS DNA/RNA Sample Storage Policy

DNA and RNA samples sent to HCGS will be stored only as long as samples are being processed, at which time the user can request the samples be sent back or request additional processing .

- GOUT J. -F., THOMAS W. K., SMITH Z., OKAMOTO K., LYNCH M. (2013). LARGE-SCALE DETECTION OF IN VIVO TRANSCRIPTION ERRORS. *PNAS*, 110(46), 8584-18589. DOI:[10.1073/PNAS.1309843110](https://doi.org/10.1073/PNAS.1309843110)
- COOPER V.S., STAPLES R.K., TRAVERSE C.C., ELLIS C.N. (2014). PARALLEL EVOLUTION OF SMALL COLONY VARIANTS IN *BURKHOLDERIA CENOCEPACIA* BIOFILMS. *GENOMICS* 104 (6A) 447-452. DOI: [10.1016/j.ygeno.2014.09.007](https://doi.org/10.1016/j.ygeno.2014.09.007).
- GHAZAL, S., HURST, S. G., MORRIS, K., ABEBE-AKELE, F., THOMAS, W. K., BADR, U. M., TISA, L. S. (2014). DRAFT GENOME SEQUENCE OF PHOTORHABDUS LUMINESCENS STRAIN BA1, AN ENTOMOPATHOGENIC BACTERIUM ISOLATED FROM NEMATODES FOUND IN EGYPT. *GENOME ANNOUNCE.*, 2(2).DOI:[10.1128/GENOMEA.00396-14](https://doi.org/10.1128/GENOMEA.00396-14)
- GHODHBANE-GTARI F., HURST S. G., OSHONE R., MORRIS K., ABEBE-AKELE F., THOMAS W. K., TISA L. S. (2014). DRAFT GENOME SEQUENCE OF FRANKIA SP. STRAIN BMG5.23, A SALT-TOLERANT NITROGEN-FIXING ACTINOBACTERIUM ISOLATED FROM THE ROOT NODULES OF CASUARINA GLAUCA GROWN IN TUNISIA. *GENOME ANNOUNC.* 2(3). DOI:[10.1128/GENOMEA.00520-14](https://doi.org/10.1128/GENOMEA.00520-14)
- HURST S. G., OSHONE R., GHODHBANE-GTARI F., MORRIS K., ABEBE-AKELE F., THOMAS W. K., TISA L. S. (2014). DRAFT GENOME SEQUENCE OF FRANKIA SP. STRAIN THR, A NITROGEN-FIXING ACTINOBACTERIUM ISOLATED FROM THE ROOT NODULES OF CASUARINA CUNNINGHAMIANA GROWN IN EGYPT. *GENOME ANNOUNC.*, 2(3). DOI:[10.1128/GENOMEA.00493-14](https://doi.org/10.1128/GENOMEA.00493-14)
- MANSOUR S.R., OSHONE R., HURST S.G. IV, MORRIS K., THOMAS W.K., TISA L.S. (2014) DRAFT GENOME SEQUENCE OF *FRANKIA* SP. STRAIN CCI6, A SALT-TOLERANT NITROGEN-FIXING ACTINOBACTERIUM ISOLATED FROM THE ROOT NODULE OF *CASUARINA CUNNINGHAMIANA*. *GENOME ANNOUNC.* 2(1):E01205-13. DOI:[10.1128/GENOMEA.01205-13](https://doi.org/10.1128/GENOMEA.01205-13)
- PETERSEN, L.M. AND TISA, L.S. (2014) MOLECULAR CHARACTERIZATION OF PROTEASE ACTIVITY IN *SERRATIA* SP. STRAIN SCBI AND ITS IMPORTANCE IN CYTOTOXICITY AND VIRULENCE, *J.BACT*, 196 (22) 3923-3926, [10.1128/JB.01908-14](https://doi.org/10.1128/JB.01908-14).