About Us

Our Resources

The GSAF is housed in approximately 2,000 square feet of controlled-access laboratory space and is an experienced NGS facility. Launched in 2008, the GSAF currently processes over 8,000 NGS samples per year.

Our equipment and capabilities include:

1. One Illumina HiSeq 4000 and two HiSeq 2500 next-generation DNA sequencers and associated peripherals. The HiSeq 4000 can generate over 1 Terabases of sequence in an 6-day run or 120 gigabases in a ~1 day rapid run. The GSAF has experience generating small RNA, mRNA, genomic DNA fragment, RAD (including ddRAD), bacterial and fungal metagenomics, and genomic DNA large-insert mate-pair libraries for the Illumina platform.

2. Two Illumina MiSeq next-generation DNA sequencers and associated peripherals. The MiSeq is intended for lower data output, faster turn-around time projects, or for projects requiring longer read lengths (up to 600 bp per template, as two 300 bp sequences).

3. Two Illumina NextSeq 500 next-generation DNA sequencer and associated peripherals. The NextSeq is ideal for intermediate scale projects, requiring more read depth than is feasible on the MiSeq platform but with faster turn-around time than the HiSeq platform.

4. Informatic tools and hardware sufficient for analysis of next-generation DNA sequencing data, including:

   a. Multiple Dell PowerEdge R900 & R720 servers with 16-32 cores each, with BWA, Bowtie, Shrimp, SOAP, and mapreads aligners, NCBI BLAST, and R/Bioconductor, and several de novo assemblers, sequence editors, and genome browsers.
   
   b. The resources of Lonestar, a 30,000 core supercomputer, and Stampede, a 400,000 core supercomputer, both hosted by UT’s Texas Advanced Computing Center, with 15 petabyte of scratch disk storage.
   
   c. The GSAF has software stacks and experience appropriate to your project and both we and TACC staff can assist you in training your students to use this resource effectively.

Lab protocols we are experienced with:

- Creation of fragment (single-end or paired-end) sequencing libraries for all Illumina next-gen sequencers
- Creation of mate-pair or “jumping” sequencing libraries between 1.5kb and 4kb for Illumina next-gen sequencers
- Creation of RNA-seq libraries from total RNA, small RNA, and immuno-precipitated RNA for Illumina next-gen sequencers
- Creation of amplicon libraries (particularly 16s and ITS regions) for the Illumina next-gen sequencers
- Human exome and custom capture with the Agilent SureSelect, Illumina TruSeq, and Nimblegen SeqCap EZ kits
- Sample and library QC using the Agilent BioAnalyzer, Picogreen and Ribogreen fluorimetry, qPCR, and spectrophotometry

Bioinformatic protocols we are experienced with:

- RNA-seq for transcript abundance, alternative splicing analysis, and variant detection
- SNP/variant analysis
- small RNA abundance and alternative editing analysis
- de novo and reference-guided assembly from fragment, paired-end, and mate-pair data on both DNA and RNA (transcriptomes)
- Whole exome data analysis

Instruments in our lab:

- Illumina HiSeq 4000 sequencer (one)
- Illumina HiSeq 2500 sequencers (two)
- Illumina MiSeq sequencers (two)
- Illumina NextSeq 500 sequencer (two)
- Covaris S220 Adaptive Focused Acoustic shearing device
- DigiLab HydroShear shearing device
- Agilent BioAnalyzer 2100
- Agilent TapeStation
- Invitrogen Qubit fluorimeter

Computational and software resources:

- The GSAF hosts a Dell R720 32-core, 196 GB server with a total of 74 TB local disk dedicated to NGS analysis. Access is available free of charge to all GSAF customers. We maintain a wide range of tools for NGS analysis and assembly on this server. Here is an explanation of the Research Computing Pod with instructions for getting an account on our server.

- In addition, the GSAF uses and works with the TACC bioinformatics group, supporting tools and applications suitable to the TACC environment.

- Want to get started? Contact us if we can help, or here's some documentation describing how to submit samples to the GSAF.

- New to Unix? Check out some Unix and Perl resources for beginners.

- Need an account? Here's how you can get an account on the GSAF Research Computing Pod.

Our Mission and Vision

Vision: The GSAF’s vision is to be a world-class genomic analysis center in terms of data quality, breadth of available methods, and productivity.
Mission: The mission of the Genome Sequencing and Analysis Facility is to provide the best quality analytical results with the best value to life science researchers.

Our People

Jessica Wheeler Podnar  
Assistant Director  
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gsaf@utgsaf.org  
Jessica joined the GSAF in June 2010. Prior to joining UT Jessica worked at Sierra Sciences, a biotech company located in Reno NV, 4 years as a researcher and laboratory manager in the cell culture division. She is a graduate of Southwest Texas State University, earning a BS in Biology in 2002.

Dhivya Arasappan  
Bioinformatician  
(512) 471-7138  
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darasappan@mail.utexas.edu  
Dhivya joined the GSAF team in April 2008 and primarily deals with analysis of Next-gen sequencing data. Prior to joining UT, she was working at the National Center of Toxicological Research, FDA. At FDA, she was involved in analysis of gene expression data. She has a Masters in Bioinformatics from Virginia Commonwealth University and a Bachelors in computer science from Anna University, India.

Matt Barnette  
Lab Research Assistant  
(512) 475-9725  
Lab Research Assistant  
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Group photos

Group Lunch, August 2012.
Group Lunch, May 2011.
Scott Hunicke-Smith, Ph.D.
Former Director
Dr. Hunicke-Smith joined UT Austin in August of 2008 to start next-generation sequencing activities at UT. Prior to joining UT, he was VP and General Manager of the molecular biology Services' division of Asuragen, a spin-out of Ambion. He joined in Ambion in July of 2003 as Director of Business Development, Instrumentation. He was promoted to Vice President, Business Development in March of 2004 and to Vice President, Ambion Services in September of 2005. Prior to joining Ambion, Dr. Hunicke-Smith served as founder and CEO of GeneMachines, a molecular biology equipment firm, from 1997 through March of 2003. Dr. Hunicke-Smith also served on the Board of Directors of Silicon Genetics, a bioinformatics software firm, from 1998 until Agilent acquired it in 2004. He received his Ph.D. from Stanford University in the laboratory of Ron Davis in 1997 and is an inventor on seven issued patents. Dr. Hunicke-Smith is currently Vice President for Molecular Diagnostics at Sonic Reference Lab, a division of the multinational Sonic Healthcare. He can be reached at shunikkesmith@sonicreferencelab.com.
Research Assistant
Meredith was an undergraduate research assistant in 2009 and 2010 and then worked with the GSAF on her senior honors thesis. She is now a graduate student at the University of North Carolina.

Arindam Bhattacharya
Arindam was an undergraduate research assistant with the GSAF in 2010 and 2011.

Ellia (Kim) Kim
Kim was an undergraduate research assistant with the GSAF in 2010 and 2011.

Alice Seol
Alice was an undergraduate research assistant with the GSAF in 2010.

Michelle Byrom
Michelle was instrumental in the founding of the GSAF and helped us work out many initial preps. She is now part of the Ellington Lab at UT Austin

Aaron Chevalier
Aaron was a graduate research assistant in 2008 and 2009 and was accepted to the Graduate program at the University of Washington

Andrew Adey
Andrew graduated in 2009 and was accepted to the Graduate program in the Institute for Systems Biology at the University of Washington