Home Page NEW

Ready to submit samples? Use these links

7/25/13 NOTE: UT's new version of Confluence requires you to “Log In” in the upper right corner BEFORE selecting an online submission form link.

To submit a new project or get detailed pricing information, use these links. You'll be given a 6-digit request ID to refer to your request later. Your requests stay here until you're ready to submit samples. You return to this link when you're ready to submit your samples.

Choose your project type:

- **Bacterial metagenomics project** - Simplified submission page for bacterial 16S metagenomics (you must log in first - upper right corner)
  - Metagenomics assay: This service starts with normalized (i.e. equal concentration) DNA samples and includes amplification of the V4/V5 regions of the bacterial 16S gene as shown on this web page and at least 10,000 2x250 bp paired-end sequences from the Illumina MiSeq platform for at least 95% of the samples submitted. PCR is performed in triplicate to minimize jackpot effects. Gel-based QC is performed on a sampling of 10% of the samples post amplification. DNA is expected as input; the GSAF does not provide DNA extraction services at this time. See this web page for sample input guidelines and note that DNA concentrations should be normalized before submission. (The GSAF can normalize your sample concentrations for an additional charge.)
- **All other projects** (you must log in first - upper right corner)
  - [Download sample submission template](#)
  - For the general, non-bacterial metagenomics submission page ONLY: Projects must be submitted via the online project submission form above to specify project details like platform, contact info, etc., but if you'd rather fill out an Excel template for your sample info instead of the web form, use this template. You'll upload it when you request a new sequencing job. This form is required for more than 30 samples; suggested for more than 10.

Latest news

24 Nov 13
The GSAF is proud to announce several major additions and changes to our service offerings. All are effective immediately, and the costs listed below are for internal UT researchers. We have integrated these new NGS prices into our LIMS job/sample submission system so you will have an accurate price for any platform and prep before you submit your samples.

1. **Gene synthesis** (in partnership with ARL) - particularly when you need many distinct mutants. The base price is $0.22/base, but can be significantly lower when creating libraries of mutants. More details are listed below and can be found here. Please contact Randy Hughes for further details (hughes at mail.utexas.edu).
2. **16S rRNA bacterial metagenomics** for the standard price of $20/sample including prep and sequencing (plus $200 for projects of less than 176 samples).
3. **Genotyping-by-sequencing** for the standard price of $25/sample including sequencing (plus $200 for projects of less than 176 samples).
4. **Lower library prep prices** - Thanks to well-validated automation, DNA fragment libraries are now $60/sample (>=8 samples) and directional RNA libraries including poly-A mRNA enrichment are now $130/sample (>= 8 samples). In addition to being less expensive, we have also found fewer sequencing issues with libraries prepared at the GSAF and want to pass that savings on to you.
5. **Lower sequencing prices** - our efficiency has improved thanks to hard work in process optimization and automation and we can pass that on to you. The new MiSeq and HiSeq instruments are now functioning smoothly and our queue times have been reduced substantially since this past summer. Both MiSeq instruments are capable of the higher output (20-25 million reads) 2x300 bp Version 3 sequencing chemistry, and both HiSeq 2500's are capable of Rapid (up to 2x150 bp) and High Output ("standard" - up to 2x100 bp) runs.

As always, please let us know if you have any questions, concerns, or comments.

Sincerely,
Scott, Jessica, and all the GSAF staff and Randy Hughes and all the ARL staff.

Getting started

- New to the GSAF? Expand here to get started...
  1. Review this self-paced training presentation.
  2. Read this page further to learn what instruments we have and what we're experienced with.
  3. Attend UT's Next-gen sequencing club meetings on the first and third Thursdays of the first month of each semester, 3:00 pm., MBB
2.204 - a great place to start learning about NGS techniques applied to real projects. Sign-up on our mailing list by joining "gsafusers" at UT's list server - just select "subscribe" and enter "gsafusers".

4. If you want to submit samples for the first time, first get a UT EID if you don’t have one, then go to our sample submission section for more info, to check our queues, etc..

Get directions here

Protocols, instruments, computers, and software of the UT GSAF

The GSAF serves a wide array of customers and has gained considerable experience in preparing samples and analyzing data for NGS projects. We have industry-leading platforms and some user-accessible instruments. If you're just considering a project or are ready to sequence, we're here to give you great data quickly and affordably. Click to expand...

Lab protocols we are experienced with:

- Creation of fragment (single-end or paired-end) sequencing libraries for the Life Technologies SOLiD and Roche 454 FLX next-gen sequencers
- Creation of mate-pair or "jumping" sequencing libraries between 1.5kb and 8kb for the Life Technologies SOLiD and Roche 454 FLX next-gen sequencers
- Creation of RNA-seq libraries from total RNA, small RNA, and immuno-precipitated RNA for the Life Technologies SOLiD next-gen sequencer
- Creation of amplicon libraries for the Roche 454 FLX next-gen sequencer
- Expression profiling from total RNA on the Nimblegen microarray platform
- 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 2500 sequencer
- Roche/454 FLX sequencer
- Covaris S220 Adaptive Focused Acoustic shearing device
- DigiLab HydroShear shearing device
- Agilent BioAnalyzer 2100
- Agilent TapeStation
- Turner Biosystems Modulus fluorometer
- NanoDrop ND1000 spectrophotometer

Computational and software resources:

- The GSAF hosts a Dell R900 16-core, 64 GB server with a 4 TB high-speed fiberchannel disk array 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 are instructions to 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.
- Need to start analysing your data? get an account on our computational server. New to Unix? Check out some Unix and Perl resources for beginners.

Need Accounts? Here's how you can get an account on the GSAF server

Welcome to the UT GSAF Wiki - a central source of information for next-gen sequencing at UT Austin.

All are welcome to explore. With a UT EID you may also edit and contribute. Please sign up for our user group email to get notifications of upcoming seminars, NGS club meetings, and changes to service. Just hit "subscribe", enter your email address, and "submit". You don't have to be at UT to subscribe.

Reference Pages (GSAF and user contributed)
Browse the wiki:

**Software and Reference Genomes**

The [Software](#) section of the [BioITeam wiki site](#) lists software available on the GSAF Server Fourierseq and/or TACC and how to use it. The [Reference Genomes and Databases](#) section lists pre-installed reference genomes and their mapping indexes.

**Lab Protocols and Oligo Sequences**

[Lab Protocols](#) and [Oligo Sequences](#) are useful if you are designing experiments or preparing your own libraries.

**User Project Analysis Pages**

Use [User Project Pages](#) to work with the GSAF about an ongoing analysis project - **user editable**, share with your PI! Note that in-process laboratory status updates are not stored here.

**How to...**

How to submit samples to the GSAF

Thanks to Craig Dupree of CCBB for pointing us to the UT Wikis infrastructure!

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