Home

This is the home of the Bioinformatics Team (BioITeam) at the University of Texas at Austin.

The BioITeam (bio - i - team, short for bioinformatics team) is a consortium of bio-computing scientists at the University of Texas comprised of scientists from TACC, CCBB, CSSB, GSAF, TI-3D, and SSC.

Latest News

Make sure you have the BioITeam's environment sourced in your Stampede and Lonestar profiles

Here are some simple instructions to give you access to even more Bio-related resources at TACC.

Run BLAST+ an order of magnitude faster on Lonestar

The split_blast wrapper is now available to make running BLAST queries in parallel easy on Lonestar. You can specify how you want to split your input data, and the wrapper script takes care of the rest: splitting the data, BLASTing it in parallel, and then reassembling the outputs. Run your BLAST query 10 times (roughly!) faster by splitting your input across 10 nodes!

Use launcher_creator.py on Stampede

The venerable launcher_creator.py has been updated to automatically detect whether it's being executed on Lonestar or Stampede, and will generate either an SGE or SLURM launcher as appropriate. The same launcher_creator.py commands that worked on Lonestar should now work on Stampede. launcher_creator.py has also been updated with some new options.

Mission of the BioITeam:

Provide "one-stop" unified support for bioinformatics:

- software tools
- educational resources and
- implementation support.

We are initially, but not exclusively, focused on tools for next-generation sequencing (NGS) analysis. We are a group of users interested in pooling our efforts with others to reduce the time we spend implementing new software and databases and on training ourselves and others we work with.

Our general model is that TACC serve as the reference implementation for stable software releases so most of the "power computing" can be done at TACC, but in addition acknowledge that most of us use resources in addition to TACC, and often need tools, databases, or other resources not globally supported at TACC.

Due to the number of tools available and the pace of change, we have formed a community to help keep up with documentation, testing, implementation, and education. You are encouraged to become a contributor - just contact one of the BioITeam core members: Scott Hunicke-Smith (UT GSAF), Matt Vaughn (TACC), Dhivya Arasappan (UT GSAF), or Anna Battenhouse (UT - Iyer lab).

Resources available here:

1. How to join the BioITeam
2. Relevant classes offered at UT System Schools
3. SSC Intro to NGS Bioinformatics Course
4. Wish list
5. Documentation of software (DRAFT) at TACC, CCBB, and GSAF systems
6. Documentation of reference genomes, databases, indexes, etc
7. BioITeam meeting minutes
8. Self Service Pipelines and Scripts
9. BME 383J Course Content
10. Results of surveys...
11. Other helpful resources
12. Appsoma-based pipeline development

Bioinformatic Jobs at UT

Recently Updated

- **Byte Club**
  Dec 06, 2017 • updated by Jessica W Podnar • view change

- **RNA-Seq Presentation.pptx**
  Dec 06, 2017 • attached by Jessica W Podnar

- **Testing for Differential Expression**
  Dec 04, 2017 • updated by Dhivya Arasappan • view change

- **BCG Full Service Pipelines**
  Nov 29, 2017 • updated by Benjamin M Goetz • view change

- **genotyping with mpileup**
  Nov 21, 2017 • updated by Groves B Dixon • view change

- **BCG Full Service Pipelines**
  Nov 21, 2017 • updated by Dhivya Arasappan • view change

- **Introduction to RAD-seq short course 2017**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **Intro_to_RAD_short_course_2017.pptx**
  Nov 05, 2017 • attached by Groves B Dixon

- **Admixture**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **PCAs from SNPs**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **vcftools**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **Mapping ddRAD to a reference**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **demultiplex 2bRAD**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **Demultiplexing ddRAD**
  Nov 05, 2017 • updated by Groves B Dixon • view change

- **Predicting number of loci**
  Nov 05, 2017 • updated by Groves B Dixon • view change

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Test Appsoma Embed