National Center for Genome Analysis Support

Indiana University Pervasive Technology Institute

About   Contact   Request Allocation   Services   Software
Who We Are

Research Technologies

XSEDE

SDSC

TACC

nsf.gov

About the NCGAS

U.S. researchers are in the midst of dramatic developments in genome sequencing capabilities, driven by the availability of high throughput, low cost next-generation gene sequencers. To help address the scientific challenges of understanding this new wealth of gene sequence information, the **National Science Foundation** (NSF) has awarded **Indiana University** a **$1.5-million grant** (NSF Award #1062432 - *ABI Development: National Center for Genome Analysis Support*) to establish the **National Center for Genome Analysis Support** (NCGAS).

NCGAS supports the national community of NSF-funded researchers who undertake genome science, critical to new opportunities in biological discovery.

The NCGAS is the culmination of more than a decade of focused support for bioinformatics by University Information Technology Services, spearheaded initially by Dr. Richard Repasky and now led by Dr. William Barnett.

News, Events, Outreach

- UPCOMING: NCGAS Bioinformaticians and High Performance Applications specialists to present on the Optimization of Trinity at the XSEDE '12 Conference, Chicago Illinois. July, 2012
- UPCOMING: NCGAS to lead genomics BOF at XSEDE '12, Chicago Illinois. July, 2012
- Dr. William Barnett presented on **NCGAS international infrastructure design** at **Bio-IT World Asia**, June 6-8, 2012
- NCGAS Bioinformaticians from Indiana University and TACC presented a workshop on Trinity Use and Applications at the Jamboree RNA Data Analysis and Intrepretation, sponsored by the European Science Foundation and the Center for Genomics and Bioinformatics in Bloomington, IN, May 22, 2012
- Dr. William Barnett presented on **NCGAS national Infrastructure pilot** at **Bio-IT World**, April 25, 2012
- NEWS: '**Long Distance Analysis**' article on national infrastructure for genomics analysis (GenomeWeb Daily News, March 2012)
- NEWS: Dr. Richard LeDuc Joins IU as the new Manager of NCGAS: March 1, 2012
- Dr. Tom Doak gives **NCGAS Poster** at 2012 PAG Conference

- Dr. Tom Doak gives **NCGAS Poster** at 2012 Pacific Symposium on Biocomputing

2011

- NCGAS bandwidth challenge demo at Supercomputing 2011
- Press Release: **IU to address unique challenges of genome research with NSF grant.**
- NEWS: **Indiana to Host Computational Core for NSF-Funded Genomics** (GenomeWeb Daily News)
- NEWS: **IU to Establish Genome Research Center** (Inside Indiana Business)

National Center for Genome Analysis Support

Indiana University Pervasive Technology Institute

About   Contact   Request Allocation   Services   Software
Who We Are

Research Technologies

XSEDE

SDSC

TACC

nsf.gov

Services We Provide

The NCGAS provides the following services:

- Consulting services for biologists who want to undertake genome analysis on our systems. **Request an allocation** to be connected to our staff.
- Assistance in running genome analysis software on NCGAS systems
- Hardened and optimized **genome analysis software**
- An equitable and easy to use allocations process to submit requests for NCGAS computational resources. **Request an allocation**
- If you are submitting a grant to NSF, NCGAS can provide a **letter of support** for your project, and we are happy to discuss partnership arrangements as well.

For more information on using NCGAS resources at Indiana University, see the following Knowledge Base articles:

- **What is the National Center for Genome Analysis Support (NCGAS)?**
- **Mason at Indiana University**

Indiana University has contributed **Mason**, a large memory computational cluster, to support the efforts of the NCGAS. Mason is a 16 node system, each node with four Intel Xeon L7555 8-core processors (32 cores total) and 512 GB of RAM (8 TB RAM total).

If you use our services, please acknowledge our support in the following way:

This research is based upon work supported by the National Science Foundation under Grant No. ABI-1062432 to Indiana University. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation, the National Center for Genome Analysis Support, or Indiana University.

National Center for Genome Analysis Support

Indiana University Pervasive Technology Institute

About   Contact   Request Allocation   Services   Software
Who We Are

Research Technologies

XSEDE

SDSC

TACC

nsf.gov

Software We Support

Below is the list of software we currently support on Mason, the IU system committed to NCGAS. If you want to request additional software be installed, please complete this **software request form**.

ABySS de novo, parallel, paired-end sequence assembler

ALLPATHS-LG short read genome assembler

Arachne 2 toolkit for Whole Genome Shotgun Assembly

bedtools A collection of utilities for common genomics tasks

Bowtie ultrafast, memory-efficient short read aligner

BWA Burrows-Wheeler Aligner

BioPerl perl modules for bioinformatics

CD-HIT cluster Database at High Identity with Tolerance

Celera Assembler de novo whole-genome shotgun (WGS) DNA sequence assembler

Edena de novo short reads assembler

EULER fragment assembler using eulerian superpath approach

GATK The genome Analysis toolkit

GenomeMapper short read mapping tool

MUMmer rapid aligner for the entire genomes

NINJA Software for inferring large-scale neighbor-joining phylogenies

Novoalign program for mapping next-generation sequencing reads

Picard java-based command-line utilities that manipulate SAM files

RAxML fast implementation of maximum-likelihood (ML) phylogeny estimation

SAMtools A collection of utilities for manipulating alignments in the SAM format

SHORE A mapping and analysis pipeline for short DNA sequences

SOAPdenovo de novo short-read assembler

Trinity RNA-Seq A method for the de novo reconstruction of transcriptomes from RNA-Seq data

Velvet Sequence assembler for very short reads

GNU compiler collection C, C++, Fortran, Objective-C, Java and Ada compilers

Java Oracle/Sun java SDK and JRE

MPICH An older implementation of the MPI standard

OpenMPI An open source MPI-2 implementation

Vampir Open Trace Profile Viewer

Vampir Trace VAMPIR is a tool set for analyzing the performance and message-passing characteristics of parallel applications

PGI Portland Group Optimizing Compilers

Intel compiler suite

R The R Project for Statistical Computing

matlab A high-level language (license limited to IU users)

COMSOL COMSOL Multiphysics

SAS A powerful data analysis system (license limited to IU users)

PAPI Performance Application Programming Interface

If there are genome analysis packages you want to use, particularly those that are memory intensive, and do not see them here, please contact us. We can install software packages for you.

National Center for Genome Analysis Support

Indiana University Pervasive Technology Institute

About   Contact   **Request Allocation**   Services   Software
Who We Are

Research Technologies

XSEDE

SDSC

TACC

nsf.gov

Request Allocation

The NCGAS allows you to request an allocation to use our computational resources to support your NSF-funded genomics research. Right now we are in 'Early User' mode, which means you need only fill out a simple web form (below) to request access to our systems. As NCGAS evolves, we intend to evolve our allocations process to integrate with the XSEDE program as a Tier 2 resource. We hope that will happen by the middle of 2012. In the meantime, we want to make NCGAS resources available immediately to support your genomics research.

REQUEST AN ALLOCATION

For an allocation request, you'll be asked to provide information about the Grant PI, Project (including NSF award number), and personal information about each of the people that will need accounts on NCGAS systems. Our staff are happy to work with you to ensure you have all the information you need to get your research done.

There is no set allocation size for now. We will establish allocation size parameters as we work with our first cadre of research partners.

By using our services, you agree to acknowledge our support in the following way:

This research is based upon work supported by the National Science Foundation under Grant No. ABI-1062432 to Indiana University. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the National Science Foundation, the National Center for Genome Analysis Support, or Indiana University.

National Center for Genome Analysis Support

Indiana University Pervasive Technology Institute

**About   Contact   Request Allocation   Services   Software
Who We Are**

Research Technologies

XSEDE

SDSC

TACC

nsf.gov

Contact the NCGAS

Right now, the NCGAS is working to develop the processes and workflow support for NSF-funded biologists and other researchers to undertake genomics analyses on Mason and other NCGAS affiliated systems. Please expect more information to appear as soon as we have these in place. For more information see:

What is the National Center for Genome Analysis Support?

If you have questions for which you cannot find answers on this site or would like more information, please feel free to contact us at:

ncgas@iu.edu

If you wish to request an allocation to use NCGAS, please visit our **Request Allocations page**.

Thank you,

Bill Barnett, Director, NCGAS

Rich LeDuc, Manager, NCGAS