



Introduction to R

25 March 2022

Getting Started Using the Grace Cluster

<https://hprc.tamu.edu/>

TEXAS A&M HIGH PERFORMANCE RESEARCH COMPUTING

Home User Services Resources Research Policies Events About **Portal**

Quick Links

- New User Information
- Accounts
 - Apply for Accounts
 - Manage Accounts
- User Consulting
- Training
- Knowledge Base
- Software
- FAQ

User Guides

- Terra
- Grace

Click on
“Portal”

Getting Started Using the Grace Cluster

<https://hprc.tamu.edu/>

The screenshot shows the homepage of the Texas A&M High Performance Research Computing (HPRC) website. The browser address bar displays <https://hprc.tamu.edu/>. The website header includes the TAMU logo and the text "TEXAS A&M HIGH PERFORMANCE RESEARCH COMPUTING". A navigation menu contains links for Home, User Services, Resources, Research, Policies, Events, About, and Portal. Below the menu is a banner image of server racks. A yellow box highlights the "Grace Portal" link, with a yellow arrow pointing to it from a callout box on the right. The "Terra Portal" link is also visible above it. On the left side, there is a "Quick Links" sidebar with a list of links: New User Information, Accounts (with sub-links for Apply for Accounts and Manage Accounts), User Consulting, Training, Knowledge Base, Software, and FAQ. Below this is a "User Guides" section with links for Terra and Grace. At the bottom of the page, there is a large image of a molecular structure visualization.

Click on
"Grace Portal"

Getting Started Using the Grace Cluster

Central Authentication Service
DIVISION OF INFORMATION TECHNOLOGY

Activate Your NetID

LOG IN

Current Users

NetID or Email Address

Password

Next

[Forgot your password?](#)

[New Student or Employee? Activate your NetID](#)

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For additional information, please see the [Privacy and Security Statement](#).

ATM | TEXAS A&M UNIVERSITY | Division of Information Technology | [Site Policies](#) | [Accessibility](#)

Log in to CAS

Getting Started Using the Grace Cluster

TAMU HPRC OnDemand (Grace) Files Jobs Clusters **Interactive Apps** My Interactive Sessions

OnDemand provides an integrated, single access point for all of your HPC resources.

Message of the Day

IMPORTANT POLICY INFORMATION

- Unauthorized use of HPRC resources is prohibited and subject to criminal prosecution.
- Use of HPRC resources in violation of United States export control laws and regulations is prohibited. Current HPRC staff members are US citizens and legal residents.
- Sharing HPRC account and password information is in violation of State Law. Any shared accounts will be DISABLED.
- Authorized users must also adhere to ALL policies at: <https://hprc.tamu.edu/policies>

!! WARNING: THERE ARE ONLY NIGHTLY BACKUPS OF USER HOME DIRECTORIES. !!

powered by **OPEN OnDemand** OnDemand version: v1.8.20

Click on
“Interactive
Apps”

Getting Started Using the Grace Cluster

The screenshot shows the TAMU HPRC OnDemand (Grace) dashboard. The top navigation bar includes links for Files, Jobs, Clusters, Interactive Apps, Dashboard, My Interactive Sessions, Develop, Help, and Log Out. The user is logged in as 'wbrashear'. The main content area features a 'Message of the Day' section, 'IMPORTANT POLICY INFORMATION' with a list of rules, and a 'Servers' section. The 'Interactive Apps' dropdown menu is open, listing various applications. 'RStudio R 4.0.3, 3.6.3' is highlighted with a red box, and a red arrow points from this box to a separate box on the right. The footer includes the 'powered by OPEN OnDemand' logo and the version 'OnDemand version: v1.8.20'.

OnDemand provides an integrated, secure environment for your HPC resources.

Message of the Day

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!! WARNING: THERE ARE ONLY NIGHTLY BACKUPS !!

powered by **OPEN OnDemand** OnDemand version: v1.8.20

RStudio R
4.0.3,3.6.3

Getting Started Using the Grace Cluster

Home / My Interactive Sessions / RStudio R 4.0.3, 3.6.3

Interactive Apps

- BIO
- Beauti
- CRISPR-Local
- Gap5
- IGV
- Mauve
- Structure
- GUI
- ANSYS Workbench
- Abaqus/CAE (testing)
- MATLAB
- ParaView
- VNC
- Imaging
- ChimeraX
- cisTEM
- Servers
- Jupyter Notebook
- JupyterLab
- RStudio R 4.1.2
- RStudio R 4.0.3, 3.6.3**
- Spark-Jupyter Notebook

RStudio R 4.0.3, 3.6.3

This app will launch **RStudio Server** an IDE for **R** on the **Grace** cluster.

R version

4.0.3

Select an R version. Some R packages are not available in all R versions.

See [documentation](#) for installing R packages.

Number of hours

6

Number of cores:

1

Specify the number of cores [1-48] allocated on a node from the **Grace** cluster.

Total memory (GB)

8

Requested total memory (2 - 360GB)

Account

This field is optional.

Email

This field is optional

I would like to receive an email when the session starts

Launch

Increase to 6 hours

Click "Launch"

Getting Started Using the Grace Cluster

The screenshot displays the TAMU HPRC OnDemand (Grace) web interface. At the top, a navigation bar includes 'TAMU HPRC OnDemand (Grace)', 'Files', 'Jobs', 'Clusters', 'Interactive Apps', 'Dashboard', and 'My Interactive Sessions'. A user is logged in as 'wbrashear'. A green notification bar at the top left states 'Session was successfully deleted.' Below this, a breadcrumb trail shows 'Home / My Interactive Sessions'. On the left, a sidebar lists various 'Interactive Apps' such as BIO, Beauti, CRISPR-Local, Gap5, IGV, Mauve, Structure, ANSYS Workbench, Abaqus/CAE (testing), MATLAB, ParaView, VNC, ChimeraX, cisTEM, Jupyter Notebook, and JupyterLab. The main content area features a card for an 'RStudio R 4.1.2 (3776972)' session, which is 'Running' on '1 node | 1 core'. The session details include 'Host: c001', 'Created at: 2022-03-23 10:10:58 CDT', 'Time Remaining: 5 hours and 57 minutes', and 'Session ID: 0db5cfef-ed48-401b-9c25-54ba5b73d770'. A red 'Delete' button is visible. A blue button labeled 'Connect to RStudio Server' is highlighted with a red arrow pointing to it from a text box on the right. The text box contains the instruction: 'Wait for session to start and then click to connect'.

Getting Started Using the Grace Cluster

Click on File, then Open File

Files	Plots	Packages	Help	Viewer
Install	Update			
Name	Description	Version		
System Library				
<input type="checkbox"/> abc	Tools for Approximate Bayesian Computation (ABC)	2.1		
<input type="checkbox"/> abc.data	Data Only: Tools for Approximate Bayesian Computation (ABC)	1.0		
<input type="checkbox"/> abe	Augmented Backward Elimination	3.0.1		
<input type="checkbox"/> abind	Combine Multidimensional Arrays	1.4-5		
<input type="checkbox"/> acepack	ACE and AVAS for Selecting Multiple Regression Transformations	1.4.1		
<input type="checkbox"/> actuar	Actuarial Functions and Heavy Tailed Distributions	3.2-1		
<input type="checkbox"/> adabag	Applies Multiclass AdaBoost.M1, SAMME and Bagging	4.2		
<input type="checkbox"/> ade4	Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	1.7-18		
<input type="checkbox"/> ADGofTest	Anderson-Darling GoF test	0.3		
<input type="checkbox"/> affy	Methods for Affymetrix Oligonucleotide Arrays	1.72.0		
<input type="checkbox"/> affyio	Tools for parsing Affymetrix data files	1.64.0		
<input type="checkbox"/> aggregation	p-Value Aggregation Methods	1.0.1		
<input type="checkbox"/> AICcmodavg	Model Selection and Multimodel Inference Based on (Q)AIC(c)	2.3-1		
<input type="checkbox"/> airway	RangedSummarizedExperiment for RNA-Seq in airway smooth muscle cells, by Himes et al PLoS One 2014	1.14.0		
<input type="checkbox"/> akima	Interpolation of Irregularly and Regularly Spaced Data	0.6-2.2		
<input type="checkbox"/> alabama	Constrained Nonlinear Optimization	2015.3-1		
<input type="checkbox"/> AlgDesign	Algorithmic Experimental Design	1.2.0		
<input type="checkbox"/> amap	Another Multidimensional Analysis Package	0.8-18		
<input type="checkbox"/> Amelia	A Program for Missing Data	1.8.0		
<input type="checkbox"/> AnalyzefMRI	Functions for Analysis of fMRI Datasets Stored in the ANALYZE or NIFTI Format	1.1-24		
<input type="checkbox"/> animation	A Gallery of Animations in Statistics and Utilities to Create Animations	2.7		
<input type="checkbox"/> annotate	Annotation for microarrays	1.72.0		
<input type="checkbox"/> AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.56.2		
<input type="checkbox"/> AnnotationFilter	Facilities for Filtering Bioconductor Annotation Resources	1.18.0		
<input type="checkbox"/> AnnotationForge	Tools for building SQLite-based annotation data packages	1.36.0		

Getting Started Using the Grace Cluster

The screenshot shows the RStudio web interface. The terminal window displays the following text:

```
R 4.1.2 · /scratch/user/wbrashear/RNA_class/counts/
R version 4.1.2 (2021-11-01) -- "Bird Hippie"
Copyright (C) 2021 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

An 'Open File' dialog box is open, showing the file name field containing `/scratch/data/training/r`. A red arrow points from a text box to this field. The dialog also shows a file list with the following entries:

File Name	Size	Modified
..		
IntroductionToR_25March2022.Rmd	44.4 KB	Mar 23, 2022, 9:41 AM

The background shows the RStudio interface with a package list on the right side, including packages like 'Tools for Approximate Bayesian Computation (ABC)', 'Data Only: Tools for Approximate Bayesian Computation (ABC)', 'Augmented Backward Elimination', etc.

Go to
“/scratch/data/training/r”
and open the file that is
in that directory

Getting Started Using the Grace Cluster

Go to File -> Save As...

Save a copy to your personal scratch directory
"/scratch/user/username"

Package Name	Description	Version
Tools for Approximate Bayesian Computation (ABC)	Tools for Approximate Bayesian Computation (ABC)	2.1
Tools for Approximate Bayesian Computation (ABC)	Tools for Approximate Bayesian Computation (ABC)	1.0
Backward Elimination	Backward Elimination	3.0.1
Multidimensional Arrays	Multidimensional Arrays	1.4-5
AS for Selecting Multiple Regression Transformations	AS for Selecting Multiple Regression Transformations	1.4.1
Functions and Heavy Tailed Distributions	Functions and Heavy Tailed Distributions	3.2-1
Multiclass AdaBoost.M1, SAMME and Bagging	Multiclass AdaBoost.M1, SAMME and Bagging	4.2
Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	1.7-18
Anderson-Darling GoF test	Anderson-Darling GoF test	0.3
Methods for Affymetrix Oligonucleotide Arrays	Methods for Affymetrix Oligonucleotide Arrays	1.72.0
Tools for parsing Affymetrix data files	Tools for parsing Affymetrix data files	1.64.0
p-Value Aggregation Methods	p-Value Aggregation Methods	1.0.1
Model Selection and Multimodel Inference Based on (QAIC(c)	Model Selection and Multimodel Inference Based on (QAIC(c)	2.3-1
RangedSummarizedExperiment for RNA-Seq in airway smooth muscle cells, by Himes et al PLoS One 2014	RangedSummarizedExperiment for RNA-Seq in airway smooth muscle cells, by Himes et al PLoS One 2014	1.14.0
Interpolation of Irregularly and Regularly Spaced Data	Interpolation of Irregularly and Regularly Spaced Data	0.6-2.2
Constrained Nonlinear Optimization	Constrained Nonlinear Optimization	2015.3-1
Algorithmic Experimental Design	Algorithmic Experimental Design	1.2.0
Another Multidimensional Analysis Package	Another Multidimensional Analysis Package	0.8-18
A Program for Missing Data	A Program for Missing Data	1.8.0
Functions for Analysis of fMRI Datasets Stored in the ANALYZE or NIFTI Format	Functions for Analysis of fMRI Datasets Stored in the ANALYZE or NIFTI Format	1.1-24
A Gallery of Animations in Statistics and Utilities to Create Animations	A Gallery of Animations in Statistics and Utilities to Create Animations	2.7
Annotation for microarrays	Annotation for microarrays	1.72.0
Manipulation of SQLite-based annotations in Bioconductor	Manipulation of SQLite-based annotations in Bioconductor	1.56.2
Facilities for Filtering Bioconductor Annotation Resources	Facilities for Filtering Bioconductor Annotation Resources	1.18.0
Tools for building SQLite-based annotation data packages	Tools for building SQLite-based annotation data packages	1.36.0

Getting Started Using the Grace Cluster

Click "Run Document"

```
1 ---
2 title: "Introduction to R"
3 output: learnr::tutorial
4 author: Wesley Brashear, Ridham Patoliya, Zhenhua He, Richard Lawrence, Dhruva Chakravorty
5 runtime: shiny_prerendered
6 ---
7
8 ```{r setup, include=FALSE}
9 library(learnr)
10 library(ggplot2)
11 knitr::opts_chunk$set(echo = FALSE)
12
13
14 ```
15
16 ## **R as a calculator**
17
18 In it's simplest form, R can be used as a calculator (although it can do so much more!). Let's get started in R by
19 doing some basic arithmetic!
20
21 > Arithmetic Operators
22
23 * Addition: `+`
24 * Subtraction: `-`
25
26 Introduction to R
```

R 4.1.2 · /scratch/user/wbrashear/RNA_class/counts/

R version 4.1.2 (2021-11-01) -- "Bird Hippie"
Copyright (C) 2021 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

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