CoGAPS on SciServer

June, 2023

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# About this Course

This introductory course will provide a quick overview of how the Bayesian NMF algorithm, CoGAPS (Coordinated Gene Activity across Pattern Subsets), can provide new insights into single cell datasets. Through these exercises you will analyze a real dataset using the SciServer compute platform.

## 0.1 Available course formats

This course is available in multiple formats which allows you to take it in the way that best suits your needs. You can take it for certificate (for free) using Leanpub.

* The material for this course can be viewed without login requirement on this [Bookdown website](https://practicalgenomics.github.io/cogaps-on-sciserver/). This format might be most appropriate for you if you rely on screen-reader technology.
* This course can be taken for [free certification through Leanpub](LINK%20HERE).
* Our courses are open source, you can find the [source material for this course on GitHub](https://github.com/PracticalGenomics/cogaps-on-sciserver).

# 1 Introduction

This introductory course will provide a quick overview of how the Bayesian NMF algorithm, CoGAPS (Coordinated Gene Activity across Pattern Subsets), can provide new insights into single cell datasets. Through these exercises you will analyze a real dataset using the SciServer compute platform.

## 1.1 Motivation

If you would like to perform sparse matrix factorization on any data. And when this data represents biomolecules, to do gene set analysis. This can be done with CoGAPS, which can be used by anyone; no machine learning experience is required.

## 1.2 Target Audience

The course is intended for anyone! No software or prior coding experience is required.

## 1.3 Curriculum

The course covers:

* How to join the compute platform, SciServer
* How to access and launch cellxgene
* How to load packages, data, configure/run CoGAPS, visualize patterns, find pattern markers, and document software in RStudio

devtools::session\_info()

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## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library

# 2 Getting Started with SciServer

## 2.1 What is SciServer?

SciServer is an online platform that provides access to big data resources to researchers worldwide. It is used by scientists studying astronomy, biology, oceanography, and more. It is free to use as long as you are using it for scientific research. Through using SciServer, you don’t need a fancy computer or need to install any special programs on your computer, you can simply log in with your internet browser to start doing research. For this course, we have set up SciServer with customized collections of programs for RNA-seq analysis, as well as the data that we’ll be analyzing. Once you sign up for SciServer and are added to the group for this course, you will be able to access these tools and begin your data analysis journey!

## 2.2 Why use SciServer?

In this course, we will use the online SciServer platform in order to perform data analysis. The purpose of this assignment is to register for a SciServer account, and then to inform the instructor of your username so that you can be added to the SciServer group for this course and access course materials.

## 2.3 Learning Objectives

This chapter will cover:

* How to create an account on SciServer
* How to confirm your email address
* How to share your username with your instructor

## 2.4 Create an Account on SciServer

1. Open [sciserver.org](https://sciserver.org) in a web browser.
2. TIP: Bookmark this page so that you can easily access it throughout the course.
3. Click “**Login to Sciserver**”
4. Click “**Create a new account**”
5. Enter a username, email, etc. and click “**Create account**”
6. Note that you cannot change your username.

## 2.5 Confirm Your Email Address

1. **Important!**: Click the verification link in your email inbox.
2. If you don’t verify your account, you will get locked out and will need to contact your instructor to unlock your account.
3. If you don’t see an email, try checking your spam folder.
4. After clicking the verification link, confirm that your username appears on the upper right hand corner of the webpage.

### 2.5.1 Resources

[sciserver.org](https://sciserver.org) [How to add a bookmark in Chrome](https://support.google.com/chrome/answer/188842) [SciServer Help page](https://sciserver.org/support/how-to-use-sciserver/)

### 2.5.2 References

Cox, K., & Tan, F. (2022, January 25). Join SciServer. C-MOOR. Retrieved June 27, 2023, from <http://www.c-moor.org/miniCURE-RNA-seq/join-sciserver.html>

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# 3 cellxgene

## 3.1 Learning Objectives

* Confirm access to STAC Administrators Group
* Launch cellxgene
* Edit SciServer Dashboard

## 3.2 Instructions

### 3.2.1 Confirm Access

1. Go to <sciserver.org> and click on “**Login to SciServer**”.
2. Log in with the SciServer account you created in Part 1.
3. Once logged in, you will see options on the top menu bar of the homepage/Dashboard (Home, Files, Groups, and various options for Compute). Confirm that you received and accepted the invitation to the STAC Administrators Group by clicking on “**Groups**” in the top menu bar.
4. Click on “**STAC Administrators**” in the left sidebar menu. You should see your username in the Members list on the right sidebar. You should also have access to the Shared Data Volume “STAC” and Share Compute Image “single-cell-explorer”.

### 3.2.2 Launch cellxgene

1. In order to explore the available datasets, click on “**Files**” in the top menu bar.
2. Click on “**Data Volumes**” in the left sidebar menu.
3. Scroll down the page to find the data volume “**STAC**”. Click on the name to access the dashboard.
4. Under the “Available datasets” heading, click on “**PDAC** [**cellxgene**](#cellxgene)”.
5. cellxgene should now launch with your dataset of interest ready to explore!

### 3.2.3 Edit Dashboard

1. Click on “**Files**” in the top menu bar.
2. Click on “**Data Volumes**” in the left sidebar menu.
3. Scroll down the page to find the data volume “**STAC**”. Click on the name to access the dashboard.
4. Scroll to the bottom of the page and find the “README.md” file. Click on the three dots, then click “**View/Edit**”.
5. You should now be able to edit and improve the README file using standard Markdown syntax.

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| **Pedagogy** |  |
| Lead Content Instructor(s) | [FirstName LastName](link%20to%20personal%20website) |
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| Content Editor(s)/Reviewer(s) | Checked your content |
| Content Director(s) | Helped guide the content direction |
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| **Art and Design** |  |
| Illustrator(s) | Created graphics for the course |
| Figure Artist(s) | Created figures/plots for course |
| Videographer(s) | Filmed videos |
| Videography Editor(s) | Edited film |
| Audiographer(s) | Recorded audio |
| Audiography Editor(s) | Edited audio recordings |
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| Funder(s) | Institution/individual who funded course including grant number |
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## remotes 2.2.0 2020-07-21 [1] RSPM (R 4.0.3)   
## rlang 1.1.0 2023-03-14 [1] CRAN (R 4.0.2)   
## rmarkdown 2.10 2023-03-28 [1] Github (rstudio/rmarkdown@02d3c25)  
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## sessioninfo 1.1.1 2018-11-05 [1] RSPM (R 4.0.3)   
## stringi 1.5.3 2020-09-09 [1] RSPM (R 4.0.3)   
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## yaml 2.2.1 2020-02-01 [1] RSPM (R 4.0.3)   
##   
## [1] /usr/local/lib/R/site-library  
## [2] /usr/local/lib/R/library

# 4 References