

# ABACBS 2023 Stereo-seq Spatial Data Challenge

## The Data Challenge

Welcome to the ABACBS 2023 Stereo-seq Spatial Data Challenge. Are you ready to explore the dynamic world of high-resolution spatial transcriptomics? Get set to dive into a thrilling challenge that offers not just the excitement of discovery but the chance to win extraordinary prizes. Whether you're a seasoned data maverick or a curious newcomer, this challenge is your ticket to experiencing the power of spatial data analysis. The Challenge will be open from **9th-30 November 2023**. Embrace this chance to make your mark in spatial transcriptomics, and win epic prizes such as STOmics Cloud subscriptions valued up to \$9,500, Fitbit Smart Watches, gaming keyboard & mouse set, magic 8 balls for bioinformaticians, and more. Seize this opportunity to wield the power of Stereo-seq, the most accessible spatial platform brought to you by [MGI](#) and [STOmics](#), participants will embark on a journey through a series of tasks to perform spatial data analysis using the StereoPy software. The challenge encompasses four compulsory tasks, each focusing on different facets of the Stereo-seq data analysis. A comprehensive **Jupyter Notebook** document will be provided, including the assigned tasks, step-by-step guidance, and the required output or images as proof of task completion. Participating in this challenge offers participants the unique opportunity to explore the capabilities of Stereo-seq technology and StereoPy software, elevating their skills and deepening their understanding of spatial transcriptomics analysis.

**Important Details:** Once you sign up, you'll receive our handy info pack, complete with task descriptions and details on joining our vibrant Slack community support group. No matter your technical experience, we've got your back!

**Judgment Criteria:** Participant rankings will be based on the number of successfully completed tasks and the percentage of tasks completed. In cases where multiple participants complete the same number of tasks, submission times will serve as tiebreakers to determine their positions in the rankings, ensuring fairness and precision.

**The Challenge:** The challenge features four (4) tasks in total that progress from preprocessing data, conducting basic analysis, to engaging in more advanced functional analysis, fully harnessing the power of single-cell resolution offered by Stereo-seq spatial transcriptomics technology. Task names include:

- Task 1: Data Filtering and Square Bin Analysis
- Task 2: Cell Bin and Marker Genes
- Task 3: ROI Extraction & Batch Integration
- Task 4: Cell-Cell Interaction & Cell Communication Analysis

**Eligibility:** To enter the challenge, you must be a registered delegate for the ABACBS 2023 conference. If you haven't registered yet be sure to register for the conference then you're eligible to attend the challenge.

**Minimum Computer Requirements:** Prepare for a seamless experience by ensuring your computer meets these specs:

- Operating system: Windows or Linux (preferred)
- Processor: Intel i5 or AMD Ryzen 5 with at least four cores
- RAM: Minimum 16GB
- Storage: At least 15GB
- Administrative rights to install Conda and related packages in your development environment

**Prerequisite Knowledge & Skills:** Participants should have a grasp of:

- Using a command-line interface (CLI) for running simple commands
- Basic Python knowledge, including importing external packages and libraries

### Important Dates

Open date: The challenge will be open with the data set and assignments available for download **12 pm (noon) AEST, 9/11/2023 (Thurs)**

Close date: The link for submissions will be closed at **12 pm (noon) AEST, 30/November/2023 (Thurs)**.

The Challenge will be open at **12 pm (noon) on 9th November Thursday** i.e. the challenge data set will be available from that time forward until the close time. The submission link closes at **12 pm (noon) on 30th November, Thursday**. We'll send you email reminders as we approach the cut-off time, and you can also stay in the loop on our Slack channel. The OneDrive folder will be provided to you which contains all you need including data sets to instructions and references for downloads, the submission link to showcase your work.

**Winner Announcement:** The challenge winners will be revealed during the STOmics Morning Workshop on 7<sup>th</sup> December on UQ campus at the ABACBS 2023 conference. Get ready to take a bow and collect your well-deserved rewards.

**How to Sign up:** through the Sign-up Form link <https://forms.office.com/r/xDqtqdK9RP>

### Prizes and Winner Announcement:

**Prizes:** Don't miss your chance to have fun with spatial data while winning incredible prizes. Four (4) tiers of prizes will be offered including

- 1<sup>st</sup> Platinum Awards:

Three top winners will receive the coveted 1st Platinum Award. Winners will receive substantial STOmics Cloud\* subscriptions subject to their rankings of valued at up to AU\$9,500 in credit, which will grant access to the analysis of data from 12, 8, or 4 STOmics libraries on the high-resolution Stereo-seq 1x1cm chip. It's a golden opportunity to dive deep into the world of spatial data analysis.

- 2<sup>nd</sup> Gold Awards:

The 2nd Gold Awards are all about staying active and in tune with your brilliant mind. Two winners will take home Fitbit Smartwatches, perfect companions for a fit and data-savvy lifestyle.

- 3<sup>rd</sup> Silver Award:

The 3rd Silver Award brings versatility to your computing experience. Two fortunate winners will receive an Ergonomic Wireless Keyboard and Mouse set. Whether it's for work or play, these high-quality peripherals are perfect for bioinformaticians and all computer enthusiasts, adding comfort and efficiency to your everyday tasks.

- 4<sup>th</sup> Excellence Award:

Rewarding mental agility and fun, the 4<sup>th</sup> Excellence Award celebrates the joy of staying mentally fit. Ten lucky winners will receive iconic Rubik's Cubes, perfect for bioinformaticians and puzzle enthusiasts to keep their minds sharp and entertained. It's also a token of appreciation for your participation in the Stereo-seq Spatial Data Challenge.

**Winner announcement:** The Challenge winners will be revealed during the STOmics Morning Workshop at the ABACBS 2023 conference to be held on UQ campus on 7<sup>th</sup> Dec. 2023 (details will be provided closer to the date). Get ready to take a bow and collect your well-deserved rewards. For catering purposes please confirm your attendance at our workshop when you fill out your sign-up form.

## Slack Support Hub



Our Support hub on Slack is your go-to destination for all things related to the Challenge. Whether you're seeking technical assistance, clarifications on tasks, or just looking to connect with fellow participants, our hub is here to make your journey smoother. Get ready to dive into spatial data analysis with confidence, and don't hesitate to reach out to our supportive community. Join us on Slack

[https://join.slack.com/t/stomicsabacbs2023/shared\\_invite/zt-26hcbp1qo-knvuk7ssmRvkaEJeSTUhTw](https://join.slack.com/t/stomicsabacbs2023/shared_invite/zt-26hcbp1qo-knvuk7ssmRvkaEJeSTUhTw) and let's unravel the mysteries of spatial transcriptomics together!

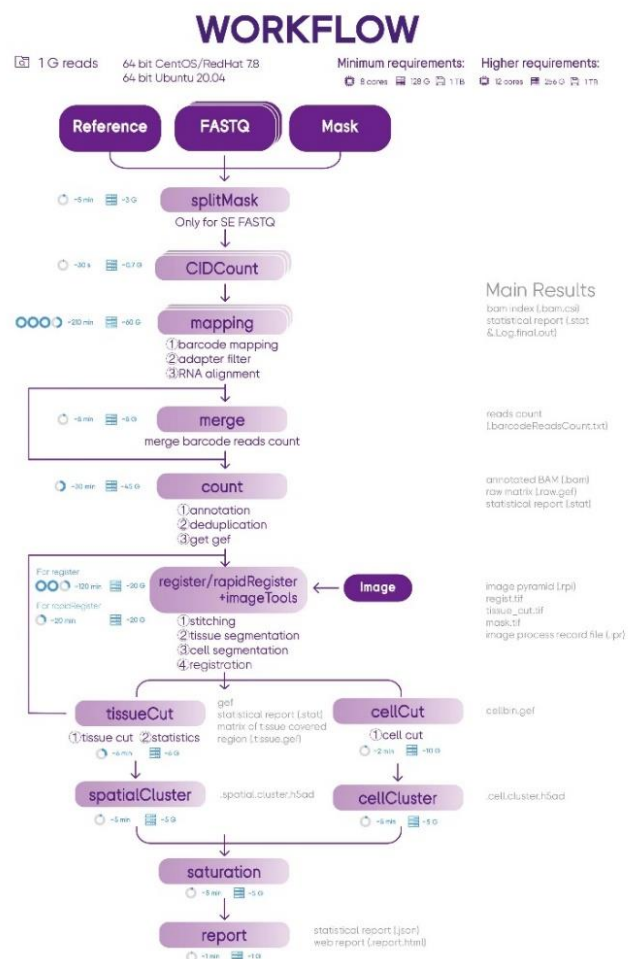
## Technology Background

### Spatial Technology Stereo-seq

Stereo-seq is an advanced spatial transcriptomics technology, reaching an impressive resolution of 500nm, one of the highest resolutions in the global market. This cutting-edge technology enables researchers to achieve single-cell resolution, providing valuable insights into the spatial organization and gene expression patterns within complex biological tissues. By integrating high-resolution imaging with transcriptomic profiling, Stereo-seq™ empowers researchers to unravel the molecular landscapes of tissues in single cell resolution, uncovering the spatial distribution of gene expression and its impact on tissue functionality. The Stereo-seq technology is powered by **STOmics**. To find more information about Stereo-seq please visit the [STOmics website](https://www.stomics.com).

### Stereo-seq Bioinformatics Solution Overview

There are a few bioinformatics tools that will be utilized in the challenge. Familiarizing yourself with these tools is essential for successfully completing the tasks and gaining a deeper understanding of Stereo-seq data analysis. The tools we will cover include StereoPy, Anaconda, and Jupyter. While the sample data provided are output from the Stereo-seq Analysis Pipeline (SAW), and therefore, SAW will not be used as part of the challenge, it is also crucial to know what it does and the files output from the pipeline.



- **SAW – Stereo-seq Analysis Pipeline**

SAW is a crucial component of the Stereo-seq data analysis workflow. It plays a vital role as a plug-and-play tool and pipeline that map sequenced reads to their spatial location on the tissue section, quantify the corresponding gene expression levels and visually present spatial gene expression distribution.

Its design as a Linux CLI tool, optimizes for massive parallel computation, ensuring efficient processing of Stereo-seq sequencing reads. Aiming to act as the standard pipeline for analysis of Stereo-seq data, shorten the learning curve and allow bioinformaticians to jumpstart their analysis when first encounter Stereo-seq technology, and enabling them to spend more time to delve deep into the data, and look for its biological significance that is important to the research question at hand.

Refer to the following diagram for the pipeline included in SAW. In brief, it takes in the 4 input files: The sequencing .FASTQ files; The .H5 mask file provided by STOmics upon purchase of the Stereo-seq chips that contain the spatial information and its corresponding coordinate ID (CID) barcode; The reference genome for the corresponding species for sequence mapping, and; the Image Process Record (.IPR) file storing the processed nuclear stained image of the tissue sample, and in the end of the pipeline, various output files are generated that serves as the input for downstream analysis using the StereoPy library.

You can find a more detailed description and file structure in the “Stereo-seq analysis workflow file format manual” in the sample data pack provided.

- **StereoPy**

StereoPy is a fundamental and comprehensive tool for mining and visualization based on spatial transcriptomics data, such as Stereo-seq. With StereoPy, you can dig deep into the rich world of spatial transcriptomics, exploring the intricate dance of genes within tissues. It helps you analyse and visualize Stereo-seq data effortlessly, giving you a ticket to the front row of the gene expression show.

After setup, this library streamlines complex analysis tasks by offering an integrated, interactive environment for various analyses. StereoPy is a versatile tool that can assist with tasks such as gene expression tracking, cell type identification, the exploration of spatial hotspots, and more.

If you're exploring the world of spatial transcriptomics, StereoPy is a reliable tool to help you unravel the intricacies concealed within tissue samples. You may find the detailed documentation on the library, from installation, usage principles, tutorials to API here <https://stereopy.readthedocs.io/en/latest/>.

## Terms and conditions

- Participation Agreement

By participating in the Stereo-seq Spatial Data Challenge, all participants agree to comply with the following terms and conditions.

- Eligibility

To participate in the challenge, you must be a registered delegate for the ABACBS 2023 conference. No other eligibility criteria are required for participation.

- Organizer's Rights

The organizers of the challenge reserve the right to amend or modify the rules and regulations, as well as the structure of the challenge, at any time without prior notice. We also retain the right to interpret and enforce these rules at our discretion.

- Data Usage and Ownership

Participants are provided with data sets and resources for the challenge, but they acknowledge that the data remains the property of the organizers. By participating, participants grant the organizers and their affiliates the right to use their work, including submissions, for promotional and educational purposes.

- Liability

The organizers are not liable for any data loss, technical issues, or any other complications that may arise during the challenge. Participants assume all risks and responsibilities associated with their participation.

- Disqualification

Any participant found to be in violation of the rules or engaged in unethical conduct may be disqualified. The decision of disqualification is at the sole discretion of the organizers.

- Prizes

Prize distribution is at the discretion of the organizers. The organizers reserve the right to substitute prizes with others of equivalent value.

- Personal Information

The personal information collected during registration will be used solely for the purpose of the challenge and will not be shared with third parties for marketing purposes.

- Termination

The organizers reserve the right to terminate the challenge or disqualify participants at any time if deemed necessary.

- Jurisdiction

These terms and conditions are governed by the applicable laws of Queensland, Australia, and any disputes are subject to the exclusive jurisdiction of the courts within the state of Queensland.

## Frequently Asked Questions

### 1. Who can participate in the Stereo-seq Spatial Data Challenge?

The challenge is open to all registered delegates of the ABACBS 2023 conference. If you haven't registered yet you may register for the conference at the ABACBS website [here](#).

### 2. Do I need to be an expert in spatial data analysis to participate?

No, the challenge is designed to accommodate participants with varying levels of experience, from beginners to experts. The provided Jupyter notebook offers step-by-step guidance to assist you. Subject to your level of experience and familiarity with Conda, you may need to spend 3 to 6 hours in total to complete all the tasks.

### 3. What are the minimum computer requirements for participation?

To ensure a smooth experience, participants should have a Windows or Linux (preferred) operating system, an Intel i5 or AMD Ryzen 5 processor with at least four cores, a minimum of 16GB of RAM, at least 15GB of storage space, and administrative rights to install Conda and related packages in their development environment.

#### 4. How will participants be judged and ranked in the challenge?

Participant rankings will be based on the number of successfully completed tasks. In the event that multiple participants complete the same number of tasks, submission time will be used as a tiebreaker.

#### 5. Where can I find support during the challenge if I have questions or encounter technical issues?

We have a dedicated Slack support group where you can seek assistance, interact with fellow participants, and get your questions answered. Sign up now and we'll send you the details.

#### 6. How do I register for the challenge?

You can register for the challenge through the Sign-up Form [here](#). Once you're registered, you'll receive instructions on how to participate in the challenge.

#### 7. What are the prizes for the challenge?

We're offering a range of exciting prizes, including STOmics Cloud subscriptions, Fitbit Smartwatches, ergonomic wireless keyboard and mouse sets, Rubik's cubes, and more. Visit the challenge landing page for detailed information on prizes.

#### 8. When does the challenge start and end?

The challenge opens from 12 pm (noon), 9<sup>th</sup> November and closes at 12 pm (noon) 30<sup>th</sup> November, 2023. Be sure to submit your work before the closing date.

#### 9. How can I stay updated on challenge announcements and reminders?

We'll send email reminders during the challenge period. You can also follow our Slack channel, where we'll be posting important updates and reminders.

#### 10. How can I access the necessary resources and data for the challenge?

Once the challenge begins, a OneDrive folder will be provided to all participants. It will contain the data set, instructions, references for downloads, and the submission link for your work.

#### 11. Can I stop in the middle of a task and come back later to complete it?

Yes, for each individual task, you have the flexibility to pause your progress in the middle of the task and return to it at your convenience. You can put the task window aside, but it needs to remain open until you complete that specific task. Once a task is finished and your Jupyter Notebook is saved successfully onto your local drive, you are free to close the task window.

#### 12. Can I stop between tasks?

Certainly! You have the flexibility to stop or take breaks between tasks. The tasks are not interrelated, so you can choose to proceed to the next one at your own pace, allowing for a comfortable and adaptable experience during the challenge. Your progress between tasks can be managed according to your preference. However, remember that submission times are tiebreakers if you and other participants submit the work with the same level of completion.

#### 13. When I submit my work, what are the submission requirements?

To submit your work, please follow these guidelines:

- Place all your output files into a folder and name it in the format "FirstName\_LastName\_Institute."



- Zip the entire folder and use the same name for the zip file as the output folder.
- Upload the zip folder to our OneDrive Submission Link.
- Once you have uploaded your submission, a timestamp will be generated to confirm the submission time. Please ensure that your submission adheres to these requirements for a successful entry into the challenge.

#### 14. How do I know if I've successfully uploaded the files?

After you've uploaded your files to our OneDrive Submission Link, a successful notification will be sent to your provided email address, confirming that your submission has been received and recorded. This confirmation ensures that your entry is in good standing for the challenge. Because the organising team will need to manually check the files submitted on a daily basis, please expect a turnaround time of up to 24 hours for confirmation of receipt.

#### 15. Can I join the challenge after it's already open?

Yes, you can still join the challenge even after it has started. The challenge is open for participation from the 9th to the 30th of November. So, there's plenty of time to explore, learn, and submit your work. Don't worry about joining late; it's about the experience and the opportunity to delve into the world of spatial data analysis. Your participation is valuable!

#### 16. When is the cut-off time for submissions?

The cut-off time for submissions is 12 pm on 30<sup>th</sup> November Thursday, 2023, when the submission link will be deactivated. Please ensure that you submit your work before this deadline to be eligible for consideration in the challenge.

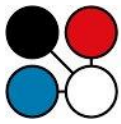
#### 17. When and how will I be informed about the challenge results?

The results of the Challenge will be announced at the STOmics Morning Workshop on 7<sup>th</sup> December during the ABACBS 2023 conference. You will also receive an email notification with the results and further instructions closer to the ABACBS conference.

#### 18. What are the terms and conditions for claiming the prizes?

There are terms and conditions that participants should be aware of when claiming their prizes:

- All prizes will be given out to the winners at the Winner Announcement during the STOmics Morning Workshop during the ABACBS 2023 conference (9-10am 7<sup>th</sup> Dec 2023 in UQ St. Lucia). Attendees can join the event physically or online. Please click the option of attendance when you sign up. Failure to attend may result in forfeiture of the prizes.
- Redemption Period: The first tier of prizes i.e. the STOmics Cloud subscriptions must be claimed within one year from the date they are awarded. After this period, unclaimed subscriptions will expire, and no compensation will be available.
- Non-transferable: The STOmics Cloud subscriptions are intended for the personal use of the winners and are not to be used for any commercial purposes. They are not to be sold, assigned, or otherwise transferred to another party.
- Compliance: The STOmics subscription winners are expected to comply with the terms and conditions of the STOmics Cloud service provider, including any usage policies and restrictions.
- Modification: The terms and conditions of the STOmics Cloud subscriptions are subject to change by the service provider, and winners are expected to adhere to any such changes.



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- Cancellation: The service provider reserves the right to cancel or suspend subscriptions in cases of misuse, abuse, or violation of their policies.

This bioinformatics data analysis competition **ABACBS 2023 Stereo-seq Spatial Data Challenge** is made possible by the joint support from [MGI](#), a world-leading life science innovator, and [STOmics](#), a cutting-edge spatial technology pioneer. Find more information on their company websites.

Updated on 7<sup>th</sup> Nov. 2023