

**STOmics**

**Stereo-seq  
ANALYSIS WORKFLOW  
SOFTWARE SUITE  
USER MANUAL**

Software Version: V5.5.0

Manual Version: A5

# REVISION HISTORY

**Manual Version:** A0  
**Software Version:** V1.0.0  
**Date:** Nov. 2021  
**Description:** Initial release

**Manual Version:** A1  
**Software Version:** V2.1.0  
**Date:** Dec. 2021  
**Description:**

- **New feature:** addition of manual registration function, some fine-tuning will be automatically performed after manually registering;
- **Improvement:** performance improvement for **mapping**; the order of sequencing saturation calculation has switched, in v2.1.0 we only compute the saturation of tissue-covered region;
- **Bug fix:** fixed the bug of indexing at **mapping** step; fix the bug of long waiting time at **register** step.

**Manual Version:** A1.1  
**Software Version:** V2.1.0  
**Date:** Jan. 2022  
**Description:**

- Add error handling;
- Update demo output.

**Manual Version:** A2  
**Software Version:** V4.1.0  
**Date:** Apr. 2022  
**Description:**

- **New feature:** support to process fused microscopic images; employ Stereopy in clustering; new gene expression matrix file format; including a file format convertor and a **mapping** memory estimator;
- **Improvement:** performance improvement for **mapping**; update gene annotation approach in **count**; update image stitching and tissue segmentation model for better performance on image stitching and segmentation for tissue with voids.

**Manual Version:** A3  
**Software Version:** V5.1.3  
**Date:** Aug. 2022  
**Description:**

- **New feature:** addition of cell segmentation on microscopic image in **register** pipeline module and **cellCut** pipeline module to extract cell expression matrix; design IPR file to store image processing record information and TIFF images produced in **register**; output exon expression matrix along with total MID count; addition of cell clustering analysis; addition of cell bin statistic result and image information in HTML report; add pipeline modules to support single-end FASTQ data; addition of option for selecting multi-mapped reads; addition of score system in image processing;
- **Improvement:** addition of poly A filtration in **mapping**; performance improvement for **merge**, **tissueCut** and **saturation**; add data scaling and upgrade clustering analysis pipeline;
- **Bug fix:** fix the bug of plotting scatter plot in **tissueCut**, review and modify the ambiguous metrics names and explanations in HTML report.

**Manual Version:** A4  
**Software Version:** V5.4.0  
**Date:** Nov. 2022  
**Description:**

- **New feature:** render a more elegant way of organizing SE FASTQs input into **mapping**; addition of header for **count** output TXT file; upgrade **ipr2img** to **imageTools** which allows you to merge TIFF images to check segmentation result and plot templates on the panoramic image or registered image to check the result of stitching and registration;
- **Improvement:** change data struct of gene index in the GEF file from uint16 to uint32 to store more genes;
- **Bug fix:** fix the typo in the manual.

**Manual Version:** A3.1  
**Software Version:** V5.1.3  
**Date:** Dec. 2022

**Description:**

- **Bug fix:** fix the typo in the manual.
- 

**Manual Version:** A5  
**Software Version:** V5.5.0  
**Date:** Jan. 2023

**Description:**

- **New feature:** addition of **manualRegister** and **lasso** pipeline modules, which acquire parameters and essential files from offline visualization software **StereoMap**; addition of error code function in each module, and the explanation has been organized in appendix D;
- **Improvement:** upgrade **tissueCut** pipeline module for better performance and improved accuracy of tissue recognition directly from gene expression matrix; upgrade clustering analysis pipelines; addition of image layers in HTML report which allow users to switch images displayed with gene expression distribution plot; the stitching deviation heatmap(s) and the frame of axes in the HTML report have been adjusted according to the registration parameters.

**Note: Please download the latest version of the manual and use it with the software specific to this manual.**

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# WORKFLOW

1 G reads

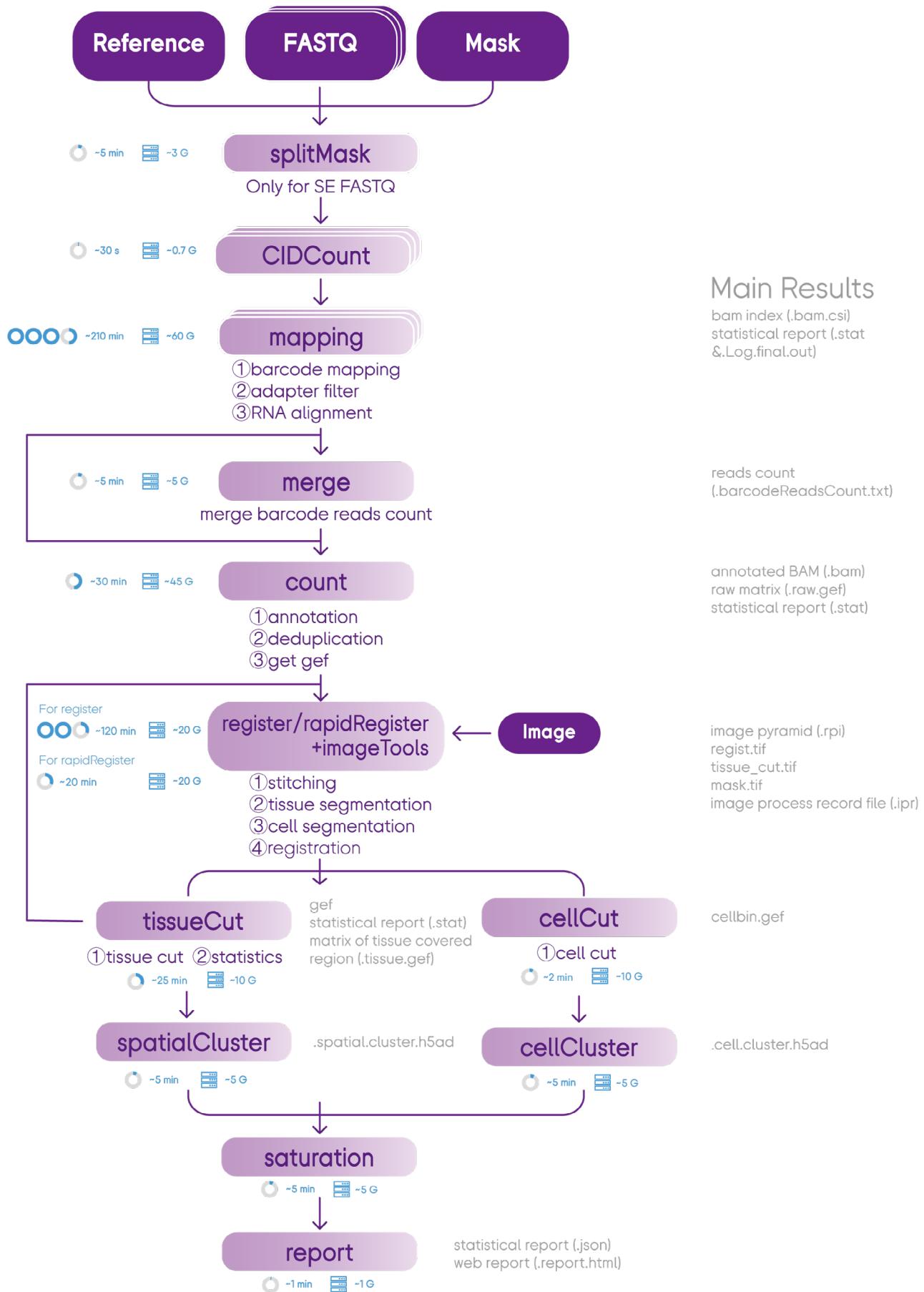
64 bit CentOS/RedHat 7.8  
64 bit Ubuntu 20.04

Minimum requirements:

8 cores 128 G 1 TB

Higher requirements:

12 cores 256 G 1 TB



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**CRITICAL STEPS:** Pay extra attention to these instructions/steps to avoid problematic results.



**SOLUTION:** Provides a solution to handling common errors.

# **CHAPTER 1**

## **STEREO-SEQ ANALYSIS WORKFLOW SOFTWARE SUITE**

## 1.1. Software Introduction

Stereo-seq Analysis Workflow<sup>1</sup> (SAW) software suite is a set of pipelines bundled to position sequenced reads to their spatial location on the tissue section, quantify spatial gene expression and visually present spatial expression distribution. SAW processes the sequencing data of Stereo-seq<sup>2</sup> to generate spatial gene expression matrices, and then users could take these files as the starting point to perform downstream analysis. SAW includes thirteen essential and suggested pipelines and auxiliary tools for supporting other handy functions:

- **splitMask:** Split Stereo-seq Chip T mask file into several pieces according to CID indexing in the SE FASTQ files.
- **CIDCount:** Counting CIDs in the Stereo-seq Chip T mask file and roughly estimating memory required to do mapping.
- **mapping:** Corresponds *in situ* captured sequenced reads recorded in FASTQ<sup>3,4</sup> files by Stereo-seq with their spatial information. It also aligns reads to the reference genome and generates coordination sorted BAM files.
- **merge (optional):** Combines CID (same as barcodes) listed files with reads count from multiple runs of mapping. Only for an analysis that requires to combine multiple pairs of FASTQ.
- **count:** Reads BAM files generated from mapping to perform gene annotation, de-duplication, and gene expression analysis on the aligned reads.
- **register:** Align microscopic tissue staining image with gene expression matrix file (GEF) generated from count.register is an optional pipeline when image failed QC or input image is absent.
- **imageTools:** Convert TIFF images from IPR, such as template-aligned stitched TIFF image, binarized tissue segmentation and cell segmentation images. Optional module when image failed QC or input image is absent.
- **tissueCut:** Identify tissue coverage area on the chip and extract gene expression matrix of the corresponding spatial location by taking inputs from both count and register or count pipeline alone.
- **spatialCluster:** Perform clustering analysis for spots (bin200) according to the gene expression matrix of the tissue covered area generated from tissueCut.
- **cellCut:** Identify cell coverage area on the staining image and extract gene expression matrix of the corresponding spatial location by taking inputs from both count and register&imageTools pipeline. Optional module when image failed QC or input image is absent.
- **cellCluster:** Perform clustering analysis for cell bins according to the gene expression matrix which is generated from cellCut. Optional module when image failed QC or input ssDNA image is absent.
- **saturation:** Calculate sequencing saturation of tissue coverage area based on the file that was used for sampling data generated from count.
- **report:** Generate a JSON format statistical summary report that integrate the analysis result from each step, as well as an HTML web analysis report, showing spatial expression distribution of genes, key statistical metrics, sequencing saturation plots, clustering analysis results. Depending on the image input state and register mode, HTML reports may or may not have cell bin statistical data and image processing key results.

Other handy functions:

- **Other applications of cellCut:** Manipulating GEF file.
- **rapidRegister:** Run registration without performing cell segmentation.
- **checkGTF:** Check GTF/GFF file is prepared in the correct format, otherwise, re-format one that meets the compatibility requirements for count.
- **Other applications of imageTools:** 1) Merge two to three TIFF images in R-G-B order, which is useful for checking segmentation result. 2) Plot templates on the panoramic image to assist the evaluation of stitching and registration result. 3) Write TIFF images into RPI format.



- **manualRegister:** Acquire manual registration operation parameters from **StereoMap visualization software** and run **manualRegister** to modify registration records in IPR. Users can turn on the "fine-tune" switch to let **manualRegister** perform an automatic adjustment to the manually operated result to make the registration more precise.
- **lasso:** Acquire one or multiple cell or spatial gene expression matrix subsets according to the GEOJSON file, which stores the coordinates data of manually delineated region(s) from **StereoMap visualization software**.

## 1.2. System Requirements

SAW runs on Linux systems that meet the following minimum requirements:

8-core Intel or AMD processor (>24 cores recommended)
128GB RAM (>256GB recommended)
1TB free disk space or higher
64-bit CentOS/RedHat 7.8 or Ubuntu 20.04

To install and run SAW, please install one kind of the following softwares:

<b>docker</b> <sup>5</sup> : version 20.10.8 or higher
<b>singularity</b> <sup>6</sup> : version 3.8 or higher

## 1.3. Related Software

- **ImageQC:** STOmics microscope **ImageQC software** is a desktop application intended for assessing the quality of microscope images. The fluorescent image should pass the **ImageQC** evaluation to ensure that it fulfills requirements for SAW pipelines. SAW >= 5.0.0 requires **imageQC** version >= 1.1.0 that provides IPR file for recording image processing data. The final version of **ImageQC** is v1.2.0 and will be no longer updated.
- **ImageStudio:** **ImageStudio** is a fully upgraded image process desktop application which integrates the entire **ImageQC** functionality. It contains four main image processing modules: image QC, manual stitching, manual tissue segmentation, and manual cell segmentation. The outputs of each module can be input into SAW for further analysis. SAW >= 5.5.0 requires **ImageStudio** version v1.0.0.
- **Stereo-Map:** **StereoMap** is a HD visualization desktop application intended for displaying Stereo-seq analysis results. SAW outputs such as gene expression matrix GEF file, image RPI and IPR files, clustering results can be visualized via **StereoMap**. Currently, **StereoMap** version v1.0.0 supports SAW >= 5.4.0.

## 1.4. SAW Docker Image Installation

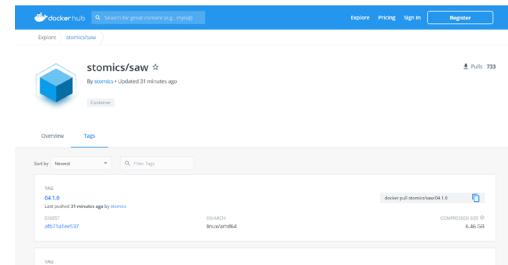
SAW is delivered as a docker image that bundles all of its required software dependencies. You can pull the SAW docker image from Docker Hub to your local system and run analyses offline.

Please download the latest version of the software and use it with the corresponding [Stereo-seq Analysis Workflow Software Suite User Manual](#) version.

Docker Hub link: <https://hub.docker.com/r/stomics/saw/tags>

We support using Singularity and Docker to install and run the SAW.

Here we take **SAW version 5.5.0** as an example.



### 1.4.1. SAW Installation via Singularity



**Please replace the yellow highlighted inputs with your own data path.**

Step 1: Pull the SAW docker image (2 options):

```
...  
$ singularity build SAW_v5.5.0.sif docker://stomics/saw:05.5.0 ## option 1  
$ singularity build --sandbox SAW_v5.5.0/ docker://stomics/saw:05.5.0 ## option 2
```

For non-root users, especially who don't have enough space in the `/home/` directory, please try:

```
...  
$ export SINGULARITY_CACHEDIR=/path/to/build  
$ singularity build --sandbox SAW_v5.5.0/ docker://stomics/saw:05.5.0
```

Step 2: Run pipelines (3 options):



**Please Note! All the requested paths need to be mounted before input. For example, it is necessary to bind directories that store input files (`/path/to/data`), reference genome (`/path/to/genomeDir`), and outputs (`/path/to/output`).**

```
...  
$ export SINGULARITY_BIND="/path/to/data,/path/to/genomeDir,/path/to/output"
```

Option 1: Run pipelines within the container from the host system.

```
...  
$ /path/to/SAW_v5.5.0.sif <application> ## option 1.1  
$ singularity exec /path/to/SAW_v5.5.0.sif <application> ## option 1.2
```

Option 2: Shell into the SAW container and interactively run bash commands. Run `exit` to exit the environment.

```
...  
$ /path/to/SAW_v5.5.0.sif /bin/bash ## option 2.1  
Singularity>  
Singularity> <shell-command>  
Singularity> exit  
$  
$ singularity shell /path/to/SAW_v5.5.0.sif ## option 2.2  
Singularity>  
Singularity> <shell-command>  
Singularity> exit  
$  
$ singularity shell SAW_v5.5.0 ## option 2.3 for sandbox  
Singularity>  
Singularity> <shell-command>  
Singularity> exit  
$
```

Option 3: Use “`--B directory on the host-machine:directory in the container`” to mount a host directory into the container and execute the command in the container.

```
...  
* $ singularity shell -B /path/to/directory/on/the/host-machine:/path/to/directory/  
mounted/in/the/container /path/to/SAW_v5.4.0.sif  
Singularity>  
Singularity> <shell-command>  
Singularity> exit  
$
```

\* Please be noted that these two lines belong to the same line of command.

## 1.4.2. SAW Installation via Docker

Step 1: Pull the SAW docker image

```
...  
$ docker pull stomics/saw:05.5.0
```

Step 2: Run pipelines

```
...  
$ docker run -d -v /path/to/data:stomics/saw:05.5.0 /bin/sh -c "<shell-command>"
```

## 1.5. SAW Github

SAW GitHub: <https://github.com/BGIResearch/SAW>

Please visit GitHub for instruction regarding the **installation of singularity** and **indexing reference genome**. The page also provides **SAW shell script** examples for users.

 **Please Note! Please build your reference before running SAW analysis.**



## 1.6. SAW Test Data

SAW test data can be downloaded from SAW GitHub page. Key outputs are shown in [\*\*Chapter 3 Test Data Demonstration\*\*](#). The reference genome version for SAW testing is:

- genome-build: GRCm38.p6
- genome-version: GRCm38
- genome-date: 2012-01
- genome-build-accession: NCBI:GCA\_000001635.8

## 1.7. SAW Output File Format

Please check [\*\*Stereo-seq File Format Manual\*\*](#) to get more information on SAW output files format.

# **CHAPTER 2**

## **SAW PIPELINES & ARGUMENTS**

## 2.1 splitMask

**splitMask** is designed for splitting Stereo-seq Chip T mask file according to the SE FASTQ CID. The split count is directly related to the number of split FASTQs while writing FASTQ out from sequencer.

Run **splitMask** requires the following files:

- Stereo-seq Chip T mask file (**.h5**)
- ⌚ Expected running time for 1 cm x 1 cm chip: ~5 min, Memory: ~3G

### 2.1.1 Arguments and Options

Table 2-1 **splitMask** Arguments and Options

Parameter index	Function
[1]	(Required) Stereo-seq Chip T mask file path (.h5).
[2]	(Required) Output directory stores split mask files.
[3]	(Required) Set the number of threads to be used.
[4]	(Optional) Split count. This count number needs to be set the same as SE FASTQ count. The options are the powers of 4, and the commonly used options are 16 and 64. If a library contains two barcodes sequenced in the same lane and the two barcodes were split when written out FASTQs, then the split count is 16; otherwise, if the barcodes were not split, then 64.
[5]	(Optional) CID position, commonly used option is “2_25”. <b>splitMask</b> uses 24 bases (out of 25, 25 is the read length of CID) to split Stereo-seq Chip T mask file. This CID position parameter is a string that combines two index numbers with “_”. The two numbers indicate the start and the end base index in the CID, and the bases in this range are used for splitting. For example, “2_25” means start from the 2 <sup>nd</sup> base to the 25 <sup>th</sup> base that are used for splitting mask file.

### 2.1.2 Usage Example

 Please Note! Replace **{SN}** with your Stereo-seq Chip T serial number (SN, e.g. SS200000135TL\_D1 or A00135D1)

```
...$ mkdir /path/to/output/00.splitmask
$ singularity exec SAW_v5.5.0.sif splitMask \
  /path/to/data/{SN}.barcodeToPos.h5 \ ## Mask path
  /path/to/output/00.splitmask \ ## output directory
  8 \ ## threads
  16 \ ## split count
  2_25 ## CID position
```

## 2.1.3 Outputs

The output files of **splitMask** are organized as below:

```
$ tree /path/to/output/00.splitmask
/path/to/output/00.splitmask
|-- 01.SN.barcodeToPos.bin
|-- 02.SN.barcodeToPos.bin
|-- 03.SN.barcodeToPos.bin
|-- 04.SN.barcodeToPos.bin
|-- 05.SN.barcodeToPos.bin
|-- 06.SN.barcodeToPos.bin
|-- 07.SN.barcodeToPos.bin
|-- 08.SN.barcodeToPos.bin
|-- 09.SN.barcodeToPos.bin
|-- 10.SN.barcodeToPos.bin
|-- 11.SN.barcodeToPos.bin
|-- 12.SN.barcodeToPos.bin
|-- 13.SN.barcodeToPos.bin
|-- 14.SN.barcodeToPos.bin
|-- 15.SN.barcodeToPos.bin
`-- 16.SN.barcodeToPos.bin

0 directories, 16 files
```

## 2.2 CIDCount

**CIDCount** is a program for computing the number of CIDs in the Stereo-seq Chip T mask file and roughly estimating memory used in **mapping**.

Run **CIDCount** requires the following files:

- Stereo-seq Chip T mask file (**.h5**)
- ⌚ Expected running time for 1 cm x 1 cm chip: ~30 s, Memory: ~0.7G

### 2.2.1 Arguments and Options

Table 2-2 **CIDCount Arguments and Options**

Parameter	Function
<b>-i</b>	(Required) Stereo-seq Chip T mask file path (.h5 or .bin).
<b>-s</b>	(Required) A string of species name.
<b>-g</b>	(Required) Genome file size in GB.

## 2.2.2 Usage Example

For PE FASTQ input cases, run **CIDCount** as below:

```
...$ singularity exec SAW_v5.5.0.sif CIDCount \
    -i /path/to/data/{SN}.barcodeToPos.h5 \ ## Stereo-seq Chip T mask file path
    -s {speciesName} \ ## species name
    -g {genomeSize} ## genome file size in GB, can be acquired by "ls -l
--block-size=GB ${Genome file of the species after STAR indexing}"
```

For SE FASTQ input cases that require to run **splitMask** first, users may run **CIDCount** only once because the results for each individual small mask are close to each other. For chip size larger than 1 cm x 1 cm, we would recommend to run **CIDCount** for each CID class/small mask.



**Please Note!** **{index}** needs to be replaced by the real index number of the split mask file.

```
...$ singularity exec SAW_v5.5.0.sif CIDCount \
    -i /path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin \ ## Stereo-seq Chip T mask file path
    -s {speciesName} \ ## species name
    -g {genomeSize} ## genome file size in GB, can be acquired by "ls -l
--block-size=GB ${Genome file of the species after STAR indexing}"
```

## 2.2.3 Outputs

The output of **CIDCount** is shown as below,

```
...$ singularity exec SAW_v5.5.0.sif CIDCount -i SN.barcodeToPos.h5 -s mouse -g 3
645784920 ## CID count
62 ## estimated memory for mapping
```

## 2.3 mapping

Each Stereo-seq sequenced read contains a CID sequence which is used as a key to spatially map the read back to its original location on the tissue section. **mapping** pipeline matches CID of the original sequencing reads stored in the FASTQ file with the records of CID-coordinates key-value pairs saved in the Stereo-seq Chip T mask file (allow 1 mismatch). Coordinate information for reads that CID could be paired with will be added based on the records of the mask file. Coordinate information for reads that CID could be paired with will be added based on the records of the mask file. Reads that get the coordinate annotations are Valid CID mRNA Reads (**Valid CID Reads**). After discarding reads with unqualified MID reads which do not satisfy with further analysis, filtering reads with adapter, and filtering short reads (read length less than 30 after trimming consecutive A bases), the filtered **Valid CID Reads** are the **Clean Reads**. **mapping** pipeline maps **Clean Reads** to the reference genome, and output sorted BAM<sup>7</sup> format alignments and summary report.

Run **mapping** requires the following files:

- Stereo-seq sequenced reads FASTQ files (**.fq.gz**)
  - Stereo-seq Chip T mask file (**.h5**)
  - Indexed reference genome
  - bcPara file (**.bcPara**), please check the content of **Table 2-4**
-  Expected running time for ~1G reads: ~4 h, Memory: ~67G

### 2.3.1 Arguments and Options

As **mapping** encapsulate STAR<sup>8</sup> function, it accepts additional options beyond those shown in the table below.

**Table 2-3 mapping Arguments and Options**

Parameter	Function
<b>--outSAMattributes spatial</b>	Set to turn on spatial BAM file format mode.
<b>--outSAMtype BAM SortedByCoordinate</b>	(STAR option) Set output BAM file sorted by coordinate.
<b>--genomeDir</b>	(STAR option) Path to the directory where the genome indices are stored.
<b>--runThreadN</b>	(STAR option; defaults to 1) Set the number of threads to be used. Usually set to 8 or higher.
<b>--outFileNamePrefix</b>	(STAR option) Custom output file prefix.
<b>--sysShell /bin/bash</b>	(STAR option) Path to the shell binary.
<b>--stParaFile</b>	(Required) Name of a parameters file defines CID mapping options. Options are specified in Table 2-4.
<b>--readNameSeparator \"\\"</b>	(STAR option) Character(s) separating the part of the read names that will be trimmed in output.
<b>--limitBAMsortRAM</b>	(STAR option) Maximum available RAM (bytes) for sorting BAM.
<b>--limitOutSJcollapsed</b>	(STAR option) Max number of collapsed junctions.
<b>--limitIObufferSize</b>	(STAR option) Max available buffers size (bytes) for input/output, per thread.
<b>--outBAMsortingBinsN</b>	(STAR option; defaults to 50) number of genome bins for coordinate-sorting. If the read2 FASTQ file size is greater than 200, it is better to set this value to 100.



Table 2-4 mapping --stParaFile Arguments and Options

Parameter	Function
<b>in</b>	(Required) Path to the Stereo-seq Chip T mask file (PE) or split mask file (SE).
<b>in1</b>	(Required) Path to the FASTQ file. For PE sequences specify the path to the FASTQ file of read1 here. For SE sequences, input FASTQ file with the same split index as the mask file. A more elegant way to input a long list of SE FASTQs is to organize them in a <b>FQ_{index}.list</b> file. Please check <a href="#">2.3.2 Usage Example SE scenario 2</a> to get more information.
<b>in2</b>	(Optional) Path to the FASTQ file of read2. Only valid for PE sequencing.
<b>encodeRule</b>	(Required for PE) Encoding rule for the four bases. ACTG stands for A->0, C->1, T->2, G->3.
<b>out</b>	(Optional) Set output file prefix.
<b>action</b>	(Required; defaults to 1) Action number. Set to 4 in <b>mapping</b> . Valid options: 1=CID stat, 2=CID overlap, 3=get CID position map, 4=map CID to slide, or 5=merge CID list.
<b>barcodeReadsCount</b>	(Required) Mapped CID list file with reads counts for each CID. This is an output file in <b>mapping</b> .
<b>platform</b>	(Optional) Sequencing platform. Valid options include but not limited to: <b>SEQ500, G400, T1, T7, T10</b> .
<b>barcodeStart</b>	(Required; defaults to 0) CID start position. Set to 0.
<b>barcodeLen</b>	(Required; defaults to 25) CID length. Set to 25 for PE, 24 for SE.
<b>umiStart</b>	(Required; defaults to 25) MID start position.
<b>umiLen</b>	(Required; defaults to 10) MID length.
<b>umiRead</b>	(Required; defaults to 1) Declare the read contains MID.
<b>mismatch</b>	(Required; defaults to 0) Max mismatch tolerant. Usually set to 1 in <b>mapping</b> .
<b>bcNum</b>	(Required) CID count in mask. Please check <a href="#">2.2 CIDCount</a> for more information.
<b>polyAnum=15</b>	(Optional) Number of consecutive A in the read that will be trimmed. Recommend to set this value to 15.
<b>mismatchInPolyA=2</b>	(Optional) Number of mismatch bases in searching poly A. Recommend to set this value to 2

## 2.3.2 Usage Example

Two scenarios for preparing **mapping --stParaFile** input file **{lane}.bcPara** with PE FASTQ input:



**Note!** Replace **{SN}** with your Stereo-seq Chip T serial number (**SN**, e.g. **SS200000135TL\_D1** or **A00135D1**), and **{lane}** with the FASTQ lane name prefix (e.g. **E100026571\_L01**)

The same applies to all examples.

PE scenario 1: Prepare `{lane}.bcPara` file for PE one pair FASTQ as `mapping` input:

```
...
$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{lane}.bcPara
in=/path/to/data/{SN}.barcodeToPos.h5
in1=/path/to/data/{lane}_read_1.fq.gz
in2=/path/to/data/{lane}_read_2.fq.gz
encodeRule=ACTG
out={lane}
barcodeReadsCount=/path/to/ouptut/01.mapping/{lane}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=25
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=645784920 ## Input the first line from output of CIDCount
polyAnum=15
mismatchInPolyA=2
```

PE scenario 2: Prepare `{lane}.bcPara` file for PE multiple pair of FASTQ as `mapping` input:

```
...
$ mkdir /path/to/multi_lane_output/01.mapping
$ vim /path/to/multi_lane_output/01.mapping/{lane}.bcPara
in=/path/to/data/{SN}.barcodeToPos.h5
in1=/path/to/data/{lane}_read_1.fq.gz
in2=/path/to/data/{lane}_read_2.fq.gz
encodeRule=ACTG
out={lane}
barcodeReadsCount=/path/to/multi_lane_output/01.mapping/{lane}.barcodeReadsCount.
txt
action=4
platform=T10
barcodeStart=0
barcodeLen=25
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=645784920 ## Input the first line from output of CIDCount
polyAnum=15
mismatchInPolyA=2
```

Run **mapping** for PE input:

```
...$ singularity exec SAW_v5.5.0.sif mapping \
    --outSAMattributes spatial \
    --outSAMtype BAM SortedByCoordinate \
    --genomeDir /path/to/genomeDir \
    --runThreadN 8 \
    --outFileNamePrefix /path/to/output/01.mapping/{lane}. \
    --sysShell /bin/bash \
    --stParaFile /path/to/output/01.mapping/{lane}.bcPara \
    --readNameSeparator \" \" \
    --limitBAMsortRAM 38582880124 \
    --limitOutSJcollapsed 10000000 \
    --limitIObufferSize=280000000 \
    --outBAMsortingBinsN 50 \
    > /path/to/output/01.mapping/{lane}_barcodeMap.stat
```

Two scenarios for preparing **mapping --stParaFile** input file **{index}.bcPara** with SE FASTQ input:

**SE scenario 1:** Prepare **{index}.bcPara** file for SE FASTQ that contains one barcode in library or did not split barcode when writing FASTQ:

 Please Note! **{index}** need to be replaced by the index of the split mask file which is corresponding to the index of the SE FASTQ file.

```
...$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{index}.bcPara
in=/path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin ## split mask file
in1=/path/to/data/{lane}_{index}.fq.gz ## {index}th FASTQ file in {lane}
out={SN}.bc.out${index}
barcodeReadsCount=/path/to/ouptut/01.mapping/{index}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=24
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=38284877 ## Input the first line from output of CIDCount
polyAnum=15
mismatchInPolyA=2
```

**SE scenario 2:** Prepare `{idx}.bcPara` file for SE FASTQ that has multiple barcodes in the library and split when writing FASTQ:



**Please Note!** `{index}` needs to be replaced by the real index number of the split mask file and `{idx}` needs to be replaced by the index number of the input FASTQ file. For example, if a library contains 2 barcodes that sequenced in the same lane, the `{index}` and `{idx}` for the third FASTQ file of barcode 1 are 01 and 03, respectively.

```
...
$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{idx}.bcPara
in=/path/to/output/00.splitmask/{index}.{SN}.barcodeToPos.bin ## split mask file
in1=/path/to/data/{lane}_{index}.fq.gz ## {index}th FASTQ file in {lane}. FASTQ
files for different barcode usually stores in different directory, so /path/to/
data/ might change to /path/to/data/{barcode_n}
out={SN}.bc.out${idx}
barcodeReadsCount=/path/to/ouptut/01.mapping/{idx}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=24
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=38284877 ## Input the first line from output of CIDCount
polyAnum=15
mismatchInPolyA=2
```

In case there are too many FASTQ files that need to be processed, an easier way is to organize them into a `FQ_{index}.list` file. The requirement for preparing a `FQ_{index}.list` file is to gather all the FASTQs with the same index as the split mask together, since these files are all split by the same logic.



```
...
$ cat SN_SE_fastq_16.list ## a FASTQ list file gathers all the FASTQs whose index
is 16
/path/to/data/lane_1_16.fq.gz
/path/to/data/lane_2_16.fq.gz
```

Then input the path of `FQ_{index}.list` file for `in1` parameter in the `{idx}.bcPara` file. The `{index}` of `FQ_{index}.list` and the `{index}` of split mask file have to be the same.

```
...
$ mkdir /path/to/output/01.mapping
$ vim /path/to/output/01.mapping/{idx}.bcPara
in=/path/to/output/00.splitmask/{index}._{SN}.barcodeToPos.bin ## split mask file
in1=/path/to/output/{SN}_SE_fastq_{index}.list
out={SN}.bc.out${idx}
barcodeReadsCount=/path/to/output/01.mapping/{idx}.barcodeReadsCount.txt
action=4
platform=T10
barcodeStart=0
barcodeLen=24
umiStart=25
umiLen=10
umiRead=1
mismatch=1
bcNum=38284877 ## Input the first line from output of CIDCount
polyAnum=15
mismatchInPolyA=2
```

### Run mapping pipeline

```
...
$ singularity exec SAW_v5.5.0.sif mapping \
    --outSAMattributes spatial \
    --outSAMtype BAM SortedByCoordinate \
    --genomeDir /path/to/genomeDir \
    --runThreadN 8 \
    --outFileNamePrefix /path/to/output/01.mapping/{index}. \ ## {index} or {idx} depending on the scenario
    --sysShell /bin/bash \
    --stParaFile /path/to/output/01.mapping/{index}.bcPara \ ## {index} or {idx} depending on the scenario
    --readNameSeparator \" \" \
    --limitBAMsortRAM 38582880124 \
    --limitOutSJcollapsed 10000000 \
    --limitI0bufferSize=280000000 \
    --outBAMsortingBinsN 50 \
    > /path/to/output/01.mapping/{index}_barcodeMap.stat ## {index} or {idx} depending on the scenario
```



### 2.3.3 Outputs

PE scenario 1 output files are organized as below:

```
...
$ tree /path/to/output/01.mapping/
/path/to/output/01.mapping/
└── lane.Aligned.sortedByCoord.out.bam
    ├── lane_barcodeMap.stat
    ├── lane.barcodeReadsCount.txt
    ├── lane.bcPara
    ├── lane.Log.final.out
    ├── lane.Log.out
    ├── lane.Log.progress.out
    └── lane.SJ.out.tab
```

PE scenario 2 output files are organized as below (Here showing example of 2 pairs of FASTQ):

 If one sample has multiple FASTQ files, you need to run mapping for each FASTQ pair.

```
...
$ tree /path/to/multi_lane_output/01.mapping
/path/to/multi_lane_output/01.mapping
└── 01.mapping
    ├── lane1.Aligned.sortedByCoord.out.bam
    ├── lane1_barcodeMap.stat
    ├── lane1.barcodeReadsCount.txt
    ├── lane1.bcPara
    ├── lane1.Log.final.out
    ├── lane1.Log.out
    ├── lane1.Log.progress.out
    ├── lane1.SJ.out.tab
    ├── lane2.Aligned.sortedByCoord.out.bam
    ├── lane2_barcodeMap.stat
    ├── lane2.barcodeReadsCount.txt
    ├── lane2.bcPara
    ├── lane2.Log.final.out
    ├── lane2.Log.out
    ├── lane2.Log.progress.out
    └── lane2.SJ.out.tab
```

SE scenario 1 (one barcode in library or did not split barcode when writing FASTQ) output files are organized as below:

```
$ tree /path/to/output/01.mapping
/path/to/output/01.mapping
└── 01.mapping
    ├── 01.Aligned.sortedByCoord.out.bam
    ├── 01_barcodeMap.stat
    ├── 01.barcodeReadsCount.txt
    ├── 01.bcPara
    ├── 01.Log.final.out
    ├── 01.Log.out
    ├── 01.Log.progress.out
    └── 01.SJ.out.tab
...
└── 16.Aligned.sortedByCoord.out.bam
    ├── 16_barcodeMap.stat
    ├── 16.barcodeReadsCount.txt
    ├── 16.bcPara
    ├── 16.Log.final.out
    ├── 16.Log.out
    ├── 16.Log.progress.out
    └── 16.SJ.out.tab
```

SE scenario 2 (multiple barcodes in the library and split when writing FASTQ) output files are organized as below (Here showing example of 2 barcodes):

```
$ tree /path/to/output/01.mapping
/path/to/output/01.mapping
└── 01.mapping
    ├── 01.Aligned.sortedByCoord.out.bam
    ├── 01_barcodeMap.stat
    ├── 01.barcodeReadsCount.txt
    ├── 01.bcPara
    ├── 01.Log.final.out
    ├── 01.Log.out
    ├── 01.Log.progress.out
    └── 01.SJ.out.tab
...
└── 128.Aligned.sortedByCoord.out.bam
    ├── 128_barcodeMap.stat
    ├── 128.barcodeReadsCount.txt
    ├── 128.bcPara
    ├── 128.Log.final.out
    ├── 128.Log.out
    ├── 128.Log.progress.out
    └── 128.SJ.out.tab
```

## 2.4 merge (optional)

SAW `merge` pipeline is used to combine the results of `mapping`.

Run `merge` requires the following file:

- `mapping` output mapped CID list files (`.txt`)
-  Expected running time for ~1G reads 2 lanes: ~5 min, Memory: ~5G

### 2.4.1 Arguments and Options

Table 2-5 `merge` Arguments and Options

Parameter	Function
[1]	(Required) Path to the Stereo-seq Chip T mask file.
[2]	(Required) Mapped CID list files with reads counts for each CID.
[3]	(Required) Mapped CID list file which merges all input files.

### 2.4.2 Usage Example

```
...
$ mkdir /path/to/multi_lane_output/02.merge
$ singularity exec SAW_v5.5.0.sif merge \
/path/to/data/{SN}.barcodeToPos.h5 \
/path/to/multi_lane_output/01.mapping/{lane1}.barcodeReadsCount.txt,/path/to/multi_
lane_output/01.mapping/{lane2}.barcodeReadsCount.txt \ ## change {lane} to {index}
or {idx} for SE and change /path/to/multi_lane_output/ to /path/to/output/ for SE
single lane scenario
/path/to/multi_lane_output/02.merge/{SN}.barcodeReadsCount.txt
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

### 2.4.3 Outputs

The output file of `merge` has been organized as below:

```
...
$ tree /path/to/multi_lane_output/02.merge
/path/to/multi_lane_output/02.merge
└── {SN}.barcodeReadsCount.txt
```

## 2.5 count

SAW **count** is an efficient general-purpose read annotation pipeline that label reads with their overlapped genomic features and outputs statistics information for the overall summarization result. Through quantification of annotated reads, **count** generates spatial gene expression data after de-duplicate reads according to CID, gene ID, and MID information. Usually, SAW **count** is run on the **Uniquely Mapped Reads** filtered from **mapping** output based on the reference genome annotation records. Starting from SAW v5.1.3, **count** allows the utilization of some Multi-Mapped Reads in quantification (**--multi\_map**). The gene expression level in SAW pipeline is the summation of both intron and exon MID count. To support downstream analysis that might be required to differentiate genomic features, **count** also output exon MID count separately.

Run **count** requires the following files:

- **mapping** output BAM file (**.bam**)
  - Reference genome annotation GFF/GTF<sup>9,10</sup> file (**.gff / .gtf**)
-  Expected running time for ~1G reads: 0.5 h, Memory: ~45 G

### 2.5.1 Arguments and Options

Table 2-6 **count** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) <b>mapping</b> output BAM file. Separate multiple files by comma.
<b>-o</b>	(Required) Set the <b>count</b> output BAM file name.
<b>-a</b>	(Required) Gene annotation GFF/GTF file.
<b>-s</b>	(Required) Set the <b>count</b> output statistical summary report file name.
<b>-e</b>	(Required) Set the <b>count</b> output gene expression file name.
<b>--umi_len</b>	(Required; defaults to 10) MID length.
<b>--sn</b>	(Required) Stereo-seq Chip T serial number (SN).
<b>-c</b>	(Optional; defaults to detected) CPU core number to use. Minimum value is 8, recommended value is 24.
<b>--save_lq</b>	(Optional; defaults to false) Save low quality reads if set.
<b>--save_dup</b>	(Optional; defaults to false) Save duplicate reads if set.
<b>--umi_on</b>	(Optional; defaults to false) Correct MID if set.
<b>--sat_file</b>	(Optional; defaults to None) Set the saturation sampling file name which is prepared for sequencing saturation (requires <b>--umi_on</b> ).
<b>-m</b>	(Optional; defaults to detected) Set available memory (GB).
<b>--multi_map</b>	(Optional; defaults to disable) Set to enable multi-mapped reads correction. This correction consists of two logics. 1) The first logic is the correction of multi-gene reads which is a read mapped uniquely to a genomic region where multiple genes overlap. In this scenario, the read has to overlap with a genomic locus greater than 50% of its read length. If the genomic feature (exon, intron, or intergenic) of all the mapped genes includes exon and intron, then select the alignment record mapped to exon in preference to intron. If more than one gene locus belongs to the same genomic feature type, then pick the one that has the longest overlap. Otherwise, label the read to “intergenic.” 2) The second logic is to select and correct one of the multi-mapped reads and add the count to gene expression matrix. The first step is to group reads by QNAME. Select reads in the group mapped to exon in preference to those mapped to intron. Then correct the longest overlapped reads (at least overlapped greater than 50% of its read length) in the group to unique read and correct its MAPQ to 255. Set the MAPQ of the remaining reads to 0.



## 2.5.2 Usage Example

```
...
$ mkdir -p /path/to/output/03.count
$ geneExp=/path/to/output/03.count/{SN}.raw.gef
$ saturationSamplingFile=/path/to/output/03.count/{SN}_raw_barcode_gene_exp.txt
$ singularity exec SAW_v5.5.0.sif count \
    -i /path/to/output/01.mapping/{lane}.Aligned.sortedByCoord.out.bam \
    -o /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
[*] target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
[*] target.bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 24 \
    -m 128
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/03.count ## change /path/to/multi_lane_out-
put/ to /path/to/output/ for SE single lane scenario
$ geneExp=/path/to/multi_lane_output/03.count/{SN}.raw.gef
$ saturationSamplingFile=/path/to/multi_lane_output/03.count/{SN}_raw_barcode_gene_
exp.txt
$ singularity exec SAW_v5.5.0.sif count \
    -i /path/to/multi_lane_output/01.mapping/{lane1}.Aligned.sortedByCoord.out.
[*] bam,/path/to/ multi_lane_output/01.mapping/{lane2}.Aligned.sortedByCoord.out.bam \
## change {lane} to {index} or {idx} for SE
[*] -o /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.
[*] merge.q10.dedup.target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.
[*] merge.q10.dedup.target.bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 24 \
    -m 128
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

For dealing with multi-mapped reads,

```
...$ singularity exec SAW_v5.5.0.sif count \
    -i /path/to/output/01.mapping/{lane}.Aligned.sortedByCoord.out.bam \
    -o /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.bam \
    -a /path/to/reference/genes.gtf \
    -s /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.
bam.summary.stat \
    -e ${geneExp} \
    --umi_len 10 \
    --sat_file ${saturationSamplingFile} \
    --sn {SN} \
    --umi_on \
    --save_lq \
    --save_dup \
    -c 24 \
    -m 128 \
    --multi_map
```

## 2.5.3 Outputs

The **count** output files are organized as below:

```
...$ tree /path/to/output/03.count
/path/to/output/03.count
└── SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam
    ├── SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.csi
    ├── SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.summary.stat
    ├── SN_raw_barcode_gene_exp.txt
    └── SN.raw.gef
```

## 2.6 register

SAW **register** pipeline aligns the microscopic tissue staining image with the plot of the gene expression matrix generated by **count** based on the track lines on the chip while establishing the mapping relationship between images and spatial gene expression distribution. SAW **register** includes four main modules, stitching, tissue segmentation, cell segmentation, and registration. Stitching combines microscopic images with overlapping sections to create a panoramic image (skip stitching if the input image is already a panoramic image). Tissue and cell segmentation modules detect and mask out tissue and cell coverage region, respectively. Registration module aligns stitched image and the expression matrix, and at the same time registered masks from segmentation modules with the gene expression matrix using the same parameters. Image stitching and segmentation modules can be run separately with registration.

Run **register** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)
- ImageQC processed microscopic tissue staining image file (**.tar.gz**)
- ImageQC Image process record file (**.ipr**)
- ⌚ Expected running time for 1 cm x 1 cm Stereo-seq Chip T image: ~2 h, Memory: ~20 G
- 🕒 **Cell segmentation is the most time consuming part. You may run rapidRegister to skip cell segmentation, but still perform stitching, tissue segmentation and registration. Please check [2.14.2 rapidRegister](#) to get more information about rapidRegister.**

### 2.6.1 Arguments and Options

Table 2-7 **register** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) ImageQC/ImageStudio processed staining image TAR.GZ file or image pre-processed output directory.
<b>-c</b>	(Required) ImageQC/ImageStudio IPR (image process record) file. IPR is designed to efficiently hold images and process records generated from each image processing step along with metadata in various data types. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on the IPR file.
<b>-v</b>	(Optional. Depends on <b>-i</b> ) <b>count</b> output gene expression matrix GEF file.
<b>-o</b>	(Required) Path to the directory where to store the <b>register</b> outputs.

## 2.6.2 Usage Example

Scenario 1: Process images from ImageQC/ImageStudio output data and gene expression matrix. Perform stitching, tissue segmentation, cell segmentation, and registration with gene expression matrix.

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name {SN}*.tar.gz | head -1)
$ imageQC=$(find ${image} -maxdepth 1 -name {SN}*.ipr | head -1)
$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.5.0.sif register \
    -i ${image4register} \
    -c ${imageQC} \
    -v /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/04.register
```

Scenario 2: Process images from ImageQC/ImageStudio output data. Perform stitching, tissue segmentation, and cell segmentation without doing registration with the gene expression matrix.

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name {SN}*.tar.gz | head -1)
$ imageQC=$(find ${image} -maxdepth 1 -name {SN}*.ipr | head -1)

$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.5.0.sif register \
    -i ${image4register} \
    -c ${imageQC} \
    -o /path/to/output/04.register
```

Scenario 3: Process images from scenario 2. register processed images with gene expression matrix.

```
...
$ imageQC=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.5.0.sif register \
    -i /path/to/output/04.register ## -i input scenario 2 output directory
    -c ${imageQC} ## scenario 2 output IPR
    -v /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/04.register
```

## 2.6.3 Outputs

`register` output files of scenario 1 and scenario 3 (if `-i` and `-o` are identical) are organized as below:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
└── attrs.json
└── fov_stitched_transformed.tif
└── SN_date_time_version.ipr
└── SN_tissue_bbox.csv
└── transform_thumb.png
```

`register` output files of scenario 2:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
└── attrs.json
└── fov_stitched_transformed.tif
└── SN_date_time_version.ipr
└── transform_thumb.png
```

`register` output files of scenario 3 if `-i` and `-o` are two different paths:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip logs
└── SN_date_time_version.ipr
└── SN_tissue_bbox.csv
```

## 2.7 imageTools

SAW **imageTools** is a handy toolkit designed to play with image data in SAW. **imageTools ipr2img** (or **ipr2img**, available from SAW ST >= v5.0.0) is required in SAW core pipeline “decode” images from the processed IPR file. SAW **imageTools ipr2img** output TIFF images from IPR such as pre-registered ssDNA stitched image, tissue segmentation and cell segmentation mask TIFFs, as well as registered three types of images.

Run **imageTools ipr2img** requires the following files:

- ImageQC/ImageStudio processed microscopic tissue staining image file (**.tar.gz**)
  - **register** processed Image process record file (**.ipr**)
-  Expected running time for 1 cm x 1 cm Stereo-seq Chip T image: ~5 min, Memory: ~10 G

### 2.7.1 Arguments and Options

Table 2-8 **imageTools ipr2img** Arguments and Options

Command	Parameter	Function
<b>ipr2img</b>	<b>-i</b>	(Required) ImageQC/ImageStudio processed staining image TAR.GZ file.
	<b>-c</b>	(Required) IPR (image process record) file. IPR is designed to efficiently hold image information generated from each processing step and datasets in various compound types along with metadata. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on IPR file.
	<b>-d</b>	(Required) Segmentation module names. Convert segmentation mask TIFF from IPR for the selected modules. Valid options: <b>tissue</b> and <b>cell</b> . Separate modules by space.
	<b>-r</b>	(Required; default to True) Whether output registered images or pre-registered images. “Pre-registered” state stands for the images that have been stitched to a single panoramic image and transformed to have the same scale with the gene expression matrix, but still need to be flipped, 90°rotated, or translated. The options are True for output registered images and False for output pre-registered images.
	<b>-o</b>	(Required) Path to the directory where to store the <b>ipr2img</b> outputs.



Please check [2.14.4 Other applications of imageTools](#) to learn more about **imageTools**.

## 2.7.2 Usage Example

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name ${SN}*.tar.gz | head -1)
$ imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name ${SN}*.ipr | head -1)
## has to be a processed IPR

$ singularity exec SAW_v5.5.0.sif imageTools ipr2img \
  -i ${image4register} \
  -c ${imageIPR} \
  -d tissue cell \ ## output both tissue and cell segmentation mask TIFF
  -r True \
  -o /path/to/output/04.register
```

## 2.7.3 Outputs

`imageTools ipr2img` output files (if the parent directory path of `-c` IPR and `-o` are identical) are organized as below:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
├── attrs.json
├── fov_stitched_transformed.tif
├── matrix_template.txt
├── SN_date_time_version.ipr
├── SN_mask.tif
├── SN_regist.tif
├── SN.rpi
├── SN_tissue_bbox.csv
├── SN_tissue_cut.tif
├── transform_template.txt
└── transform_thumb.png
```

`imageTools ipr2img` output files (if the parent directory path of `-c` IPR and `-o` are two different paths) are organized as below:

```
...
$ tree /path/to/output/04.register_tmp
/path/to/output/04.register_tmp
... ## skip logs and image folder
├── fov_stitched_transformed.tif
├── matrix_template.txt
├── SN_mask.tif
├── SN_regist.tif
├── SN.rpi
├── SN_tissue_bbox.csv
├── SN_tissue_cut.tif
└── transform_template.txt
```

## 2.8 tissueCut

SAW **tissueCut** pipeline can delineate and extract the tissue coverage area based on the aligned image generated from **register** and **imageTools** or from the plot of gene expression matrix (if microscopic tissue staining images are not available). **tissueCut** outputs expression data in GEF format.

 If the output of **tissueCut** doesn't match the morphology of the tissue, user could handle this issue with the help of ImageStudio, StereoMap or Stereopy<sup>11</sup>. If the **tissueCut** was run with an image, users could manually redo tissue segmentation for the image via ImageStudio and run **register**, **imageTools** and **tissueCut** again. Otherwise, manually delineate tissue coverage region from the gene expression distribution plot via StereoMap and then put the result into the SAW-lasso pipeline (2.14.6 lasso), or do lasso selection and expression matrix extraction via Stereopy ([Stereopy->Examples->Interactive](#)).

Run **tissueCut** requires the following files:

- Mapped CID list file (**.txt**)
- **count** output gene expression matrix file (**.raw.gef**)
- **imageTools ipr2img** output tissue segmentation mask TIFF file (**.tif optional**)
-  Expected running time for ~1G reads: ~10 min, Memory: ~10 G

### 2.8.1 Arguments and Options

Table 2-9 **tissueCut** Arguments and Options

Parameter	Function
<b>--dnbfle</b>	(Optional) Mapped CID list file with reads counts for each CID. Input merged mapped CID list file if more than one list file were generated in <b>mapping</b> .
<b>-i</b>	(Required) <b>count</b> output gene expression matrix file.
<b>-o</b>	(Required) Path to the directory where to store the <b>tissueCut</b> outputs.
<b>-s</b>	(Optional) Path to the <b>imageTools ipr2img</b> output tissue segmentation mask file. Only valid when <b>register</b> has performed.
<b>--sn</b>	(Required) Stereo-seq Chip T serial number (SN).
<b>--omics,-0</b>	(Required; default to Transcriptomics) String that specifies the omics.
<b>-d</b>	(Required) Set to generate required plots for <b>report</b> .

## 2.8.2 Usage Example

Run **tissueCut** if **register** aligned microscopic staining image is provided:

```
...
$ tissueMaskFile=$(find /path/to/output/04.register -maxdepth 1 -name {SN}_
tissue_cut.tif | head -1)
$ mkdir -p /path/to/output/05.tissuecut
$ singularity exec SAW_v5.5.0.sif tissueCut \
--dnbf file /path/to/output/02.merge/{SN}.barcodeReadsCount.txt \
-i /path/to/output/03.count/{SN}.raw.gef \
-o /path/to/output/05.tissuecut \
-s ${tissueMaskFile} \
--sn {SN} -O Transcriptomics -d
```

Run **tissueCut** if image is not available:

```
...
$ mkdir -p /path/to/output/05.tissuecut
$ singularity exec SAW_v5.5.0.sif tissueCut \
--dnbf file /path/to/output/02.merge/{SN}.barcodeReadsCount.txt \
-i /path/to/output/03.count/{SN}.raw.gef \
-o /path/to/output/05.tissuecut \
--sn {SN} -O Transcriptomics -d
```

## 2.8.3 Outputs

**tissueCut** output files:

Image is provided:

```
...
$ tree /path/to/output/05.tissuecut
/path/to/output/05.tissuecut
├── SN.tissue.gef
├── tissuecut.stat
└── tissue_fig
    ├── scatter_100x100_MID_gene_counts.png
    ├── scatter_150x150_MID_gene_counts.png
    ├── scatter_200x200_MID_gene_counts.png
    ├── scatter_50x50_MID_gene_counts.png
    ├── statistic_100x100_MID_gene_DNB.png
    ├── statistic_150x150_MID_gene_DNB.png
    ├── statistic_200x200_MID_gene_DNB.png
    ├── statistic_50x50_MID_gene_DNB.png
    ├── violin_100x100_MID_gene.png
    ├── violin_150x150_MID_gene.png
    └── violin_200x200_MID_gene.png
        └── violin_50x50_MID_gene.png
```

Image is not provided:

```
...$ tree /path/to/output/05.tissuecut
/path/to/output/05.tissuecut
└── 100X100_contour_image.png  ## bin100 expression png
    ├── bin1_img.tif  ## bin1 expresion distribution TIFF file
    ├── bin1_img_tissue_cut.tif  ## tissue mask acquried from bin1 expression distribution plot
    ├── SN.tissue.gef
    ├── tissuecut.stat
    └── tissue_fig
        ├── scatter_100x100_MID_gene_counts.png
        ├── scatter_150x150_MID_gene_counts.png
        ├── scatter_200x200_MID_gene_counts.png
        ├── scatter_50x50_MID_gene_counts.png
        ├── statistic_100x100_MID_gene_DNB.png
        ├── statistic_150x150_MID_gene_DNB.png
        ├── statistic_200x200_MID_gene_DNB.png
        ├── statistic_50x50_MID_gene_DNB.png
        ├── violin_100x100_MID_gene.png
        ├── violin_150x150_MID_gene.png
        ├── violin_200x200_MID_gene.png
        └── violin_50x50_MID_gene.png
```

## 2.9 spatialCluster

SAW **spatialCluster** pipeline performs clustering analysis for spots using StereoPy. The clustering procedure includes 4 main steps: 1) preprocess gene expression data from the tissue-coverage region (normalize, logarithmize, identify highly-variable genes, and scale each gene), 2) reduce the dimensionality of the data by running PCA, 3) compute the neighborhood graph and embed neighborhood graph using UMAP, 4) and clustering by Leiden algorithm.

Run **spatialCluster** requires the following files:

- **tissueCut** output GEF file for the tissue-covered region (**.tissue.gef**)
- ⌚ Expected running time for ~1G reads: ~1 min, Memory: ~5 G

### 2.9.1 Arguments and Options

**Table 2-10 spatialCluster Arguments and Options**

Parameter	Function
<b>-i</b>	(Required) <b>tissueCut</b> output GEF file for the tissue coverage area.
<b>-o</b>	(Required) Output path for the clustering result in H5AD format.
<b>-s</b>	(Required; default to 50) Bin size.

### 2.9.2 Usage Example

```
...$ mkdir -p /path/to/output/06.spatialcluster
$ singularity exec SAW_v5.4.0.sif spatialCluster \
    -i /path/to/output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
    -s 200
```

### 2.9.3 Outputs

**spatialCluster** output files are:

```
...$ tree /path/to/output/06.spatialcluster
/path/to/output/06.spatialcluster
└── SN.spatial.cluster.h5ad
```

## 2.10 cellCut

SAW **cellCut** pipeline runs to extract expression matrix of cell nucleus based on the aligned image generated from **register** and **imageTools**. **cellCut** outputs expression data in cell bin GEF format. Run **cellCut** if cell bin results are desired.

Run **cellCut** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)
  - **register** and **imageTools** output cell segmentation mask TIFF file (**.tif**)
-  Expected running time for ~1G reads: ~2 min, Memory: ~10 G

### 2.10.1 Arguments and Options

Table 2-11 **cellCut** Arguments and Options

Commands	Parameters	Function
<b>cgef</b>	<b>-i, --input-file</b>	(Required) Input GEF file.
	<b>-m, --mask-file</b>	(Required) Input cell segmentation mask file.
	<b>-o, --output-file</b>	(Required) Output cell bin GEF file.
	<b>-b, --block</b>	(Optional; default to 256,256) Block size.
	<b>-r, --rand-celltype</b>	(Optional; default to 0) Number of random cell type.
	<b>-t, --threads</b>	(Optional; default to 1) Number of threads.
	<b>-v, --verbose</b>	(Optional) Verbose output.
	<b>-n, --cnum</b>	(Optional; default to 5000) Top level cell number.
	<b>-R, --ratio</b>	(Optional; default to 20) Other level cell number ratio.
	<b>-a, --allocat</b>	(Optional; default to 2) Allocation strategy.
<b>cellCut</b>	<b>-g, --raw-gem</b>	(Optional) Raw GEM file.
	<b>-c, --canvas</b>	(Optional; default to 0,0,90000,90000) Set canvas size, minX,minY,maxX maxY.
	<b>-l, --limit</b>	(Optional; default to 16,16) Set block limit.
	<b>-S, --split</b>	(Optional; default to 0) Split cellID to layers and blocks.
	<b>-w, --errorCode-file</b>	(Optional; default to false) Set to turn on error code mode.



Please check [2.14.1 Other applications of cellCut](#) to learn more about **cellCut**.

### 2.10.2 Usage Example

Run **cellCut** only if **register** aligned microscopic staining image is provided:

```
...
$ mkdir -p /path/to/output/051.cellcut
$ singularity exec SAW_v5.5.0.sif cellCut cgef \
    -i /path/to/output/03.count/{SN}.raw.gef \
    -m /path/to/output/04.register/{SN}_mask.tif \
    -o /path/to/output/051.cellcut/{SN}.cellbin.gef
```

## 2.10.3 Outputs

`cellCut` output files:

```
...$ tree /path/to/output/051.cellcut
/path/to/output/051.cellcut
└── SN.cellbin.gef
```

## 2.11 cellCluster

SAW `cellCluster` pipeline runs by clustering cells using the Leiden algorithm similarly to the procedures of `spatialCluster`. Run `cellCluster` if cell bin results are desired.

Run `cellCluster` requires the following files:

- `cellCut` output cell bin gene expression matrix file (**.cellbin.gef**)
- ⌚ Expected running time for ~1G reads: ~5 min, Memory: ~5 G

### 2.11.1 Arguments and Options

Table 2-12 `cellCluster` Arguments and Options

Parameter	Function
<b>-i</b>	(Required) <code>cellCut</code> output cell bin gene expression matrix file.
<b>-o</b>	(Required) Output path for the clustering result in H5AD format.

### 2.11.2 Usage Example

```
...$ mkdir -p /path/to/output/061.cellcluster
$ singularity exec SAW_v5.5.0.sif cellCluster \
    -i /path/to/output/051.cellcut/{SN}.cellbin.gef \
    -o /path/to/output/061.cellcluster/{SN}.cell.cluster.h5ad
```

### 2.11.3 Outputs

`cellCluster` output files:

```
...$ tree /path/to/output/061.cellcluster
/path/to/output/061.cellcluster
└── SN.cell.cluster.h5ad
```

## 2.12 saturation

SAW **saturation** pipeline is performed to compute the sequencing saturation for the tissue coverage area.

- Run **saturation** requires the following files:
  - **mapping** output statistical report of CID mapping (**.stat**)
  - **count** output saturation sampling file (**.txt**)
  - **count** output statistical report of annotation (**.stat**)
  - **tissueCut** output GEF file for the tissue coverage area (**.tissue.gef**)
-  Expected running time for ~1G reads: ~5 min, Memory: ~5 G

### 2.12.1 Arguments and Options

Table 2-13 **saturation** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) <b>count</b> output saturation sampling file.
<b>--tissue</b>	(Required) <b>tissueCut</b> output GEF file for the tissue coverage area.
<b>-o</b>	(Required) Path to the directory where to store the <b>saturation</b> outputs. There has to be an existing path.
<b>--bcstat</b>	(Required) <b>mapping</b> output statistical report of CID mapping. Separate multiple files by comma.
<b>--summary</b>	(Required) <b>count</b> output statistical report of annotation.

### 2.12.2 Usage Example

```
...
$ mkdir -p /path/to/output/07.saturation
$ singularity exec SAW_v5.5.0.sif saturation \
    -i /path/to/output/03.count/{SN}_raw_barcode_gene_exp.txt \
    --tissue /path/to/output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/output/07.saturation \
    --bcstat /path/to/output/01.mapping/{lane}_barcodeMap.stat \
    --summary /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.
[*] dedup.target.bam.summary.stat
```

\* Please be noted that these two lines belong to the same line of command.

For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/07.saturation
$ singularity exec SAW_v5.5.0.sif saturation \
    -i /path/to/multi_lane_output/03.count/{SN}_raw_barcode_gene_exp.txt \
    --tissue /path/to/multi_lane_output/05.tissuecut/{SN}.tissue.gef \
    -o /path/to/multi_lane_output/07.saturation \
    --bcstat /path/to/multi_lane_output/01.mapping/{lane1}_barcodeMap.stat,/path/
[*] to/multi_lane_output/01.mapping/{lane2}_barcodeMap.stat \
    --summary /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.
[*] merge.q10.dedup.target.bam.summary.stat
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



## 2.12.3 Outputs

**saturation** output files:

```
$ tree /path/to/output/07.saturation
└── plot_1x1_saturation.png
└── plot_200x200_saturation.png
└── sequence_saturation.tsv
```

## 2.13 report

SAW **report** pipeline is performed to integrate analysis report from each step and generate the report in JSON format as well as a web report in HTML format. HTML analytical report integrate genes' spatial expression distribution, key statistical metrics, sequencing saturation plots, clustering analysis result, and image processing information.

Run **report** requires the following files and information:

- **mapping** output statistical reports of CID mapping and STAR alignment (**.stat, .out**)
- **count** output statistical report of annotation (**.stat**)
- **register** processed Image process record file and image pyramid RPI file (**.ipr, .rpi**)
- **tissueCut** and **cellCut** (if available) output GEF file, statistical report of tissue-covered region, plots and image pyramid RPI file (**.gef, .stat, .png**)
- **spatialCluster** and **cellCluster** (if available) output clustering H5AD file (**.h5ad**)
- **saturation** output bin200 sequence saturation plot (**.png**)
- species, tissue, and reference information
- ⌚ Expected running time for ~1G reads: ~1 min, Memory: 1G

## 2.13.1 Arguments and Options

Table 2-14 **report** Arguments and Options

Parameter	Function
<b>-m</b>	(Required) Statistical report of CID mapping. Separate multiple files by comma.
<b>-a</b>	(Required) Statistical report of STAR alignment. Separate multiple files by comma.
<b>-g</b>	(Required) Statistical report of annotation.
<b>-l</b>	(Required) Statistical report of tissue-covered region.
<b>-n</b>	(Required) GEF file that has wholeExp/bin200. Please check <a href="#">2.14.1 Other applications of cellCut</a> to get more information of GEF completion.
<b>-b</b>	(Required) tissueCut output bin 200 scatter plot.
<b>-v</b>	(Required) tissueCut output bin 200 violin plot.
<b>-c</b>	(Required) tissueCut output bin 200 statistics plot.

Parameter	Function
--bin50Saturation	(Required) tissueCut output bin 50 scatter plot.
--bin50violin	(Required) tissueCut output bin 50 violin plot.
--bin50MIDGeneDNB	(Required) tissueCut output bin 50 statistics plot.
--bin100Saturation	(Required) tissueCut output bin 100 scatter plot.
--bin100violin	(Required) tissueCut output bin 100 violin plot.
--bin100MIDGeneDNB	(Required) tissueCut output bin 100 statistics plot.
--bin150Saturation	(Required) tissueCut output bin 150 scatter plot.
--bin150violin	(Required) tissueCut output bin 150 violin plot.
--bin150MIDGeneDNB	(Required) tissueCut output bin 150 statistics plot.
-d	(Required) spatialCluster output H5AD file.
-t	(Required) saturation output bin 200 sequence saturation plot.
-r standard_version	(Required) Set to specifying report version.
-s	(Required) The Stereo-seq Chip T serial number.
--pipelineVersion	(Required) Set to specifying analysis pipeline version.
-o	(Required) The directory to store outputs.
--species	(Required) A string of species name.
--tissue	(Required) A string of tissue type.
-reference	(Required) A string of reference used for mapping
--rpi_resolution	(Optional; default to 100) The resolution of RPI. Valid options: <b>2, 10, 50, 100, 150</b> .
-i	(Optional) The image pyramid RPI file.
--iprFile	(Optional) A processed IPR (image process record) file.
--cellBinGef	(Optional) The cell bin GEF file.
--cellCluster	(Optional) cellCluster output H5AD file.

## 2.13.2 Usage Example

Run **report** if **register** aligned microscopic staining image is provided and have cell bin output:

 Please Note! Replace **{SN}**, **{lane}**, **{species\_name}**, **{tissue\_type}**, **{reference\_index}** with the real information.

```
...
$ imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1) ## has to be a processed IPR
$ singularity exec SAW_v5.5.0.sif cellCut bgef \
  -i /path/to/output/03.count/{SN}.raw.gef \
  -o /path/to/output/05.tissuecut/{SN}.gef \
  -b 1,10,20,50,100,200,500 \
  -O Transcriptomics

$ mkdir -p /path/to/output/08.report
$ singularity exec SAW_v5.5.0.sif report \
  -m /path/to/output/01.mapping/{lane}_barcodeMap.stat \
  -a /path/to/output/01.mapping/{lane}.Log.final.out \
  -g /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.* \
  target.bam.summary.stat \
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

```

*** -l /path/to/output/05.tissuecut/tissuecut.stat \
-n /path/to/output/05.tissuecut/{SN}.gef \
-d /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
-t /path/to/output/07.saturation/plot_200x200_saturation.png \
-b /path/to/output/05.tissuecut/tissue_fig/scatter_200x200_MID_gene_counts.
png \
-v /path/to/output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.png \
-c /path/to/output/05.tissuecut/tissue_fig/statistic_200x200_MID_gene_DNB.
png \
--bin50Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_50x50_MID_
gene_counts.png \
--bin50violin /path/to/output/05.tissuecut/tissue_fig/violin_50x50_MID_gene.
png \
--bin50MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_50x50_-
MID_gene_DNB.png \
--bin100Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_100x100_-
MID_gene_counts.png \
--bin100violin /path/to/output/05.tissuecut/tissue_fig/violin_100x100_MID_-
gene.png \
--bin100MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_100x100_-
MID_gene_DNB.png \
--bin150Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_150x150_-
MID_gene_counts.png \
--bin150violin /path/to/output/05.tissuecut/tissue_fig/violin_150x150_MID_-
gene.png \
--bin150MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_150x150_-
MID_gene_DNB.png \
--cellBinGef /path/to/output/051.cellcut/{SN}.cellbin.gef \
--cellCluster /path/to/output/061.cellcluster/{SN}.cell.cluster.h5ad \
-i /path/to/output/04.register/{SN}.rpi \
-r standard_version \
-s {SN} \
--pipelineVersion SAW_v5.5.0 \
--iprFile ${imageIPR} \
--species {species_name} \
--tissue {tissue_type} \
--reference {reference_index} \
-o /path/to/output/08.report

```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



For more than one pair of FASTQ files (Here showing an example of 2 pairs of FASTQ),

```
...
$ mkdir -p /path/to/multi_lane_output/08.report
$ singularity exec SAW_v5.5.0.sif cellCut bgef \
  -i /path/to/output/03.count/{SN}.raw.gef \
  -o /path/to/output/05.tissuecut/{SN}.gef \
  -b 1,10,20,50,100,200,500 \
  -O Transcriptomics
$ singularity exec SAW_v5.5.0.sif report \
  -m /path/to/multi_lane_output/01.mapping/{lane1}_barcodeMap.stat,/path/to/
multi_lane_output/01.mapping/{lane2}_barcodeMap.stats \
  -a /path/to/multi_lane_output/01.mapping/{lane1}.Log.final.out,/path/to/
multi_lane_output/01.mapping/{lane2}.Log.final.out \
  -g /path/to/multi_lane_output/03.count/{SN}.Aligned.sortedByCoord.out.merge.
q10.dedup.target.bam.summary.stat \
  -l /path/to/multi_lane_output/05.tissuecut/tissuecut.stat \
  -n /path/to/multi_lane_output/05.tissuecut/{SN}.gef \
  -d /path/to/multi_lane_output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
  -t /path/to/multi_lane_output/07.saturation/plot_200x200_saturation.png \
  -b /path/to/multi_lane_output/05.tissuecut/tissue_fig/scatter_200x200_MID_
gene_counts.png \
  -v /path/to/multi_lane_output/05.tissuecut/tissue_fig/violin_200x200_MID_
gene.png \
  -c /path/to/multi_lane_output/05.tissuecut/tissue_fig/statistic_200x200_MID_
gene_DNB.png \
  --bin50Saturation /path/to/multi_lane_output/05.tissuecut/tissue_fig/scat-
ter_50x50_MID_gene_counts.png \
  --bin50violin /path/to/multi_lane_output/05.tissuecut/tissue_fig/vio-
lin_50x50_MID_gene.png \
  --bin50MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_
fig/statistic_50x50_MID_gene_DNB.png \
  --bin100Saturation /path/to/multi_lane_output/05.tissuecut/tissue_
fig/scatter_100x100_MID_gene_counts.png \
  --bin100violin /path/to/multi_lane_output/05.tissuecut/tissue_
fig/violin_100x100_MID_gene.png \
  --bin100MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_
fig/statistic_100x100_MID_gene_DNB.png \
  --bin150Saturation /path/to/multi_lane_output/05.tissuecut/tissue_
fig/scatter_150x150_MID_gene_counts.png \
  --bin150violin /path/to/multi_lane_output/05.tissuecut/tissue_
fig/violin_150x150_MID_gene.png \
  --bin150MIDGeneDNB /path/to/multi_lane_output/05.tissuecut/tissue_
fig/statistic_150x150_MID_gene_DNB.png \
  --cellBinGef /path/to/output/051.cellcut/{SN}.cellbin.gef \
  --cellCluster /path/to/output/061.cellcluster/{SN}.cell.cluster.h5ad \
  -i /path/to/multi_lane_output/04.register/{SN}.rpi \
  -r standard_version \

```



```
...  
-s {SN} \  
--pipelineVersion SAW_v5.5.0 \  
--iprFile ${imageIPR} \  
--species {species_name} \  
--tissue {tissue_type} \  
--reference {reference_index} \  
-o /path/to/multi_lane_output/08.report
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

Run **report** of **rapidRegister** outputs in which the microscopic image has been registered with gene expression matrix but did not perform cell segmentation. Here is an example of just one pair of FASTQ,

```
...  
$ mkdir -p /path/to/output/08.report  
$ singularity exec SAW_v5.5.0.sif cellCut bgef \  
    -i /path/to/output/03.count/{SN}.raw.gef \  
    -o /path/to/output/05.tissuecut/{SN}.gef \  
    -b 1,10,20,50,100,200,500 \  
    -O Transcriptomics  
  
$ singularity exec SAW_v5.5.0.sif report \  
    -m /path/to/output/01.mapping/{lane}_barcodeMap.stat \  
    -a /path/to/output/01.mapping/{lane}.Log.final.out \  
    -g /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.  
target.bam.summary.stat \  
    -l /path/to/output/05.tissuecut/tissuecut.stat \  
    -n /path/to/output/05.tissuecut/{SN}.gef \  
    -d /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \  
    -t /path/to/output/07.saturation/plot_200x200_saturation.png \  
    -b /path/to/output/05.tissuecut/tissue_fig/scatter_200x200_MID_gene_counts.png  
    \  
    -v /path/to/output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.png \  
    -c /path/to/output/05.tissuecut/tissue_fig/statistic_200x200_MID_gene_DNB.png  
    \  
    --bin1Saturation /path/to/output/07.saturation/plot_1x1_saturation.png \  
    --bin50Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_50x50_MID_  
gene_counts.png \  
    --bin50Violin /path/to/output/05.tissuecut/tissue_fig/violin_50x50_MID_gene.  
png \  
    --bin50MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_50x50_MID_  
gene_DNB.png \  
    --bin100Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_100x100_  
MID_gene_counts.png \  
    --bin100Violin /path/to/output/05.tissuecut/tissue_fig/violin_100x100_MID_  
gene.png \  
    --bin100MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_100x100_  
MID_gene_DNB.png \  
    --bin150Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_150x150_  
MID_gene_counts.png \  
...
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



```
*** --bin150violin /path/to/output/05.tissuecut/tissue_fig/violin_150x150_MID_gene.
png \
--bin150MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_150x150_
MID_gene_DNB.png \
-i /path/to/output/04.register/{SN}.rpi \
-r standard_version \
-s {SN} \
--pipelineVersion SAW_v5.5.0 \
--iprFile ${imageIPR} \
--species {species_name} \
--tissue {tissue_type} \
--reference {reference_index} \
-o /path/to/output/08.report
```

Run **report** for **register** aligned microscopic staining image is absent (Here showing an example of just one pair of FASTQ, similar to multiple pairs),

```
*** $ mkdir -p /path/to/output/08.report
$ singularity exec SAW_v5.5.0.sif cellCut bgef \
  -i /path/to/output/03.count/{SN}.raw.gef \
  -o /path/to/output/05.tissuecut/{SN}.gef \
  -b 1,10,20,50,100,200,500 \
  -O Transcriptomics
$ singularity exec SAW_v5.5.0.sif report \
  -m /path/to/output/01.mapping/{lane}_barcodeMap.stat \
  -a /path/to/output/01.mapping/{lane}.Log.final.out \
  -g /path/to/output/03.count/{SN}.Aligned.sortedByCoord.out.merge.q10.dedup.
target.bam.summary.stat \
  -l /path/to/output/05.tissuecut/tissuecut.stat \
  -n /path/to/output/05.tissuecut/{SN}.gef \
  -d /path/to/output/06.spatialcluster/{SN}.spatial.cluster.h5ad \
  -t /path/to/output/07.saturation/plot_200x200_saturation.png \
  -b /path/to/output/05.tissuecut/tissue_fig/scatter_200x200_MID_gene_counts.
png \
  -v /path/to/output/05.tissuecut/tissue_fig/violin_200x200_MID_gene.png \
  -c /path/to/output/05.tissuecut/tissue_fig/statistic_200x200_MID_gene_DNB.
png \
  --bin50Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_50x50_MID_
gene_counts.png \
  --bin50violin /path/to/output/05.tissuecut/tissue_fig/violin_50x50_MID_gene.
png \
  --bin50MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_50x50_
MID_gene_DNB.png \
  --bin100Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_100x100_
MID_gene_counts.png \
  --bin100violin /path/to/output/05.tissuecut/tissue_fig/violin_100x100_MID_
gene.png \
  --bin100MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_100x100_
MID_gene_DNB.png \
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.



```
...  

    --bin150Saturation /path/to/output/05.tissuecut/tissue_fig/scatter_150x150_  

MID_gene_counts.png \  

    --bin150violin /path/to/output/05.tissuecut/tissue_fig/violin_150x150_MID_  

gene.png \  

    --bin150MIDGeneDNB /path/to/output/05.tissuecut/tissue_fig/statistic_150x150_MID_gene_DNB.png \  

    -r standard_version \  

    -s {SN} \  

    --pipelineVersion SAW_v5.5.0 \  

    --species {species_name} \  

    --tissue {tissue_type} \  

    --reference {reference_index} \  

    -o /path/to/output/08.report
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

### 2.13.3 Outputs

**report** output files that have cell bin data input are organized as below:

```
...  

$ tree /path/to/output/08.report  

/path/to/output/08.report  

├── scatter_1x1_MID_gene_counts.png  

├── SN.report.html  

├── SN.statistics.json  

├── statistic_1x1_MID_gene_DNB.png  

└── violin_1x1_MID_gene.png
```

**report** output files that the cell bin data inputs are absent:

```
...  

$ tree /path/to/output/08.report  

/path/to/output/08.report  

├── SN.report.html  

└── SN.statistics.json
```



## 2.14 Other Applications

### 2.14.1 Other applications of `cellCut`

SAW `cellCut` is also an application for manipulating GEF file. SAW contains this tool to convert GEF format gene expression matrix to plain table or complete a GEF. Users may also manipulate the GEF files using the separate individual C++ compiled program geftools<sup>12</sup> or its python encapsulated package gefpy<sup>13</sup>.

#### 2.14.1.1 Arguments and Options

Table 2-15 Other applications of `cellCut` Arguments and Options

Commands	Parameters	Function
<code>view</code>	<code>-i, --input-file</code>	(Required) Input bin GEF file or cell bin GEF file.
	<code>-o, --output-file</code>	(Optional; default to stdout) Output GEM file.
	<code>-d, --exp_data</code>	(Optional; default to "") Input bin1 GEF to get cell bin GEM.
	<code>-b, --bin-size</code>	(Optional; default to 1) Set bin size for bin GEF file. Only valid for bin GEF.
	<code>-s, --serial-number</code>	(Required) Stereo-seq Chip T serial number.
	<code>-e, --exon</code>	(Optional; default to 1) Whether or not output exon group.
<code>bgef</code>	<code>-w, --errorCode-file</code>	(Optional; default to false) Determine output error code to file.
	<code>-i, --input-file</code>	(Required) Input gene expression matrix file (.gem/.gem.gz) or bin1 GEF file.
	<code>-o, --output-file</code>	(Required) Output bin GEF file.
	<code>-b, --bin-size</code>	(Required; default to 1,10,20,50,100,200,500) Comma-separate bin size list.
	<code>-r, --region</code>	(Optional; default to "") A rectangular region represented by the comma-separated list of vertex coordinates. For example, minX,maxX,minY,maxY.
	<code>-t, --threads</code>	(Optional; default to 8) Number of threads.
	<code>-s, --stat</code>	(Optional; default to true) Whether create stat group. Stat group includes a gene dataset which contains total MIDcount and E10 score for each gene.
	<code>-o, --omics</code>	(Required; default to Transcriptomics) Specify the omics.
	<code>-v, --verbose</code>	(Optional) Verbose output.
	<code>-w, --errorCode-file</code>	(Optional; default to false) Determine output error code to file.



### 2.14.1.2 Usage Examples

Function 1: GEF to plain table GEM format

```
...
$ singularity exec SAW_v5.5.0.sif cellCut view \ ## convert GEF that only contains
bin1 geneExp
  -s {SN} \
  -i /path/to/output/03.count/{SN}.raw.gef \
  -o {SN}.raw.gem
$ singularity exec SAW_v5.5.0.sif cellCut view \ ## convert a whole GEF
  -s {SN} \
  -i /path/to/output/05.tissuecut/{SN}.gef \
  -o {SN}.gem
$ singularity exec SAW_v5.5.0.sif cellCut view \ ## convert tissue GEF that only
contains bin1 geneExp
  -s {SN} \
  -i /path/to/output/05.tissuecut/{SN}.tissue.gef \
  -o {SN}.tissue.gem
$ singularity exec SAW_v5.5.0.sif cellCut view \ ## convert cellbin GEF to cellbin
GEM
  -s {SN} \
  -i /path/to/output/051.cellcut/{SN}.cellbin.gef \
  -o {SN}.cellbin.gem \
  -d /path/to/output/03.count/{SN}.raw.gef
```

Function 2: completion of a GEF

```
...
$ singularity exec SAW_v5.5.0.sif cellCut bgef \ ## complete GEF that only con-
tains bin1 geneExp group to a whole GEF, you may specify the bin size using “-b”.
Separate multiple bin size with comma
  -i /path/to/output/03.count/{SN}.tissue.gef \
  -o {SN}.tissue.complete.gef \
  -b 1,20,50,100 \
  -O Transcriptomics
```

Function 3: converting GEM to GEF

```
...
$ singularity exec SAW_v5.5.0.sif cellCut bgef \ ## convert GEM to GEF in specific
bin size. Separate multiple bin sizes with comma
  -i {SN}.gem \
  -o {SN}.gef \
  -b 1,20,50 \
  -O Transcriptomics
```

Example of GEF to GEM conversion using gefpy, users may specify the bin size.

```
...
$ python
>>> from gefpy.bgef_reader_cy import BgefR
>>> bgef=BgefR(filepath='/path/to/output/05.tissuecut/{SN}.tissue.gef',bin_
size=200,n_thread=4)
>>> bgef.to_gem('{SN}.tissue.bin200.gem')
```



## 2.14.2 rapidRegister

SAW **rapidRegister** is a lite **register** pipeline that performs all modules in the **register** except cell segmentation. The usage is the same as **register**.

Run **rapidRegister** requires the following files:

- **count** output gene expression matrix file (**.raw.gef**)
  - ImageQC processed microscopic tissue staining image file (**.tar.gz**)
  - ImageQC Image process record file (**.ipr**)
- ⌚ Expected running time for 1 cm x 1 cm Stereo-seq Chip T image: ~20 min, Memory: ~20 G

### 2.14.2.1 Arguments and Options

Table 2-16 **rapidRegister** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) ImageQC/ImageStudio processed staining image TAR.GZ file or image pre-processed output directory.
<b>-c</b>	(Required) ImageQC/ImageStudio IPR (image process record) file. IPR is designed to efficiently hold images and process records generated from each image processing step along with metadata in various data types. Please check <a href="#">Stereo-seq File Format Manual</a> to get more information on the IPR file.
<b>-v</b>	(Optional; depends on <b>-i</b> ) <b>count</b> output gene expression matrix GEF file.
<b>-o</b>	(Required) Path to the directory where to store the <b>rapidRegister</b> outputs.

### 2.14.2.2 Usage Examples

The usage of **rapidRegister** is similar to **register**. Here we only take scenario 1 as an example.

Scenario 1: Process images from ImageQC/ImageStudio output data and gene expression matrix. Perform stitching, tissue segmentation, and registration with gene expression matrix.

```
...
$ image=/path/to/data/image
$ image4register=$(find ${image} -maxdepth 1 -name ${SN}*.tar.gz | head -1)
$ imageQC=$(find ${image} -maxdepth 1 -name ${SN}*.ipr | head -1)
$ mkdir -p /path/to/output/04.register
$ singularity exec SAW_v5.5.0.sif rapidRegister \
    -i ${image4register} \
    -c ${imageQC} \
    -v /path/to/output/03.count/{SN}.raw.gef \
    -o /path/to/output/04.register
```

### 2.14.2.3 Outputs

**rapidRegister** output files are organized as below:

```
...
$ tree /path/to/output/04.register
/path/to/output/04.register
... ## skip setting files, logs and image folder
└── attrs.json
└── fov_stitched_transformed.tif
└── SN_date_time_version.ipr ## rapidRegister output IPR does not have /CellSeg/
    CellMask dataset
└── SN_tissue_bbox.csv
└── transform_thumb.png
```

### 2.14.3 checkGTF

SAW **checkGTF** is an application for checking whether the GTF/GFF file is in the correct format as the input for **count**.

Run **checkGTF** requires the following files:

- Reference genome annotation GFF/GTF<sup>9,10</sup> file (**.gff** / **.gtf**)

#### 2.14.3.1 Arguments and Options

Table 2-17 **checkGTF** Arguments and Options

Parameter	Function
<b>-i</b>	(Required) Gene annotation GFF/GTF file.
<b>-o</b>	(Required) Output a re-format GFF/GTF file.

#### 2.14.3.2 Usage Examples

```
...
$ singularity exec SAW_v5.5.0.sif checkGTF \
    -i /path/to/reference/genes.gtf \
    -o /path/to/reference/genes_new.gtf \
```

## 2.14.4 Other applications of imageTools

Besides `ipr2img`, `imageTools` has three more functions: `img2rpi`(writes images in RPI format), `merge` (merges stain image with tissue segmentation and cell segmentation images to check the segmentation result), and `overlay` (stacks inferred track line template with stitched panoramic image to check stitching result or stacks track line template from matrix with registered panoramic image to check registration result).

### 2.14.4.1 Arguments and Options

Table 2-18 Other applications of `imageTools` Arguments and Options

Commands	Parameters	Function
<code>img2rpi</code>	<code>-i</code>	(Required) Input TIFF file. Separate multiple files by comma.
	<code>-g</code>	(Required) Set the group name of the input TIFF stores in the RPI. Separate multiple files by comma, the order of groups needs to be exactly same with the input TIFF files.
	<code>-b</code>	(Required) Bin sizes. Separate multiple bin sizes with space, for example 1 10 50 100
	<code>-o</code>	(Required) Output path for the RPI file. Has to use absolute path or relative path.
<code>merge</code>	<code>-i</code>	(Required) Input TIFF files. Separate multiple files by comma. The maximum number of TIFF files to be composited is three, and the channel order is R-G-B.
	<code>-o</code>	(Required) Output path for the multichannel image.
<code>overlay</code>	<code>-i</code>	(Required) Input TIFF file. Usually input a pre-registered panoramic image if overlaid with the stitching template derived from track cross, and input a registered microscopic image if overlaid with the track line template acquired from gene expression matrix.
	<code>-c</code>	(Required) Image configuration file (.ipr) or template points file (.txt).
	<code>-o</code>	(Required) Output path of the TIFF file which has the template overlaid on the selected image.
	<code>-d</code>	(Required) Module name. Convert template from IPR for the selected modules. Valid options: <code>stitch</code> or <code>register</code> .
	<code>-l</code>	(Optional, default to 30) Cross limbs length in pixel.
	<code>-w</code>	(Optional, default to 1) Cross line thickness in pixel.

### 2.14.4.2 Usage Examples

Function 1: `img2rpi`

```
...
$ singularity exec SAW_v5.5.0.sif imageTools img2rpi \
-i /path/to/output/04.register/fov_stitched_transformed.tif \
-g ssDNA \
-b 1 10 50 100 \
-o /path/to/output/04.register/fov_stitched_transformed.rpi ## this RPI is
used for manual registration in StereoMap
```

### Function 2: `merge`

```
...
$ singularity exec SAW_v5.5.0.sif imageTools merge \
    -i /path/to/output/04.register/{SN}_regist.tif,/path/to/output/04.register/
{SN}_tissue_cut.tif,/path/to/output/04.register/{SN}_mask.tif \
    -o /path/to/output/04.register/merge.tif
```

\* Please be noted that we use the backward slash “\” to indicate the end of a line in a command that spans multiple lines.

### Function 3: `overlay`

Overlay stitching template in IPR or in a TXT format with the pre-registered panoramic image to check the stitching result.

```
...
## stitch
preRegImage=/path/to/output/04.register/fov_stitched_transformed.tif
imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
stitchTmplt=/path/to/output/04.register/transform_template.txt

singularity exec SAW_5.5.0.sif imageTools overlay \
    -i ${preRegImage} \
    -c ${imageIPR} \
    -o /path/to/output/04.register/stitch_check.tif \
    -d stitch \
    -l 60 \
    -w 3

singularity exec SAW_5.5.0.sif imageTools overlay \
    -i ${preRegImage} \
    -c ${stitchTmplt} \
    -o /path/to/output/04.register/stitch_check_tmplt.tif \
    -d stitch \
    -l 60 \
    -w 3
```

Overlay registration template in IPR or in a TXT format with the registered panoramic image.

```
...
## register
regImage=/path/to/output/04.register/{SN}_regist.tif
imageIPR=$(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
regTmplt=/path/to/output/04.register/matrix_template.txt

singularity exec SAW_5.5.0.sif imageTools overlay \
    -i ${regImage} \
    -c ${imageIPR} \
    -o /path/to/output/04.register/register_check.tif \
    -d register \
    -l 60 \
    -w 3
```

```
...
singularity exec SAW_5.5.0.sif imageTools overlay \
-i ${regImage} \
-c ${regTmplt} \
-o /path/to/output/04.register/register_check_tmplt.tif \
-d register \
-l 60 \
-w 3
```

## 2.14.5 manualRegister

SAW manualRegister pipeline is performed when automatic registration result does not meet the requirement. Users can use StereoMap, an offline visualization software, to manually register images with the gene expression matrix. The operation parameters are recorded in the JSON file and can be input into the SAW manualRegister pipeline to modify registration record in IPR. Remember to run imageTools ipr2img again to acquire transformed images.

Run **manualRegister** requires the following files and information:

- count output gene expression matrix file (**.raw.gef**)
  - An image processing output directory which needs to include a **fov\_stitched\_transformed.tif** file, usually this is **/path/to/output/04.register**
  - **register/rapidRegister** output IPR file (**.ipr**)
  - **StereoMap** manual registration output JSON file which record manual operations (**.regist.json**)
-  Expected running time for 1 cm x 1 cm Stereo-seq Chip T image: ~3 min, Memory: 7 G

### 2.14.5.1 Arguments and Options

Table 2-19 **manualRegister** Arguments and Options

Parameters	Function
<b>-i</b>	(Required) register/rapidRegister output directory which includes a <b>fov_stitched_transformed.tif</b> file.
<b>-c</b>	(Required) register/rapidRegister output IPR file. <b>manualRegister</b> would overwrite registration parameters in the IPR to the manually adjusted parameters acquired from <b>StereoMap</b> .
<b>-v</b>	(Required) count output gene expression matrix GEF file.
<b>-o</b>	(Optional; default to 0) Offset in the x and y direction from the center of the <b>fov_stitched_transformed.tif</b> image. These two values are specified as "offsetX" and "offsetY" in the <b>StereoMap</b> output JSON file created after manual registration, and will be recorded as "OffsetX" and "OffsetY" in the IPR "Register" group. The offset x and offset y are separate by space.
<b>-f</b>	(Optional; default to 0) Whether flip the image horizontally along the y-axis. This value is specified as "flip" in the <b>StereoMap</b> output JSON file created after manual registration. Valid options: 1 (flip), 0 (not flip). Flip information will be recorded as "Flip" in the IPR "Register" group.
<b>-t</b>	(Optional; default to 0) Count of counterclockwise rotation at 90 degree. This value is specified as "rot" in the <b>StereoMap</b> output JSON file created after manual registration. Valid options: 0 (no rotate), 1 (90 degree rotation), 2 (180 degree rotation), 3 (270 degree rotation). Rotation information will be recorded as "CounterRot90" in the IPR "Register" group.

Parameters	Function
<b>-a</b>	(Optional; default to False) Whether perform fine tuning for manual registration result. Turn on the fine tuning switch to perform a precise adjustment that relies on a self-developed algorithm to register manually operated image and spatial gene expression matrix according to the track-lines. Since the result of fine tuning depends highly on the accuracy of image stitching, which aligns tracklines, please check the stitching result before turning on the fine tune switch. The "OffsetX" and "OffsetY" records in the IPR "Register" group for a fine-tuned result would differ from the input offsets. Valid options: True (perform fine tuning) and False (transform image based solely on manual operation).
<b>-p</b>	(Required) Output directory.

## 2.14.5.2 Usage Examples

 **Tip: get the inputs for manualRegister from StereoMap manual registration output JSON file:**

```
...
- "offsetX":{offsetX} of -o
- "offsetY":{offsetY} of -o
- "flip":{flip} of -f
- "rot":{rot} of -t
- "isTuned":{isTuned} of -a, please input a capitalized Boolean value.
```

Scenario 1: perform fine tuning

```
...
$ mkdir -p /path/to/output/manualregister
$ cp $(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
/path/to/output/manualregister # we recommend to make a copy of IPR to prevent overwirte original file
$ regIPR=$(find /path/to/output/manualregister -maxdepth 1 -name {SN}*.ipr |
head -1)

singularity exec SAW_v5.5.0.sif manualRegister \
-i /path/to/output/04.register \
-c ${regIPR} \
-v /path/to/output/03.count/{SN}.raw.gef \
-o {offsetX} {offsetY} \
-f {flip} \
-t {rot} \
-a {isTuned} ## This need to be a capitalized 'True'
-p /path/to/output/manualregister
```

Scenario 2: transform image based solely on manual operation

```
...
$ mkdir -p /path/to/output/manualregister
$ cp $(find /path/to/output/04.register -maxdepth 1 -name {SN}*.ipr | head -1)
/path/to/output/manualregister # we recommend to make a copy of IPR to prevent overwirte original file
$ regIPR=$(find /path/to/output/manualregister -maxdepth 1 -name {SN}*.ipr |
head -1)

singularity exec SAW_v5.5.0.sif manualRegister \
-i /path/to/output/04.register \
-c ${regIPR} \
-v /path/to/output/03.count/{SN}.raw.gef \
-o {offsetX} {offsetY} \
-f {flip} \
-t {rot} \
-p /path/to/output/manualregister
```

## 2.14.6 lasso

SAW lasso pipeline is performed to extract cell or spatial gene expression matrix(ces) of one or multiple manually delineated closed regions acquired from **StereoMap**.

Run **lasso** requires the following files and information:

- GEF file that includes **wholeExp group** or **cellCut** output cell bin GEF file (**.gef** or **.cellbin.gef**)
  - **StereoMap** output coordinates list file (**.geojson**)
- ⌚ Running time and memory are highly dependent on the selected bin size and data volume.

### 2.14.6.1 Arguments and Options

Table 2-20 Lasso Arguments and Options

Parameters	Function
<b>-i</b>	(Required) GEF file that includes wholeExp group or cellCut output cell bin GEF file (.gef or .cellbin.gef)
<b>-m</b>	(Required) StereoMap output coordinates list file (.geojson)
<b>-n</b>	(Required) The Stereo-seq Chip T serial number.
<b>-o</b>	(Required) Path to the directory where to store the lasso outputs. It has to be an existing path.
<b>-s</b>	(Required for square bin) Bin size.

## 2.14.6.2 Usage Examples



**Please Note! Replace `{SN}` with your Stereo-seq Chip T serial number (SN, e.g. SS200000135TL-D1), `{bin}` with the bin size you want (e.g. 1, 10, 200), and `/upload/path/{taskID}` with the true path and task ID.**

Scenario 1: square bin lasso

```
...
$ mkdir -p /path/to/output/lasso

$ singularity exec SAW_v5.5.0.sif lasso \
  -i /path/to/output/05.tissuecut/{SN}.gef \
  -m /upload/path/{taskID}.anno.geojson \
  -o /path/to/output/lasso \
  -s {bin} \
  -n {SN}
```

Scenario 2: cell bin lasso

```
...
$ mkdir -p /path/to/output/lasso

$ singularity exec SAW_v5.5.0.sif lasso \
  -i /path/to/output/051.tissuecut/{SN}.cellbin.gef \
  -m /upload/path/{taskID}.anno.geojson \
  -o /path/to/output/lasso \
  -n {SN}
```

## 2.14.6.3 Outputs

Square bin lasso output files are:

```
...
tree /path/to/output/lasso
/path/to/output/lasso
└── segmentation
    ├── SN.lasso.mask.tif
    └── SN.lasso.label.gz
```

Cellbin lasso output files are:

```
...
tree /path/to/output/lasso
/path/to/output/lasso
└── segmentation
    ├── SN.lasso.cellbin.gef
```

# **CHAPTER 3**

## **TEST DATA**

### **DEMONSTRATION**

Users may refer to this section as a format for testing SAW process, of the files show in this chapter as the reference in testing SAW pipelines. This chapter includes the statistics results and examples of critical files for each key step.

SN: SS200000135TL\_D1



“...” in the demo stands for some lines of log information that can be omitted.

### 3.1 mapping

#### 3.1.1 Statistical Report for CID Mapping and Filtering

```
...
$ cat /path/to/output/01.mapping/E100026571_L01_trim_read_1_barcodeMap.stat
...
getBarcodePositionMap_uniqBarcodeTypes: 645784920
total_reads: 1002214171
reads_with_polyA: 131113905 13.08%
reads_filteredByPolyA: 22008148 2.20%
mapped_reads: 826344259 82.45%
reads_with_adapter: 9007116 0.90%
reads_with_dnb: 42264284 4.22%
barcode_exactlyOverlap_reads: 682746301 68.12%
barcode_misOverlap_reads: 143590127 14.33%
barcode_withN_reads: 7831 0.00%
Q10_bases_in_barcode: 99.54%
Q20_bases_in_barcode: 97.49%
Q30_bases_in_barcode: 91.74%
Q10_bases_in_umi: 99.26%
Q20_bases_in_umi: 96.32%
Q30_bases_in_umi: 89.45%
Q10_bases_in_seq: 99.47%
Q20_bases_in_seq: 97.12%
Q30_bases_in_seq: 91.08%
umi_filter_reads: 8265089 0.82%
umi_with_N_reads: 13025 0.00%
umi_with_polyA_reads: 12365 0.00%
umi_with_low_quality_base_reads: 8239699 0.82%
mapped_dnbs: 75619113
...
```

### 3.1.2 Statistical Report for Reference Genome Alignment

```
...
$ cat /path/to/output/01.mapping/E100026571_L01_trim_read_1.Log.final.out
...
Number of input reads | 766807770
Average input read length | 95
UNIQUE READS:
    Uniquely mapped reads number | 643871246
    Uniquely mapped reads % | 83.97%
    Average mapped length | 95.21
    Number of splices: Total | 67595584
    Number of splices: Annotated (sjdb) | 65674308
    Number of splices: GT/AG | 66407685
    Number of splices: GC/AG | 457595
    Number of splices: AT/AC | 41563
    Number of splices: Non-canonical | 688741
    Mismatch rate per base, % | 0.50%
    Deletion rate per base | 0.07%
    Deletion average length | 3.91
    Insertion rate per base | 0.03%
    Insertion average length | 1.25
MULTI-MAPPING READS:
    Number of reads mapped to multiple loci | 87649341
    % of reads mapped to multiple loci | 11.43%
    Number of reads mapped to too many loci | 5301054
    % of reads mapped to too many loci | 0.69%
UNMAPPED READS:
    Number of reads unmapped: too many mismatches | 0
    % of reads unmapped: too many mismatches | 0.00%
    Number of reads unmapped: too short | 28773993
    % of reads unmapped: too short | 3.75%
    Number of reads unmapped: other | 1212136
    % of reads unmapped: other | 0.16%
CHIMERIC READS:
    Number of chimeric reads | 0
    % of chimeric reads | 0.00%
```

### 3.1.3 Example of BAM mapping

```
...
$ samtools view /path/to/output/01.mapping/E100026571_L01_trim_read_1.Aligned.sortedByCoord.out.bam | head -2
E100026571L1C007R00303973559 256 1 3000644 3 100M * 0
0 GCCTCATTGTGCCCATATGTTGCCTATGTTGTGGACTTATTTCATTAAACTTAAACATCTTA-
ATTTTTCTTATTCATCATTGACCAAGCT -FCA9D?GFFD<-D<CGFEGD-DG*FGDFBE;E(9BGGE38FFF-
G9GG;0?GGFGB?E@G:GGG3GF79F0GGDG?G<D>F;EG,G?<<CD4>G=>B+C NH:i:2 HI:i:2 AS:i:94
nM:i:2 Cx:i:8839 Cy:i:7539 UR:Z:120CF
E100026571L1C003R03702347721 0 1 3001778 255 100M * 0
0 GTATGACATCTGTCCAGGATCTTAGCTTCTAGCTCTGGTGAGAAGTCTGGAGTAATTCTAATAGG-
CCTGCATTATGTTACTTGACCTTTTC EEFEDFFEFFFFFEFFFEC@EFFFFDFFEEFFFCFCEFFAFB-
FCED??FGBEFFDC:FFFDCFAF4FAFFDFDG?DFBD.F@FECA/FEDEFFAA NH:i:1 HI:i:1 AS:i:92
nM:i:3 Cx:i:12136 Cy:i:14034 UR:Z:C0808
```

## 3.2 merge

### 3.2.1 Example of Mapped CID List with Reads Count File

```
...$ head /path/to/output/02.merge/SS200000135TL_D1.barcodeReadsCount.txt
7127    18002    48
4348    19028    1
14130    8635     1
7618    14537    24
4912    10945    5
16783    12914    1
15539    8177     1
9288    8082     14
7274    16533    59
9087    10657    10
```

## 3.3 count

### 3.3.1 Statistical Report for MID Filtering and Gene Annotation

```
...$ cat /path/to/output/03.count/SS200000135TL_D1.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.summary.stat
## FILTER & DEDUPLICATION METRICS
TOTAL_READS      PASS_FILTER      ANNOTATED_READS UNIQUE_READS      FAIL_FILTER_RATE
FAIL_ANNOTATE_RATE      DUPLICATION_RATE
731520587      643871246      532386027      108123310      11.98    17.31    79.69
## ANNOTATION METRICS
TOTAL_READS      MAP      EXONIC      INTRONIC      INTERGENIC      TRANSCRIPTOME      ANTISENSE
643871246      643871246      483163052      49222975      111485219      532386027
109940618
100.0    100.0    75.0     7.6      17.3      82.7      17.1
```

### 3.3.2 Example of Annotated BAM

```
...$ samtools view /path/to/output/03.count/SS200000135TL_D1.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam | head -2
E100026571L1C003R03702347721      0      1      3001778 255      100M      *      0      0
GTATGACATCTGCCAGGATCTTCTAGCTTCATAGTCTCTGGTGAGAAGTCTGGAGTAATTCTAATAGGCCTGCATTATAT-
GTTACTTGACCTTTTC      EEFEDFFFFFFFEFFFFEC@EFFFFDFFEEFFFCFCEFFAFBFCED??FGBEFFDC:FFF-
DCFAF4FAFFDFFDG?DFBD.F@FECA/FEDEFFAA      NH:i:1      HI:i:1      AS:i:92      nM:i:3      Cx:i:12136
Cy:i:14034      UR:Z:C0808      XF:i:2
E100026571L1C005R02302788444      528      1      3016331 0      100M      *      0      0
TTTATGTGGAGTCCCTTAATCCACTTAGATTGACCTTAGTACAAGGAGATAGGAATGGATCAATTGCATTCTTACATGATAACAG-
CCAGTTGTACC      ;FDF>FCFFEAD:FFEBF=@FFDEEFFFC@EFCEFDDFFCE?FDF7EEECFDEFFFCEFCCEEDEEEFFB-
FEEFFDEEFFFEEDFFEDFEEEFFEAD      NH:i:5      HI:i:1      AS:i:96      nM:i:1      Cx:i:6628      Cy:i:7872
UR:Z:EDFF9
```

### 3.3.3 Example of count Gene Expression Matrix

```
$ h5dump -n /path/to/output/03.count/SS200000135TL_D1.raw.gef
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
FILE_CONTENTS {
group /
group /geneExp
group /geneExp/bin1
dataset /geneExp/bin1/exon
dataset /geneExp/bin1/expression
dataset /geneExp/bin1/gene
}
}

$ h5dump -d /geneExp/bin1/expression /path/to/output/03.count/SS200000135TL_D1.raw.gef | head -15
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
DATASET “/geneExp/bin1/expression” {
DATATYPE H5T_COMPOUND {
H5T_STD_U32LE “x”;
H5T_STD_U32LE “y”;
H5T_STD_U8LE “count”;
}
DATASPACE SIMPLE { ( 76041339 ) / ( 76041339 ) }
DATA {
(0): {
4888,
10392,
1
},
(1): {
}
}

$ h5dump -d /geneExp/bin1/gene /path/to/output/03.count/SS200000135TL_D1.raw.gef | head -20
HDF5 “/path/to/output/03.count/SS200000135TL_D1.raw.gef” {
DATASET “/geneExp/bin1/gene” {
DATATYPE H5T_COMPOUND {
H5T_STRING {
STRSIZE 32;
STRPAD H5T_STR_NULLTERM;
CSET H5T_CSET_ASCII;
CTYPE H5T_C_S1;
} “gene”;
H5T_STD_U32LE “offset”;
H5T_STD_U32LE “count”;
}
DATASPACE SIMPLE { ( 24661 ) / ( 24661 ) }
DATA {
(0): {
“Gm1992”,
0,
132
},
(1): {
}
}
```



### 3.3.4 Example of count Sampling File

```
$ head -8 /path/to/output/03.count/SS200000135TL_D1_raw_barcode_gene_exp.txt
y x geneIndex MIDIndex readCount
10392 4888 10551 665954 4
7096 8901 10551 881671 1
7096 8901 10551 357383 20
18783 7397 10551 355789 1
13032 9155 10551 297666 1
13032 9155 10551 298690 1
11778 10617 10551 686313 4
```

## 3.4 register and imageTools

### 3.4.1 Registered image

File /path/to/output/04.register/fov\_stitched\_transformed.tif and /path/to/output/04.register/SS200000135TL\_D1\_regist.tif.

/path/to/output/04.register/  
fov\_stitched\_transformed.tif



/path/to/output/04.register/  
SS200000135TL\_D1\_regist.tif



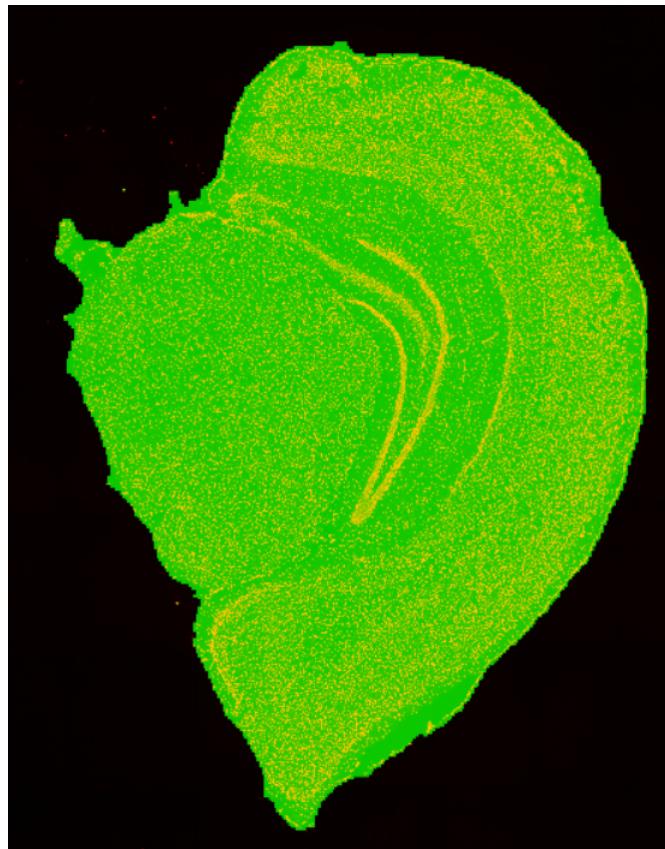
### 3.4.2 Image Process Record File

```
...
h5dump -n /path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr
HDF5 “/path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr” {
FILE_CONTENTS {
group      /
group      /CellSeg
dataset    /CellSeg/CellMask
group      /ImageInfo
dataset    /ImageInfo/RGBScale
group      /ManualState
dataset    /Preview
group      /QCInfo
group      /QCInfo/CrossPoints
dataset    /QCInfo/CrossPoints/0_0
...
dataset    /QCInfo/CrossPoints/9_7
dataset    /QCInfo/TrackDistanceTemplate
group      /Register
dataset    /Register/MatrixTemplate
group      /StereoResepSwitch
group      /Stitch
group      /Stitch/BGISTitch
dataset    /Stitch/BGISTitch/StitchedGlobalLoc
group      /Stitch/ScopeStitch
dataset    /Stitch/ScopeStitch/GlobalLoc
group      /Stitch/StitchEval
dataset    /Stitch/StitchEval/StitchEvalH
dataset    /Stitch/StitchEval/StitchEvalV
dataset    /Stitch/TemplatePoint
dataset    /Stitch/TransformTemplate
group      /TissueSeg
dataset    /TissueSeg/TissueMask
}
}

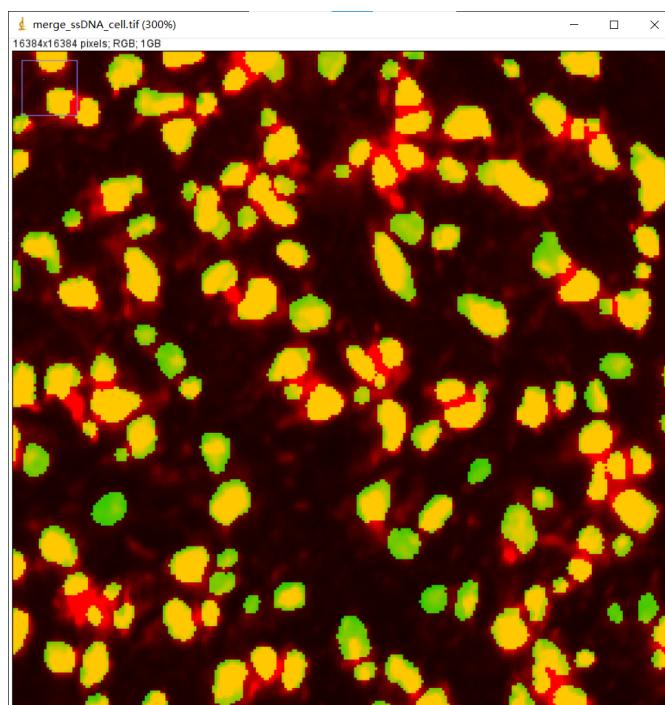
$ h5dump -A /path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr
| head -20
HDF5 “/path/to/output/04.register/SS200000135TL_D1_20220527_201353_1.1.0.ipr” {
GROUP “/” {
ATTRIBUTE “IPRVersion” {
DATATYPE H5T_STRING {
STRSIZE H5T_VARIABLE;
STRPAD H5T_STR_NULLTERM;
CSET H5T_CSET_UTF8;
CTYPE H5T_C_S1;
}
DATASPACE SCALAR
DATA {
(0): “0.0.1”
}
}
GROUP “CellSeg” {
ATTRIBUTE “CellSegShape” {
DATATYPE H5T_STD_I64LE
DATASPACE SIMPLE { ( 2 ) / ( 2 ) }
DATA {
(0): 21482, 22337
}
}
}
```

### 3.4.3 ImageTools merge

Merged image of microscopy image SS200000135TL\_D1\_regist.tif and tissue segmentation mask file SS200000135TL\_D1\_tissue\_cut.tif to check tissue segmentation performance.

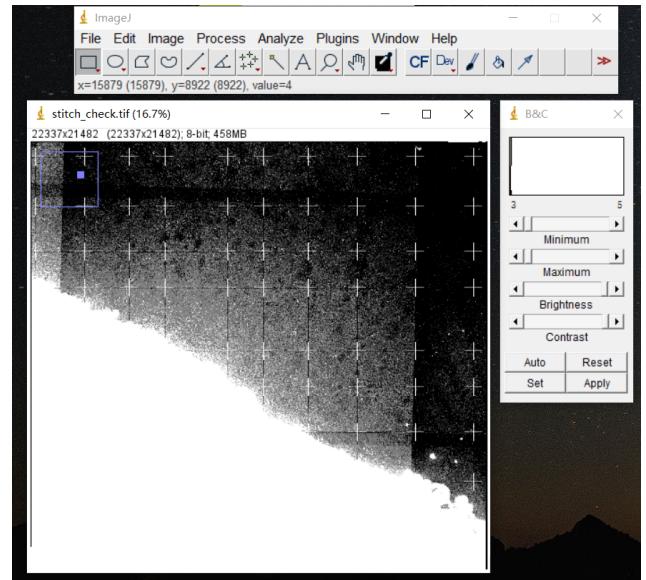
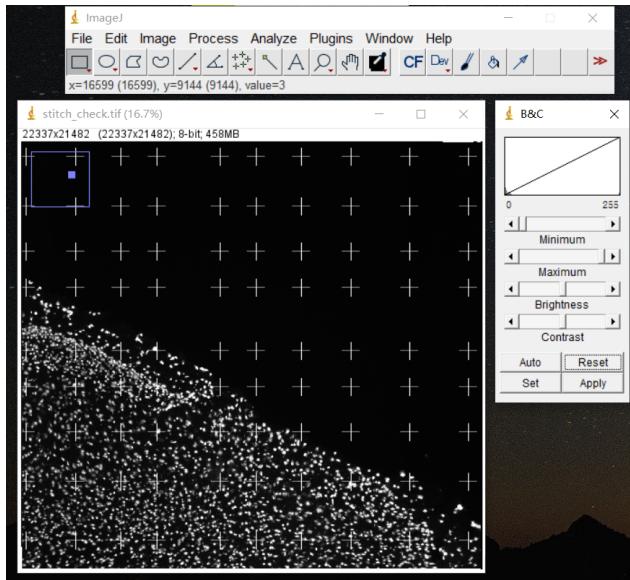


Part of merged image of microscopy image SS200000135TL\_D1\_regist.tif and cell segmentation mask file SS200000135TL\_D1\_mask.tif to check cell segmentation performance.

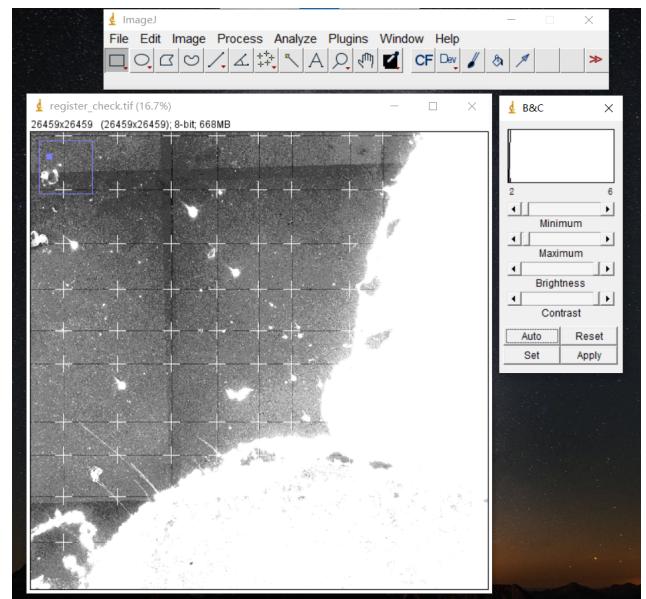
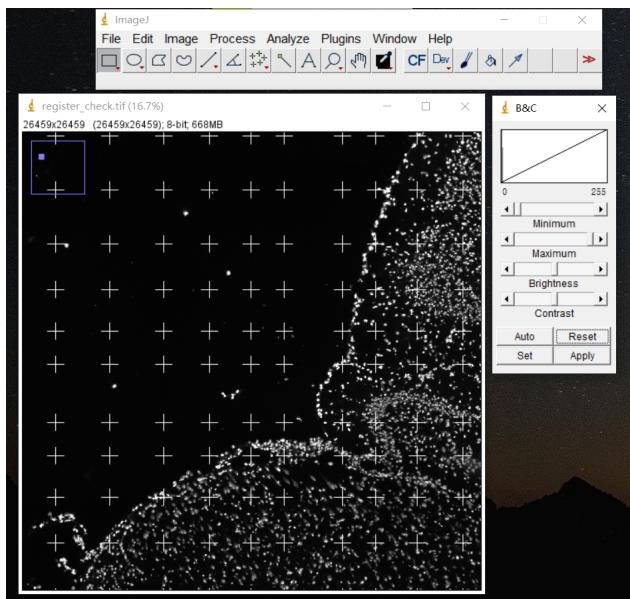


### 3.4.4 ImageTools overlay

Stack stitching template onto the `fov_stitched_transformed.tif` to check the result of stitching.



Stack registration template onto the `SS200000135TL_D1_register.tif` to check the result of registration.



### 3.5 tissueCut

#### 3.5.1 Statistical Report for Tissue Covered Region

```
...
$ cat /path/to/output/05.tissuecut/tissuecut.stat
# Tissue Statistic Analysis with Stain Image
Contour_area: 88637560
Number_of_DNB_under_tissue: 36679634
Ratio: 41.38%
Total_gene_type: 24299
MID_counts: 89816137
Fraction_MID_in_spots_under_tissue: 83.07%
Reads_under_tissue: 648371996
Fraction_reads_in_spots_under_tissue: 78.46%

binSize=1
Mean_reads_per_spot: 17.68
Median_reads_per_spot: 11.00
Mean_gene_type_per_spot: 1.71
Median_gene_type_per_spot: 1
Mean_Umi_per_spot: 2.45
Median_Umi_per_spot: 2

binSize=50
Mean_reads_per_spot: 18045.92
Median_reads_per_spot: 16198.00
Mean_gene_type_per_spot: 1151.22
Median_gene_type_per_spot: 1117
Mean_Umi_per_spot: 2499.82
Median_Umi_per_spot: 2309

binSize=100
Mean_reads_per_spot: 71116.81
Median_reads_per_spot: 64454.00
Mean_gene_type_per_spot: 3083.32
Median_gene_type_per_spot: 3081
Mean_Umi_per_spot: 9851.50
Median_Umi_per_spot: 9066

binSize=150
Mean_reads_per_spot: 157601.36
Median_reads_per_spot: 143773.00
Mean_gene_type_per_spot: 4891.22
Median_gene_type_per_spot: 5029
Mean_Umi_per_spot: 21831.83
Median_Umi_per_spot: 20242

binSize=200
Mean_reads_per_spot: 276727.25
Median_reads_per_spot: 254272.00
Mean_gene_type_per_spot: 6403.27
Median_gene_type_per_spot: 6719
Mean_Umi_per_spot: 38333.82
Median_Umi_per_spot: 35679
```

### 3.5.2 Example of Gene Expression Matrix for Tissue Covered Region



### 3.5.3 Example of Gene Expression Matrix for complete GEF

```
$ h5dump -n /path/to/output/05.tissuecut/SS200000135TL_D1.gef
HDF5 "/path/to/output/05.tissuecut/SS200000135TL_D1.gef" {
FILE_CONTENTS {
group      /
group      /geneExp
group      /geneExp/bin1
dataset    /geneExp/bin1/exon
dataset    /geneExp/bin1/expression
dataset    /geneExp/bin1/gene
group      /geneExp/bin10
dataset   /geneExp/bin10/exon
dataset   /geneExp/bin10/expression
dataset   /geneExp/bin10/gene
group      /geneExp/bin100
dataset   /geneExp/bin100/exon
dataset   /geneExp/bin100/expression
dataset   /geneExp/bin100/gene
group      /geneExp/bin20
dataset   /geneExp/bin20/exon
dataset   /geneExp/bin20/expression
dataset   /geneExp/bin20/gene
group      /geneExp/bin200
dataset   /geneExp/bin200/exon
dataset   /geneExp/bin200/expression
dataset   /geneExp/bin200/gene
group      /geneExp/bin50
dataset   /geneExp/bin50/exon
dataset   /geneExp/bin50/expression
dataset   /geneExp/bin50/gene
group      /geneExp/bin500
dataset   /geneExp/bin500/exon
dataset   /geneExp/bin500/expression
dataset   /geneExp/bin500/gene
group      /stat
dataset   /stat/gene
group      /wholeExp
dataset   /wholeExp/bin1
dataset   /wholeExp/bin10
dataset   /wholeExp/bin100
dataset   /wholeExp/bin20
dataset   /wholeExp/bin200
dataset   /wholeExp/bin50
dataset   /wholeExp/bin500
group      /wholeExpExon
dataset   /wholeExpExon/bin1
dataset   /wholeExpExon/bin10
dataset   /wholeExpExon/bin100
dataset   /wholeExpExon/bin20
dataset   /wholeExpExon/bin200
dataset   /wholeExpExon/bin50
dataset   /wholeExpExon/bin500
}
}
```



```
...
$ h5dump -d /stat/gene /path/to/output/05.tissuecut/SS200000135TL_D1.gef | head -20
HDF5 “/path/to/output/05.tissuecut/SS200000135TL_D1.gef” {
DATASET “/stat/gene” {
    DATATYPE H5T_COMPOUND {
        H5T_STRING {
            STRSIZE 32;
            STRPAD H5T_STR_NULLTERM;
            CSET H5T_CSET_ASCII;
            CTYPE H5T_C_S1;
        } “gene”;
        H5T_STD_U32LE “MIDcount”;
        H5T_IEEE_F32LE “E10”;
    }
    DATASPACE SIMPLE { ( 24661 ) / ( 24661 ) }
    DATA {
        (0): {
            “Gm42418”,
            5861037,
            60.1033
        },
        (1): {
    }
}

```

## 3.6 cellCut

### 3.6.1 Example of Gene Expression Matrix for Cell Bins

```
...
$ h5dump -n /path/to/output/051.cellcut/SS200000135TL_D1.cellbin.gef
HDF5 “/path/to/output/051.cellcut/SS200000135TL_D1.cellbin.gef” {
FILE_CONTENTS {
    group /
    group /cellBin
    dataset /cellBin/blockIndex
    dataset /cellBin/blockSize
    dataset /cellBin/cell
    dataset /cellBin/cellBorder
    dataset /cellBin/cellExon
    dataset /cellBin/cellExp
    dataset /cellBin/cellExpExon
    dataset /cellBin/cellTypeList
    dataset /cellBin/gene
    dataset /cellBin/geneExon
    dataset /cellBin/geneExp
    dataset /cellBin/geneExpExon
}
}
```

## 3.7 saturation

### 3.7.1 Example of Sequence Saturation File

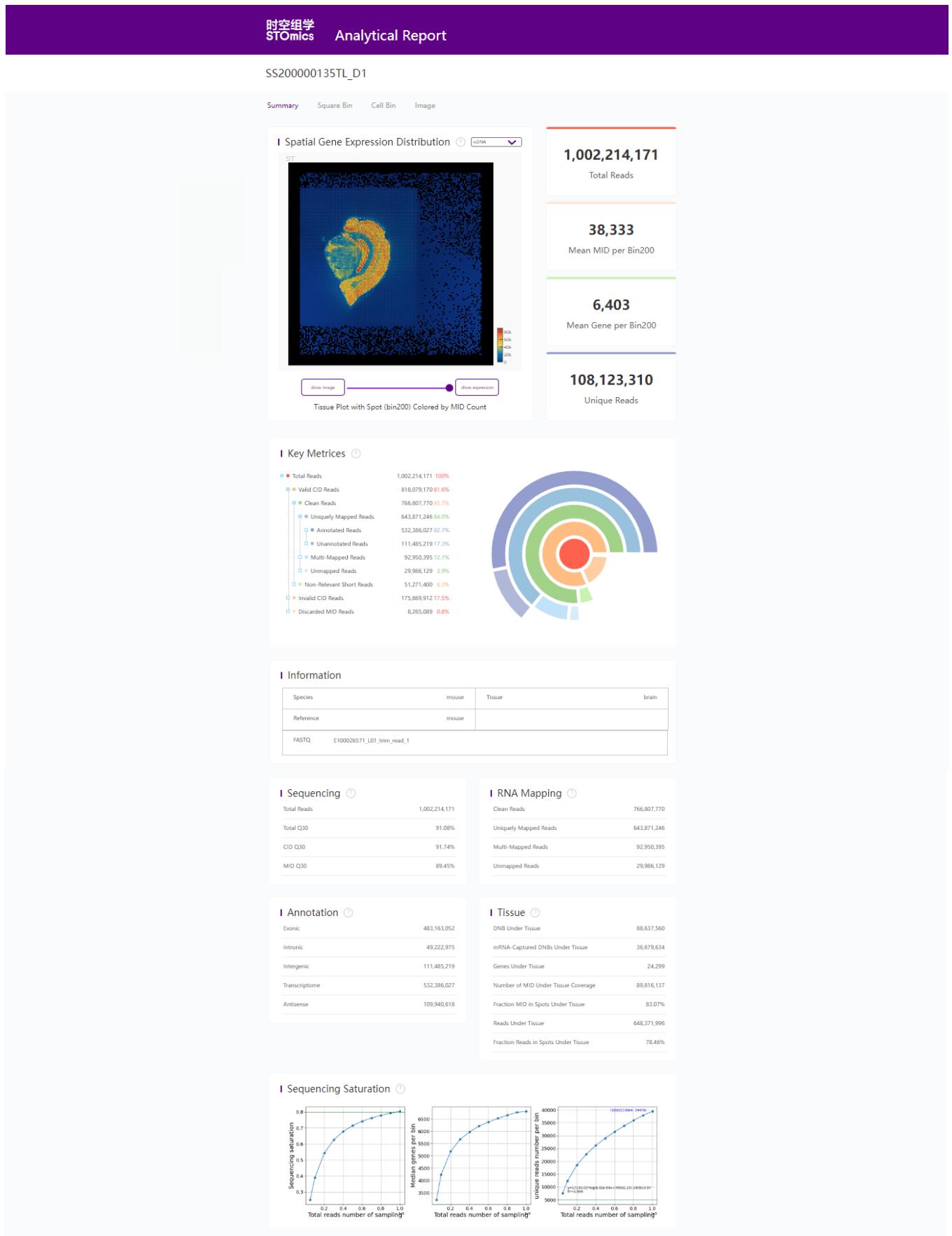
```
$ cat /path/to/output/07.saturation/sequence_saturation.tsv
sample bar_x bar_y1 bar_y2 bar_umi bin_x bin_y1 bin_y2 bin_umi
0.05 26619302 0.250959 1 19938952 26619302
0.27571 3270 7613
0.1 53238604 0.390241 1 32462699 53238604
0.41122 4268 12394
0.2 106477208 0.543149 1 48644210 106477208
0.558617 5215 18573
0.3 159715808 0.625887 1 59751787 159715808
0.638094 5693 22814
0.4 212954416 0.67839 1 68488171 212954416
0.688522 5995 26150
0.5 266193008 0.714813 1 75914701 266193008
0.723539 6204 28985
0.6 319431616 0.741736 1 82497808 319431616
0.749427 6378 31499
0.7 372670208 0.76249 1 88513055 372670208
0.769402 6517 33795
0.8 425908832 0.779116 1 94076279 425908832
0.78542 6642 35920
0.9 479147392 0.792733 1 99311385 479147392
0.798541 6747 37918
1 532386027 0.804159 1 104262941 532386027
0.809561 6840 39472
```

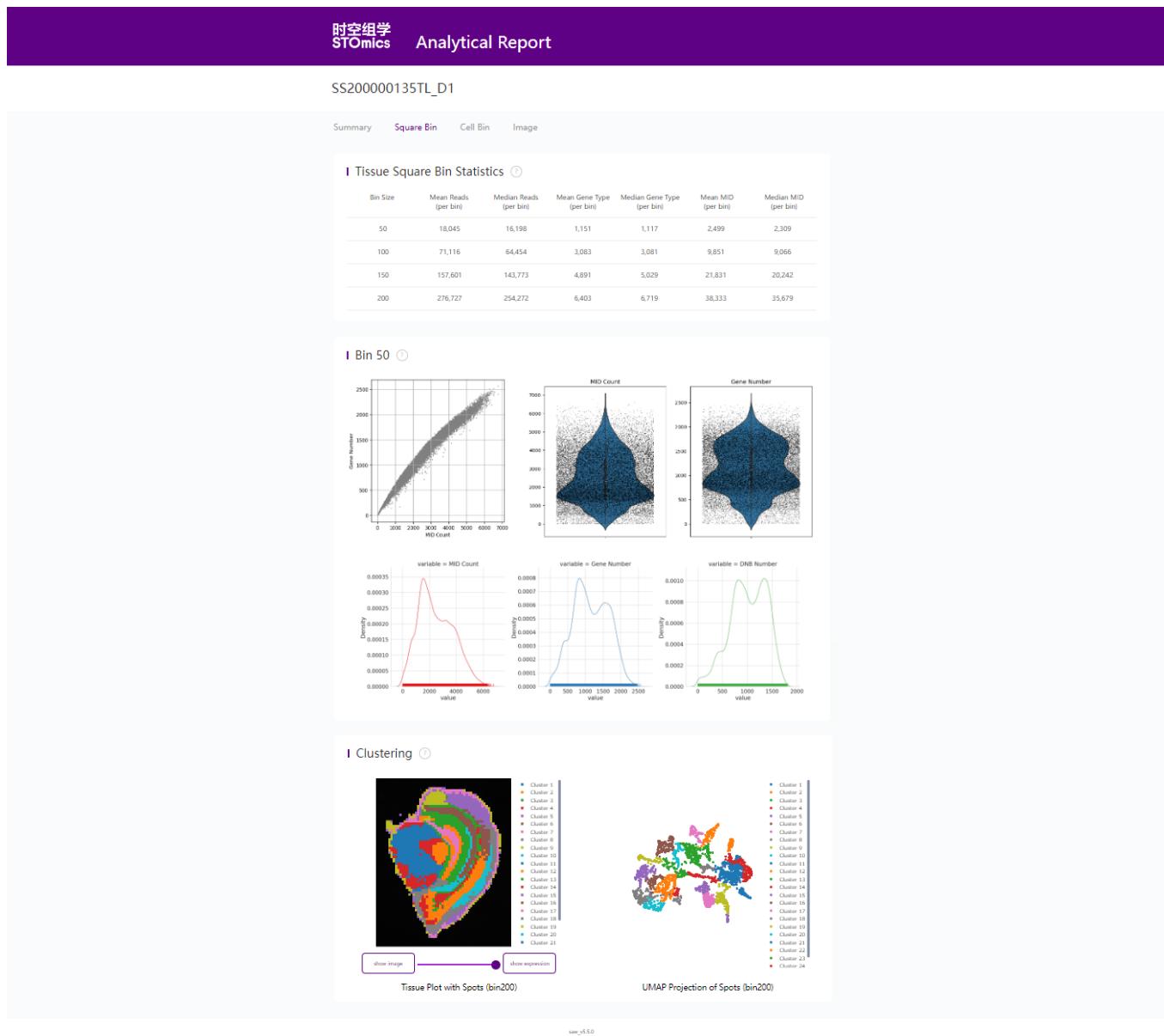
## 3.8 report

### 3.8.1 Example of Statistical Summary Report

```
$ cat /path/to/output/08.report/SS200000135TL_D1.statistics.json
{
    "version": "version_v2",
    "1.Filter_and_Map": {
        "1.1.Adapter_Filter": [
            {
                "Sample_id": "E100026571_L01_trim_read_1",
                "getCIDPositionMap_uniqCIDTypes": "645784920",
                "total_reads": "1002214171",
                "mapped_reads": "826344259(82.45%)",
                "CID_misOverlap_reads": "143590127(14.33%)",
                "CID_overlap_reads": "143590127(14.33%)"
            }
        ]
    }
}
```

### 3.8.2 HTML Report





**时空组学 STomics Analytical Report**

SS200000135TL\_D1

Summary Square Bin Cell Bin Image

### I Cell Bin Statistics

Cell Count	57,085	Median Cell Area	264
Mean Cell Area	278	Median DNB Count	231
Mean DNB Count	273	Median Gene Type	196
Mean Gene Type	223	Median MID	334
Mean MID	398		

### I Cell Bin

### I Clustering

Tissue Plot with Spots (cell bin)

UMAP Projection of Spots (cellbin)

**时空组学 STomics Analytical Report**

SS200000135TL\_D1

Summary Square Bin Cell Bin Image

### I Image Information

Manufacturer	micr
Model	Moticam50 M
Scan Time	2021-11-25 12:26:19
Overlap	0.1
Exposure Time (ms)	19.009
Scan Rows	13
Scan Columns	9
FOV Height	2,039
FOV Width	3,064
Stain Type	ssDNA
Stitched Image	No
Image Name	SS2000001351_D1_20220527_201353.11.0

### I QC

ImageQC Version	1.1.0
QC Pass	Pass
Track Line Score	70
Clarity Score	94
Good FOV Count	92
Total FOV Count	117
Stitching Score	93
Tissue Segmentation Score	100
Registration Score	99

### I Registration

ScaleX	0.866
ScaleY	0.866
Rotation	-1.603
Flip	True
Image X Offset	3,383.29
Image Y Offset	2,065
Counter Clockwise Rotation	90
Matrix X Offset	0.00
Matrix Y Offset	0.00
Matrix Height	26,459
Matrix Width	26,459

### I Stitching

Template Source Row No.	9
Template Source Column No.	6
Global Height	24,071
Global Width	25,128

# Appendices

## Appendix A: Recommended Directory Structure for Raw Data

Recommend to organize raw data as below if users prefer to use **SAW shell script** provided on the **SAW GitHub page** (<https://github.com/BGIResearch/SAW>).

```
$ tree
.
|-- image
|   |-- SS200000135TL_D1_20220527_201353_1.1.0.ipr
|   `-- SS200000135TL_D1_20220527_201353_1.1.0.tar.gz
|-- mask
|   '-- SS200000135TL_D1.barcodeToPos.h5
|-- md5
|-- reads
|   |-- E100026571_L01_trim_read_1.fq.gz
|   '-- E100026571_L01_trim_read_2.fq.gz
`-- reference
    |-- STAR_SJ100
    |   |-- Genome
    |   |-- SA
    |   '-- SAindex
    |       |-- chrLength.txt
    |       |-- chrName.txt
    |       |-- chrNameLength.txt
    |       |-- chrStart.txt
    |       |-- exonGeTrInfo.tab
    |       |-- exonInfo.tab
    |       |-- geneInfo.tab
    |       |-- genomeParameters.txt
    |       '-- genomeParameters_bkp.txt
    |           '-- sjdbInfo.txt
    |           '-- sjdbList.fromGTF.out.tab
    |           '-- sjdbList.out.tab
    |               '-- transcriptInfo.tab
    |-- genes.gtf
    '-- genome.fa

5 directories, 24 files
```

## Appendix B: SAW ST Output File List

STEP	OUTPUT	FILE DESCRIPTION
<b>splitMask</b>	<code>*.SN.barcodeToPos.bin</code>	Split Stereo-seq Chip T mask file according to the CID.
	<code>lane.Aligned.sortedByCoord.out.bam</code>	Binary Alignment/Map file, used for storing the sequence alignment information.
	<code>lane.Aligned.sortedByCoord.out.bam.csi</code>	BAM index file, which is a table of contents for the BAM file that indicating where in the BAM file a specific read or set of reads can be found.
	<code>lane.barcodeReadsCount.txt</code>	Mapped CID list file with reads counts for each CID, the three columns record x, y, and read count.
<b>mapping</b>	<code>lane.Log.final.out</code>	Summary mapping statistics after mapping job is complete (STAR output)
	<code>lane.Log.out</code>	Main log file in STAR mapping (STAR output)
	<code>lane.Log.progress.out</code>	Reports job process statistics (STAR output)
	<code>lane.SJ.out.tab</code>	Splice junctions detected in the mapping (STAR output)
	<code>lane.bcPara</code>	A parameters file defines CID mapping options
	<code>lane_barcodeMap.stat</code>	Statistical report of CID mapping, such as CID mapped reads count, reads sequencing quality, mapped DNB count, etc.
<b>merge</b>	<code>SN.barcodeReadsCount.txt</code>	Mapped CID list file with reads counts for each CID., the three columns record x, y, and read count.
	<code>SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam</code>	Annotated BAM file sorted by coordinate, includes uniquely mapped reads and multi-mapped reads whose Hl:i tag is 1.
	<code>SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.csi</code>	Index file of annotated BAM.
	<code>SN.Aligned.sortedByCoord.out.merge.q10.dedup.target.bam.summary.stat</code>	Statistical summary report file for count. Total reads in filter&de-duplication metrics stand for the total alignment record count in BAM. Pass filter and total reads in annotation metrics are the same, they represent uniquely mapped reads that will be used for annotation, MID correction and quantification.
<b>count</b>	<code>SN.raw.gef</code>	Gene expression file in hdf5 format. This is the first raw matrix that includes the expression information over a complete chip region. It only includes geneExp group for the bin size of 1. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been record as minX and minY in the attribute of geneExp/ expression dataset.
	<code>SN_raw_barcode_gene_exp.txt</code>	A space-separate file records coordinate, gene, MID, and count information. Which is prepared to be a sampling file that performs sequence saturation. The 5 columns are y, x, geneIndex, MIDIndex, readCount.
	<code>date-hh-mm-ss.log</code>	Log file.
<b>register&amp;imageTools ipr2img</b>	<code>attrs.json</code>	Height and width of gene expression matrix.
	<code>SN or other user specified name for the image folder used when input into imageQC/imageStudio</code>	This subdirectory stores raw small image pieces in TIFF format.
	<code>SN_0000_0000_YYYY-MM-DD_hh-mm-ss-n.tif</code>	Small image pieces in TIFF format.

STEP	OUTPUT	FILE DESCRIPTION
register& imageTools ipr2img	<b>fov_stitched_trans- formed.tif</b>	The stitched panoramic image that has pre-registered with the track line pattern template. So that it will not need to further rotate a non-right angle or scale.
	<b>matrix_template.txt</b>	Track line cross point template for the registered ssDNA image. Used for assessing registration result.
	<b>SN_date_time_version.ipr</b>	IPR format image process record file which records basic image information gathered from imageQC/imageStudio.
	<b>SN_mask.tif</b>	Registered cell segmentation binary image file in TIFF format.
	<b>SN_regist.tif</b>	Registered panoramic image file in TIFF format.
	<b>SN.rpi</b>	Registered panoramic image file, tissue area boundary, and cell boundaries (downsampled) that stores as an image pyramid.
	<b>SN_tissue_bbox.csv</b>	Registered panoramic image size.
	<b>SN_tissue_cut.tif</b>	The tissue segmentation result of registered panoramic image file in TIFF format.
	<b>transform_template.txt</b>	Track line cross point template for the fov_stitched_transformed.tif. Used for assessing stitching result.
	<b>transform_thumb.png</b>	A downsampled pre-registered panoramic image.
tissueCut	<b>SN.gef</b>	A gene expression file in hdf5 format. This file is a complete GEF format which includes geneExp group and wholeExp group in bin1, 10, 20, 50, 100, 200, and 500. It also includes a stat group. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been recorded as minX and minY in the attribute of geneExp/expression dataset.
	<b>SN.tissue.gef</b>	A gene expression file in hdf5 format. Tissue GEF includes the expression information of the tissue coverage region. It only includes geneExp group for the bin size of 1. The origin of expression matrix has been calibrated to (0,0), and the offset x and y has been record as minX and minY in the attribute of geneExp/expression dataset same to raw GEF.
	<b>tissue_fig</b>	This directory stores the statistical plots for the tissue coverage region
	<b>scatter_100x100_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin100)
	<b>scatter_150x150_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin150)
	<b>scatter_200x200_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin200)
	<b>scatter_50x50_MID_gene_counts.png</b>	Scatter plot of MID count and gene number in each bin (bin50)
	<b>statistic_100x100_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin100)
	<b>statistic_150x150_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin150)
	<b>statistic_200x200_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin200)
	<b>statistic_50x50_MID_gene_DNB.png</b>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis (bin50)
	<b>violin_100x100_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin100)
	<b>violin_150x150_MID_gene.png</b>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin150)

STEP	OUTPUT	FILE DESCRIPTION
<b>tissueCut</b>	<code>violin_200x200_MID_gene.png</code>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin200)
	<code>violin_50x50_MID_gene.png</code>	Violin plots show the distribution of deduplicated MID count and gene number in each bin (bin50)
	<code>tissuecut.stat</code>	Statistical report for tissue coverage region.
<b>cellCut</b>	<code>SN.cellbin.gef</code>	A gene expression file for cells in hdf5 format. Cellbin GEF includes the expression information of the cells, such as the coordinate of the centroid, boundary coordinates, expression of genes, and cell area. The cell is record by its boundary. The origin of expression matrix has been calibrated to (0,0), and the coordinate offset x and y has been recorded as offsetX and offsetY in the attribute of the GEF file same to minX and minY in the raw GEF file.
<b>spatial-Cluster</b>	<code>SN.spatial.cluster.h5ad</code>	H5AD file for spatial clustering analysis result.
<b>cellCluster</b>	<code>SN.cell.cluster.h5ad</code>	H5AD file for cell clustering analysis result.
<b>saturation</b>	<code>plot_1x1_saturation.png</code>	Sequencing saturation analysis plots for bin1. Calculated by 1-(unique reads/total reads) for each bin (bin1).
	<code>plot_200x200_saturation.png</code>	Sequencing saturation analysis plots for bin200. Calculated by 1-(unique reads/total reads) for each bin (bin1).
	<code>sequence_saturation.tsv</code>	Sequence saturation file. The nine columns are sampling component (#sample), bin1 total reads (bar_x), sequence saturation value at bin1 (bar_y1), median gene count at bin1 (bar_y2), unique reads at bin1 (bar_umi), bin200 total reads (bin_x), sequence saturation value at bin200 (bin_y1), median gene count at bin200 (bin_y2), and unique reads at bin200 (bin_umi), respectively.
<b>report</b>	<code>SN.report.html</code>	HTML analytical report.
	<code>SN.statistics.json</code>	Statistical summary report in JSON format. It gathers all important statistical metrics from the statistical report in each step.
	<code>scatter_1x1_MID_gene_counts.png</code>	Scatter plot of MID count and gene number in each cell
	<code>statistic_1x1_MID_gene_DNB.png</code>	Univariate distribution of MID count, gene numbers, and DNB numbers with rug along the x axis of each cell
	<code>violin_1x1_MID_gene.png</code>	Violin plots show the distribution of deduplicated MID count and gene number in each cell

## Appendix C: Handling Errors and Exceptions

### Common Errors

- **File access error:**

Some examples of file access error:

```
...
terminate called after throwing an instance of 'std::invalid_argument'
what(): Could not open the file: xxxxxxx
...
```

Or

```
#006: H5FDsec2.c line 352 in H5FD_sec2_open(): unable to open file: name = '/path/to/hdf5/file', errno = 2, error message = 'No such file or directory', flags = 0,
o_flags = 0
    major: File accessibility
    minor: Unable to open file
...
```



Solution:

```
...
# Attempt 1: Bind file path before execute command.
$ export SINGULARITY_BIND="/path/to/file/directory"

# Attempt 2: Turn off the HDF5 lock on the file by running the command below before
running SAW.
$ export HDF5_USE_FILE_LOCKING=FALSE
```

### mapping

- **readNameSeparator error:**

```
...
EXITING: FATAL INPUT ERROR: empty value for parameter "readNameSeparator" in input
"Command-Line"
SOLUTION: use non-empty value for this parameter
```



try to delete --readNameSeparator \\" \\\" from the command.

- **limitBAMsortRAM error:**

```
...
Error code: SAW-A10183

EXITING because of fatal ERROR: not enough memory for BAM sorting:
SOLUTION: re-run STAR with at least -limitBAMsortRAM xxxxxxxxxxx
```



Modify the value specified by the --limitBAMsortRAM refer to the SOLUTION in the stderr.

- **limitOutSJcollapsed error:**

```
...
Error code: SAW-A10182

EXITING because of fatal error: buffer size of SJ output is too small
Solution: increase input parameter --limitOutSJcollapsed
```

-  the parameters `--limitOutSJcollapsed` and `--limitIObufferSize` are paired.  
Please replace them with `--limitOutSJcollapsed 10000000 --limitIObufferSize=480000000` and try again.

## imageTools

- **OSError raises for imageTools merge**

```
...
OSError: [Errno 30] Read-only file system: '/opt/saw_v5.4.0_software/pipeline/imageTools/imagetools-1.0.0/log'
```

-  Error raises because the `-o` input is a filename without path. Try to input `/path/to/output/file.rpi` or `./file.rpi` for `-o`.

## Appendix D: Error Codes

SAW error codes are designed to catch error information and describe it in an easily understood way. Users can use these messages to fix the problem by themselves. The error messages will be output to the "errcode.log" file.

The error code is designed to express in three parts, date-time, error code, and explanation. The date-time information could help users differentiate errors in different program executions. The error code part provides information for the pipeline modules and error types. The explanation section displays the most explicit message stating the error/exception and possible solutions.

Pipeline	Code	Error Type	Examples and Error Handling
<b>splitMask</b>	SAW-A00001	Parameters invalid or missing	e.g. "parameters error" Please check your input parameters. Some required parameters might be missed. e.g. "splitBcPos error, expected 1_24 or 2_25" Please check your input CID position is either 1_24 or 2_25.
	SAW-A00002	File open failed	Please check the input file exists and has the correct access permission.
	SAW-A00003	File parse failed	e.g. "only support .bin or .h5 file." Please check your input file is in the correct file format.
	SAW-A00004	Other IO API error	e.g. "cannot write to file, /path/to/file" Please check your output directory path is an existing path.
	SAW-A00005	Other API error	Please check Appendix C or contact FAS/FBS for help.
	SAW-A00006	Software exception	Please check Appendix C or contact FAS/FBS for help.
<b>CIDCount</b>	SAW-A00021	Parameters invalid or missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A00022	File open failed	e.g. "cannot open such file, /path/to/file" Please check the input file exists and has the correct access permission.
	SAW-A00023	Failed to parser the file	Please check your input file is in the correct file format.
	SAW-A00024	Other API error	Please check Appendix C or contact FAS/FBS for help.
	SAW-A00025	Software exception	Please check Appendix C or contact FAS/FBS for help.

Pipeline	Code	Error Type	Examples and Error Handling
mapping	SAW-A10101	Parameters invalid or missing	<p>e.g. "EXITING: FATAL INPUT ERROR: unrecognized parameter name "outSAMattribute" in input "Command-Line-Initial""            Please check the spelling of your argument and parameters.</p> <p>e.g. "please check the umi position and length"            Please check the length of the reads in FQ1 are consistent with the parameters set for barcode length and umi length. For example, the length of the sum of barcode and umi set in bcPara file is 35 bp, but one of the reads in FQ1 is 30 bp, then you will see A10101 error code.            Please check the parameters set in the bcPara file are consistent with your FQs.</p>
	SAW-A10102	File open failed	<p>e.g. "Error, cannot open the file which be expected in gz or ascii format"            Please check the file permission and file format.</p> <p>e.g. "barcodePositionMapFile does not exists: /path/to/mask"            Please check the mask file exists and has the correct access permission.</p>
	SAW-A10103	File parse failed	<p>e.g. "sequence and quality have different length"            Please check the completeness of the reads in FQ. This issue may arise if the FQs are in incorrect format or the file was incompletely written or transferred.</p>
	SAW-A10104	Invalid data or data exception	Error data. Please check the file format and content.
	SAW-A10105	File deletion failed	This error arose if "_STARtmp" directory failed to be deleted. Please check whether the program has completely finished according to the *.Log.progress.out or *_barcodeMap.stat file.
	SAW-A10106	File IO failed	Please contact FAS/FBS for help.
	SAW-A10107	Failure on APIs of system and libraries	Please contact FAS/FBS for help.
	SAW-A10108	Software assert	Please contact FAS/FBS for help.
	SAW-A10109	Software exception	Please contact FAS/FBS for help.
	SAW-A10110	Allocate memory error	This error occurs when you run out of RAM. You may need to kill some jobs that use the same RAM or upgrade your hardware to get more RAM resources for your job.

Pipeline	Code	Error Type	Examples and Error Handling
mapping	SAW-A10111	Out of disk space	This error occurs when you store too many files on your hard disk. Please remove some files to free disk space.
	SAW-A10200	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A10201	CID comparison rate is too low	This error usually arises because the CID information of the input FQs is not the same as the CID in the input mask file. Please use the correct SN-FQ pairs for mapping.
	SAW-A10202	Fail to create the index for the BAM file	Please contact FAS/FBS for help.
	SAW-A10300	Fail to load indexed reference	Please check the existence, access permission, and completeness for the indexed reference.
count	SAW-A20001	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A20002	File open failed	Please check the input file exists and has the correct access permission.
	SAW-A20003	File parse failed	Please check your input BAM header is in the correct file format.
	SAW-A20004	Allocate memory error	This error occurs when you run out of RAM. You may need to kill some jobs that use the same RAM or upgrade your hardware to get more RAM resources for your job.
	SAW-A20009	Software exception	Please contact FAS/FBS for help.
count	SAW-A20101	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A20102	File open failed	Please check the file that exists and has the correct access permission.
	SAW-A20103	File parse failed	Please check your input file has a valid column number.

Pipeline	Code	Error Type	Examples and Error Handling
merge	SAW-A30001	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A30002	File open failed	Please check the input file exists and has the correct access permission.
	SAW-A30003	File parse failed	Please check your mask file is in the correct file format. Only support .h5/.bin mask file.
	SAW-A30004	Fail to create output file	Fail to create output file. Please check your writing permission of the output directory.
	SAW-A30005	Fail to open input file	Fail to open input TXT file. Please check the file that exists and have the correct access permission.
	SAW-A30006	Out of index	Record coordinates exceed the expected range. Please check the input file is the output of mapping.
	SAW-A30007	Allocate memory error	Please check whether the range of the coordinates is too large, or you have run out of RAM. You may need to kill some jobs that use the same RAM or upgrade your hardware to get more RAM resources for your job.
register & rapidRegister	SAW-A40001	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A40002	File open failed	Please check the input file that exists and has the correct access permission. Or, please check whether a stitched panoramic TIFF (.tif or .tiff) image exists in the TAR.GZ.
	SAW-A40003	File parse failed	Please check your input file is in the correct file format. The -v input gene expression matrix should be either a *tsv, barcode_gene_exp.txt, *.gem.gz, or *raw.gef.
	SAW-A40004	Invalid data or data exception	Error data. Please check the file content. This error may arise because the -v input file is empty, the CZI file in TAR.GZ is invalid, or the QCPassFlag in IPR is 0.
	SAW-A40005	Tissue segmentation error	Abnormal tissue segmentation reference score in image preprocessing.
	SAW-A40006	IPR field missing	"Stitch/BGIStitch/StitchedGlobalLoc", does not exist.

Pipeline	Code	Error Type	Examples and Error Handling
<b>register &amp; rapidRegister</b>	SAW-A40007	Tiled image missing	Please check the uncompressed image folder has tiled images.
	SAW-A40401	Parameter missing	Please check your <code>imageTools merge</code> input parameters. Some required parameters might be missed.
	SAW-A40402	File open failed	Please check the <code>imageTools merge</code> input file that exists and has the correct access permission.
	SAW-A40405	Invalid input	<code>imageTools merge</code> inputs of less than two images or more than three images.
	SAW-A40406	File pairing failed	Please check the <code>imageTools merge</code> input TIFF sizes are the same. Since the <code>merge</code> function is used for evaluating segmentation results, the input images are supposed to be the same in size and position (tissue position in the whole image).
	SAW-A40501	Parameter missing	Please check your <code>imageTools overlay</code> input parameters. Some required parameters might be missed.
	SAW-A40502	File open failed	Please check the <code>imageTools overlay</code> input file that exists and has the correct access permission.
<b>imageTools</b>	SAW-A40504	Invalid data or data exception	Error data. Please check the file content. This error may arise because the <code>-c</code> input IPR file does not include Stitch/TransformTemplate or Register/MatrixTemplate information.
	SAW-A40601	Parameter missing	Please check your <code>imageTools img2rpi</code> input parameters. Some required parameters might be missed.
	SAW-A40602	File open failed	Please check the <code>imageTools img2rpi</code> input file that exists and has the correct access permission.
	SAW-A40605	Invalid input	<code>imageTools img2rpi</code> input <code>-i</code> and <code>-g</code> have different length. These two inputs are supposed to be paired.
	SAW-A40701	Parameter missing	Please check your <code>imageTools ipr2img</code> input parameters. Some required parameters might be missed.

Pipeline	Code	Error Type	Examples and Error Handling
<b>imageTools</b>	SAW-A40702	File open failed	Please check the <code>imageTools ipr2img</code> input file exists and has the correct access permission. Or, please check whether a stitched panoramic TIFF (.tif or .tiff) image exists in the TAR.GZ.
	SAW-A40703	File parse failed	Please check your <code>imageTools ipr2img</code> input file is in the <b>imageQC/imageStudio</b> output TAR.GZ format.
	SAW-A40704	Invalid data or data exception	Error data. Please check the <code>imageTools ipr2img</code> input IPR file content. This error may arise because the CZI file in TAR.GZ is invalid, or the image has not either automatically or manually registered with the expression matrix. The second circumstance can be confirmed from IPR by checking whether the StereoResepSwitch/register is TRUE (has not performed automatic registration) or the ManualState/register is FALSE (has not performed manual registration). The third possible reason is the StereoResepSwitch/tissueseg is TRUE, therefore cannot output cell segmentation result.
	SAW-A40706	File pairing failed	Please check the shape of registered tissue segmentation images stored in the <code>imageTools ipr2img</code> input IPR are the same. Or please contact FAS/FBS for help.
<b>tissueCut</b>	SAW-A50001	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A50002	File open failed	Please check the file that exists and has the correct access permission.
	SAW-A50003	File parse failed	Please check your input file is in the correct file format.
	SAW-A50004	Fail to create output file	Fail to create output file. Please check your writing permission of the output directory.
	SAW-A50005	Fail to write TIFF	Fail to write a TIFF file.
	SAW-A50006	h5AttrWrite error	Please check the H5 file attributes.
	SAW-A50007	h5DatasetWrite error	Please check the H5 file dataset.

Pipeline	Code	Error Type	Examples and Error Handling
cellCut	SAW-A60001	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A60002	File open failed	Please check the file that exists and has the correct access permission.
	SAW-A60003	File parse failed	The file does not contain correct information. Please check the file format.
	SAW-A60110	Program version error	Please check your output GEF version. Your input GEF version might be too old.
	SAW-A60111	Call process error	e.g. "Please call freeRestriction first, or call restrictRegion function before restrictGene." This error arose because the invocation flow order was messed up. Please modify your invocation flow as prompted.
	SAW-A60120	Invalid data or data exception	Error data. Please check the file content.
	SAW-A60121	File information missing	Failed to read the file. Please check whether the file is damaged.
	SAW-A60122	File pairing failed	Please check the TIFF mask size is consistent with the size of expression matrix. Since the mask has been registered with the expression matrix, their sizes are supposed to be the same.
	SAW-A60130	Fail to create output file	Fail to create output H5 file. Please check your writing permission of the output directory or contact FAS/FBS for help.
	SAW-A60140	Allocate memory error	This error occurs when you run out of RAM. You may need to kill some jobs that use the same RAM or upgrade your hardware to get more RAM resources for your job.
	SAW-A60150	Dimensions of gene expression matrix did not match	Please contact FAS/FBS for help.

Pipeline	Code	Error Type	Examples and Error Handling
spatial-Cluster	SAW-A70001	Parameter missing	e.g. "-i or --gef_file is missing" Please check your input parameters. Some required parameters might be missed.
	SAW-A70002	File open failed	e.g. "cannot access /path/to/file: No such file or directory." Please check the file that exists and has the correct access permission.
	SAW-A70005	Value error	e.g. "The bin size is out of range, please check the range of gef binsize is in [1,10,20,50,100,200,500]." Please reset the bin size as prompted. e.g. "Gene number less than 3000, please check your gef file" Please check the content of your GEF file, and make sure there are at least 3000 genes for clustering.
	SAW-A70101	Parameter missing	e.g. "-i or --gef_file is missing" Please check your input parameters. Some required parameters might be missed.
cellCluster	SAW-A70102	File open failed	e.g. "cannot access /path/to/file: No such file or directory." Please check the file that exists and has the correct access permission.
	SAW-A70105	Value error	e.g. "The bin size is out of range, please check the range of gef binsize is in [1,10,20,50,100,200,500]." Please reset the bin size as prompted. e.g. "Gene number less than 3000, please check your gef file" Please check the content of your GEF file, and make sure there are at least 3000 genes for clustering.

Pipeline	Code	Error Type	Examples and Error Handling
<b>saturation</b>	SAW-A80001	Parameter missing	e.g. "-i is missing." Please check your input parameters. Some required parameters might be missed.
	SAW-A80002	File open failed	Please check the file that exists and has the correct access permission.
	SAW-A80003	File parse failed	Invalid GEF file. Please check the file format.
	SAW-A80004	Invalid data or data exception	e.g. "no data left after filter by coordinates." Please check the file content.
	SAW-A80005	Invalid data or data exception	e.g. "total map reads is 0, please check file format from --bcstat" Please check the file content of the input file as prompted.
	SAW-A80006	File pairing failed	e.g. "map reads less than annotated reads." Please check the input mapping statistical report and the count statistical report are from the same analysis.
	SAW-A80007	Plot error	Please contact FAS/FBS for help. PATH environment may not have python3.
	SAW-A80008	Fail to create output file	Fail to generate saturation file, please contact FAS/FBS for help.

Pipeline	Code	Error Type	Examples and Error Handling
report	SAW-A90001	Parameter missing	e.g. "-m or --barcodeMapStat is missing." Please check your input parameter as prompted. Some required parameters might be missed.
	SAW-A90002	File open failed	e.g. "cannot access *: No such file or directory." Please check the file that exists and has the correct access permission.
	SAW-A90003	File parse failed	JSON file format error. This error may arise because the input statistics files were not generated in the same SAW version as report. Or, the input mapping file prefix can not be parsed. Please contact FAS/FBS for help.
	SAW-A90004	Invalid data or data exception	e.g."information loss: fail to find 'bin_[size]' or 'ssDNA' in '*.rpi'" Please check the file content.
	SAW-A90005	Fail to create output file	Fail to create output file. Please check your writing permission of the output directory.
manualRegister	SAW-A40801	Parameter missing	Please check your input parameters. Some required parameters might be missed.
	SAW-A40802	File open failed	Please check the file that exists and has the correct access permission. Or, please check whether the pre-registered image fov_stitched_transformed.tif exists in the input directory.
	SAW-A40803	File parse failed	Please check your input file is in the correct file format. The -v input gene expression matrix should be either a *tsv, barcode_gene_exp.txt, *.gem.gz, or *raw.gef.
	SAW-A40804	Invalid data or data exception	Error data. Please check the file content. This error may arise because the -v input file is empty. The second possible reason is that the gene expression matrix information in the IPR Register module (MatrixShape, Xstart, Ystart) does not match with the input GEF file (minX, minY, maxX, maxY), because the manual registration has to be processed on the identical matrix.

## References

1. BGIResearch/SAW. Accessed October 13, 2021. <https://github.com/BGIResearch/SAW>
2. Chen A, Liao S, Cheng M, et al. Large field of view-spatially resolved transcriptomics at nanoscale resolution Short title: DNA nanoball stereo-sequencing. *bioRxiv*. Published online January 24, 2021:2021.01.17.427004. doi:10.1101/2021.01.17.427004
3. Cock PJA, Fields CJ, Goto N, Heuer ML, Rice PM. The Sanger FASTQ file format for sequences with quality scores, and the Solexa/Illumina FASTQ variants. *Nucleic Acids Res.* 2009;38(6):1767-1771. doi:10.1093/nar/gkp1137
4. Archives SR, Sra T, Nucleotide I, et al. File Format Guide 1. Published online 2009:1-11. Accessed May 21, 2021. <https://www.ncbi.nlm.nih.gov/sra/docs/submitformats/>
5. Merkel D. Docker: lightweight Linux containers for consistent development and deployment. *Linux J.* 2014;2014(239):2. Accessed October 15, 2021. <https://www.linuxjournal.com/content/docker-lightweight-linux-containers-consistent-development-and-deployment>
6. Kurtzer GM, Sochat V, Bauer MW. Singularity: Scientific containers for mobility of compute. *PLoS One.* 2017;12(5):e0177459. doi:10.1371/journal.pone.0177459
7. Sequence Alignment/Map Format Specification.; 2021. Accessed May 21, 2021. <https://github.com/samtools/hts-specs>.
8. Dobin A, Davis CA, Schlesinger F, et al. STAR: Ultrafast universal RNA-seq aligner. *Bioinformatics.* 2013;29(1):15-21. doi:10.1093/bioinformatics/bts635
9. Ensembl. GFF/GTF File Format. Published 2020. Accessed May 27, 2021. <http://www.ensembl.org/info/website/upload/gff.html?redirect=no>
10. GFF2 - GMOD. Accessed May 27, 2021. <http://gmod.org/wiki/GFF2>
11. GitHub - BGIResearch/stereopy: A toolkit of spatial transcriptomic analysis. Accessed July 4, 2021. <https://github.com/BGIResearch/stereopy>
12. BGIResearch/geftools: Tools for manipulating GEFs. Accessed April 7, 2022. <https://github.com/BGIResearch/geftools>
13. BGIResearch/gefpy: gef io, draw out from stereopy. Accessed April 7, 2022. <https://github.com/BGIResearch/gefpy>

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Please raise GitHub issues for reporting bugs and requesting features:

SAW GitHub Issue Page: <https://github.com/BGIResearch/SAW/issues>