

单细胞免疫组数据分析上机文档

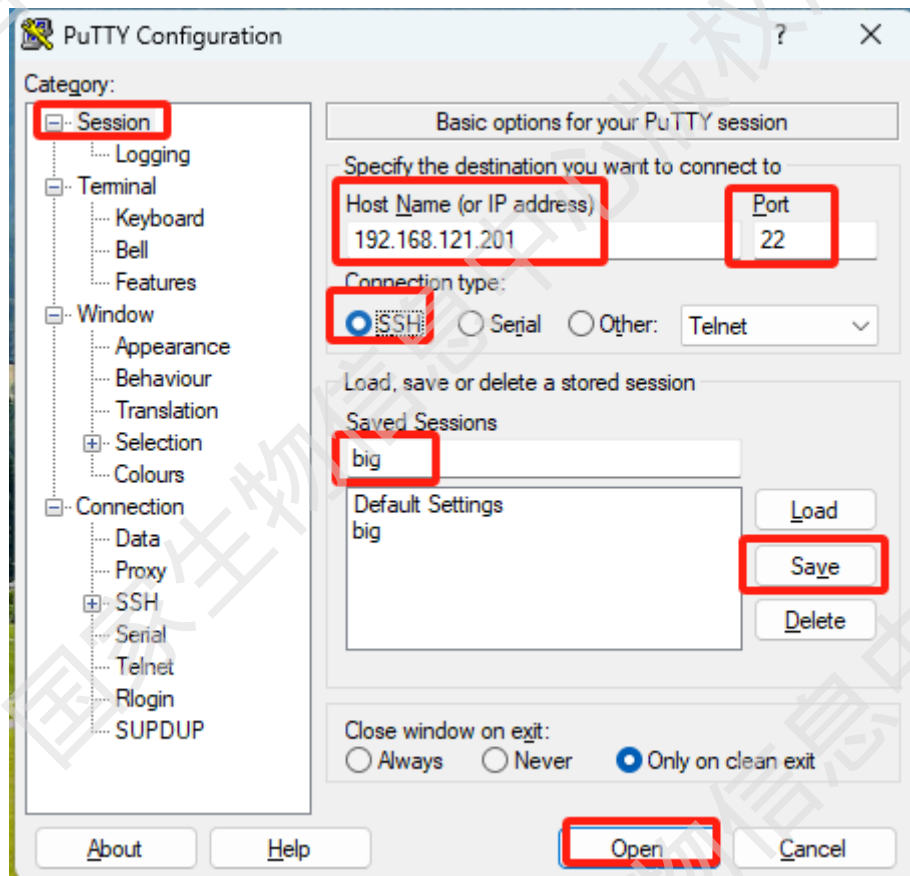
一、通过 putty 登录服务器

1. SSH 客户端 putty 安装及登录

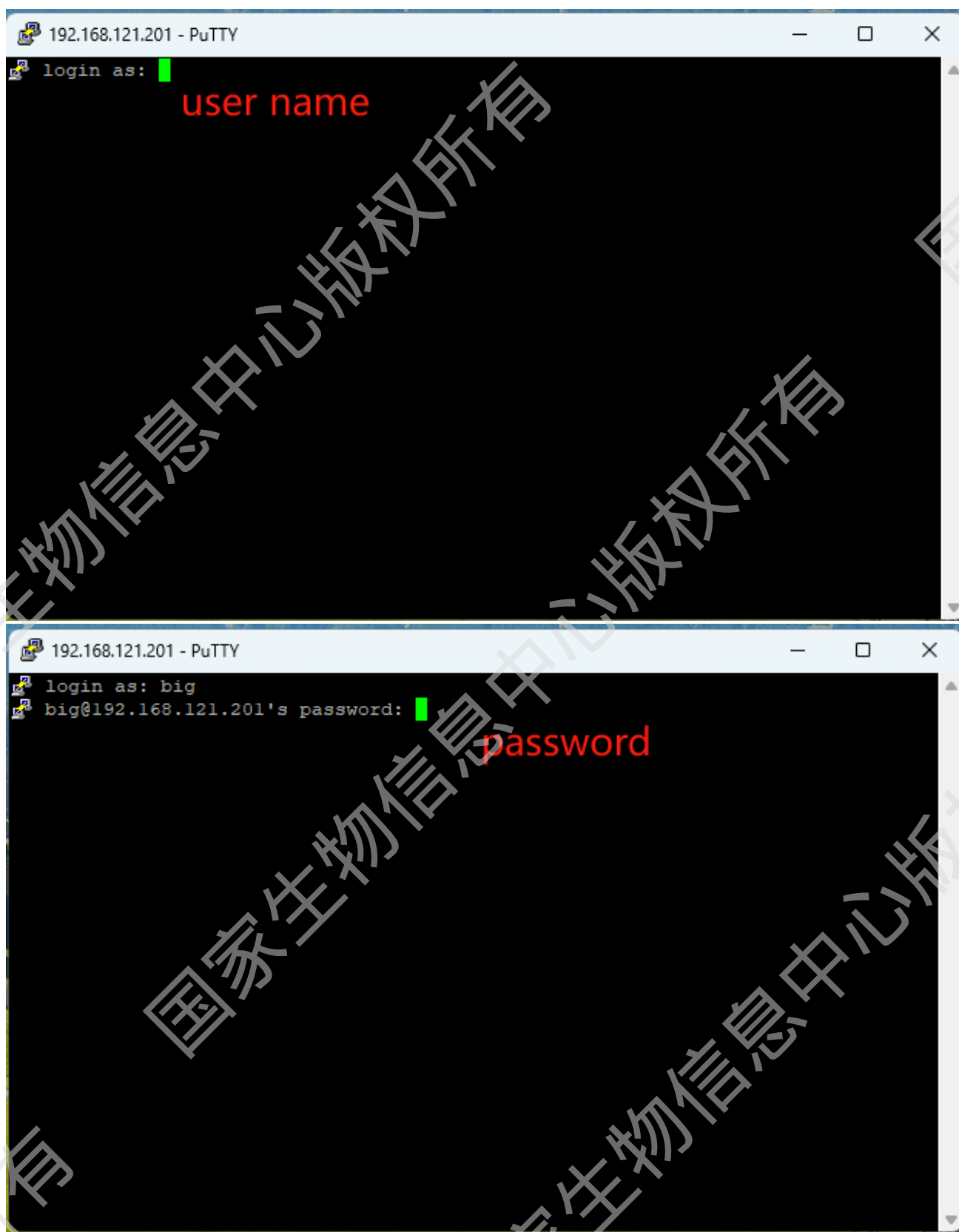
SSH 客户端 putty:

点击链接 <http://the.earth.li/~sgtatham/putty/latest/x86/putty.exe> 下载 putty.exe;

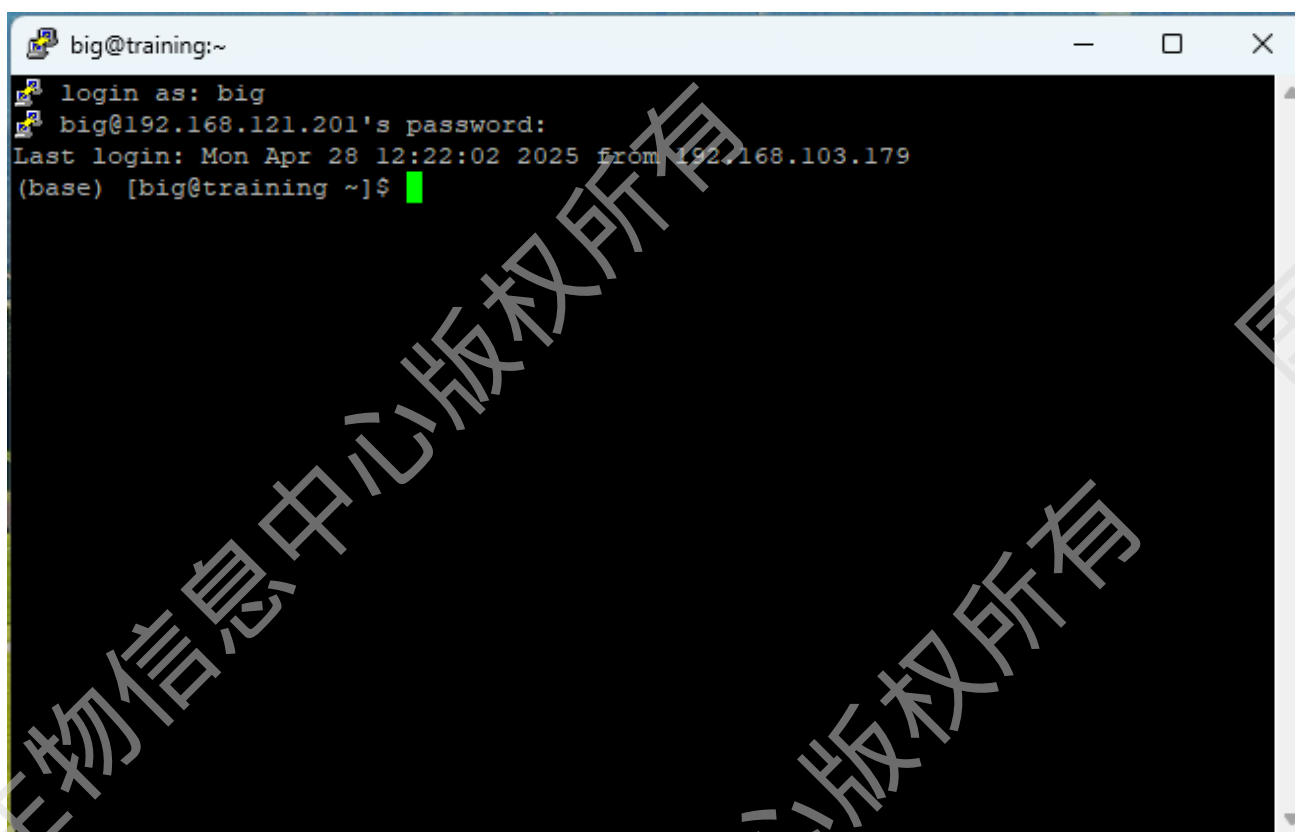
双击打开 putty，在 Session 栏的主机地址输入服务器地址 192.168.121.201；输入端口号：22；选择 ssh 链接方式；点击 Load；然后点击 open 打开。如果出现安全警告框，点击 YES。（见下图）



再输入用户名和密码登陆服务器。



远程登录服务器成功:



```
big@training:~
login as: big
big@192.168.121.201's password:
Last login: Mon Apr 28 12:22:02 2025 from 192.168.103.179
(base) [big@training ~]$
```

二、 软件和数据

1) 分析用到的软件

免疫组的序列比对部分用到的软件是：

cellranger[官网：<https://www.10xgenomics.com/support/software/cell-ranger/latest>]

免疫组的分析软件

scRepertoire [官网：<https://www.borch.dev/uploads/sc repertoire/>]

常用的学习新软件包的网址：

新 R 包：Bioconductor[官网：<https://www.bioconductor.org/>]

新 R 包/新软件：GitHub[官网：<https://github.com/>]

国内平替版（可能不全）Gitee[官网：<https://gitee.com/>]

分析软件均为开源软件，可以下载最新版本，进行安装。

2) 软件准备

Linux 系统里使用的软件 cellranger 已经安装在路径 “/data/biosoft/big/cellranger-9.0.1/cellranger”，使用的参考基因组路径为 “/data/biosoft/big/scTCR_scBCR/refdata-cellranger-vdj-GRCh38-alts-ensembl-7.1.0/”，大家可以直接使用。

3) 准备分析数据

在自己的工作目录下建立文件夹 `scTCR_scBCR` 并进入，然后把 “`/data/biosoft/big/scTCR_scBCR`” 路径下的数据拷贝到当前目录。

命令行：

```
cd
```

```
cp -r /data/biosoft/big/scTCR_scBCR .
```

```
cd scTCR_scBCR/
```

```
ll
```

```
mkdir scTCR_scBCR          #建立文件夹
cd  scTCR_scBCR            #进入文件夹
cp /home/big/scTCR_scBCR/* ./      #复制数据
ll  ./                      #查看文件夹内容
```

打开文件夹进行查看，

```
(base) [big@training scTCR_scBCR]$ ll
total 12
-rwxrwxr-x. 1 big big 268 Apr 21 11:53 1_cellranger_Sub01.sh
drwxr-xr-x. 3 big big 41 Nov 22 2022 refdata-cellranger-vdj-GRCh38-alts-ensembl-7.1.0
-rw-rw-r--. 1 big big 3350 Apr 21 11:45 Sub01_S1_L001_R1_001.fastq.gz
-rw-rw-r--. 1 big big 3350 Apr 21 11:45 Sub01_S1_L001_R2_001.fastq.gz
```

文件说明：

`refdata-cellranger-vdj-GRCh38-alts-ensembl-7.1.0` 目录是用来做比对的参考基因组，包含基因组的 `fasta` 序列以及 `cellranger` 需要用到的其他文件。

`*.fastq.gz` 文件为测序数据，这里有一个样本的 `scTCR` 双端测序数据，`Sub01` 表示测序样本 ID; `L001` 表示测序重复，`R1` 和 `R2` 表示双末端 `pair-end` 数据。

三、 分析流程

1. 基因组比对(约 7min)

1.1 认识 cellranger

基因组比对是以参考基因组为模版，把测序的短片段 `reads` 比对到参考基因组的具体位置上。10X Genomics 的 Universal 5' Gene Expression 建库方式，会检测同一个细胞的 5'scRNA-seq 和 scTCR/BCR 这两个模态。常用的 scRNA-seq 比对软件为 `cellranger count` 或 `STARsolo`，常用的 scTCR/BCR 比对软件为 `cellranger vdj`。

```
(base) [big@training scTCR_scBCR]$ /home/big/Software/cellranger-9.0.1/cellranger
cellranger cellranger-9.0.1

Process 10x Genomics Gene Expression, Feature Barcode, and Immune Profiling data

Usage: cellranger <COMMAND>

Commands:
count      Count gene expression and/or feature barcode reads from a single sample and GEM well
multi      Analyze multiplexed data or combined gene expression/immune profiling/feature barcode data
multi-template  Output a multi config CSV template
vdj        Assembles single-cell VDJ receptor sequences from 10x Immune Profiling libraries
aggr       Aggregate data from multiple Cell Ranger runs
annotate   Annotate cell-types from outputs of a CellRanger run
reanalyze  Re-run secondary analysis (dimensionality reduction, clustering, etc)
mkvdjref   Prepare a reference for use with CellRanger VDJ
mkfastq    Run Illumina demultiplexer on sample sheets that contain 10x-specific sample index sets
testrun    Execute the 'count' pipeline on a small test dataset
cloud      Invoke cloud commands
mat2csv    Convert a feature-barcode matrix to CSV format
mkref      Prepare a reference for use with 10x analysis software. Requires a GTF and FASTA
mkgtf      Filter a GTF file by attribute prior to creating a 10x reference
upload     Upload analysis logs to 10x Genomics support
sitecheck  Collect Linux system configuration information
telemetry  Configure and inspect telemetry settings and data
help       Print this message or the help of the given subcommand(s)

Options:
-h, --help    Print help
-V, --version Print version
```

1.2 输入/data/biosoft/big/cellranger-9.0.1/cellranger vdj --help 可以查看软件的帮助信息 (下图)

```
(base) [big@training scTCR_scBCR]$ /home/big/Software/cellranger-9.0.1/cellranger vdj --help
Assembles single-cell VDJ receptor sequences from 10x Immune Profiling libraries

Usage: cellranger vdj [OPTIONS] --id <ID> --fastqs <PATH>

Options:
  --id <ID>                A unique run id and output folder name [a-zA-Z0-9_]+
  --description <TEXT>      Sample description to embed in output files [default: ]
  --reference <PATH>        Path of folder containing 10x-compatible VDJ reference. Optional if '--denovo' is
                             specified
  --fastqs <PATH>           Path to input FASTQ data
  --project <TEXT>          Name of the project folder within a mkfastq or bcl2fastq-generated folder to pick
                             FASTQs from
  --sample <PREFIX>         Prefix of the filenames of FASTQs to select
  --lanes <NUMS>            Only use FASTQs from selected lanes
  --denovo                  Run in reference-free mode (do not use annotations)
  --chain <CHAIN_SPEC>      Chain type to display metrics for: 'TR' for T cell receptors, 'IG' for B cell
                             receptors, or 'auto' to autodetect [default: auto]
  --inner-enrichment-primers <PATH> If inner enrichment primers other than those provided in the 10x kits are used,
                             they need to be specified here as a textfile with one primer per line. Disable
                             secondary analysis, e.g. clustering
  --dry                    Do not execute the pipeline. Generate a pipeline invocation (.mro) file and stop
  --jobmode <MODE>          Job manager to use. Valid options: local (default), sge, lsf, slurm or path to a
                             .template file. Search for help on "Cluster Mode" at support.10xgenomics.com for
                             more details on configuring the pipeline to use a compute cluster
  --localcores <NUM>        Set max cores the pipeline may request at one time. Only applies to local jobs
  --localmem <NUM>          Set max GB the pipeline may request at one time. Only applies to local jobs
  --localmem <NUM>          Set max virtual address space in GB for the pipeline. Only applies to local jobs
  --mempercore <NUM>        Reserve enough threads for each job to ensure enough memory will be available,
                             assuming each core on your cluster has at least this much memory available. Only
                             applies to cluster jobmodes
  --maxjobs <NUM>           Set max jobs submitted to cluster at one time. Only applies to cluster jobmodes
  --jobinterval <NUM>       Set delay between submitting jobs to cluster, in ms. Only applies to cluster
                             jobmodes
  --overrides <PATH>        The path to a JSON file that specifies stage-level overrides for cores and memory.
                             Finer-grained than --localcores, --mempercore and --localmem. Consult
                             https://10xgen.com/resource-override for an example override file
  --output-dir <PATH>       Output the results to this directory
  --uiport <PORT>           Serve web UI at http://localhost:PORT
  --disable-ui              Do not serve the web UI
  --noexit                  Keep web UI running after pipeline completes or fails
  --nopreflight             Skip preflight checks
  -h, --help                Print help
```

1.3 比对（mapping）

命令行：

```
/data/biosoft/big/cellranger-9.0.1/cellranger vdj --id=Sub01 --sample=Sub01 --reference=./refdata-cellranger-vdj-GRCh38-alt-ensembl-7.1.0/ --fastqs=./ --localmem=30 --localcores=10
（不要运行，仅为示例）
```

```
cd /home/user01/scTCR_scBCR #回到工作目录，注释 user01 换成自己的ID
/home/big/Software/cellranger-9.0.1/cellranger vdj --id=Sub01 --sample=Sub01 --reference=./refdata-cellranger-vdj-GRCh38-alt-ensembl-7.1.0 --fastqs=./ --localmem=30 --localcores=10
```

软件参数说明：

- id 用户自定义一个唯一的 ID，cellranger vdj 的全部输出结果会保存在名为该 ID 的目录下
- sample 给 cellranger 读取的 fastq 的前缀名（即“Sub01_S1_L001_R1_001.fastq.gz”中的“Sub01”）
- reference 参考基因组的目录，下载网址和教程：<https://www.10xgenomics.com/support/software/cellranger/downloads#reference-downloads>
- fastqs 原始 fastq 数据所在路径
- localmem 所需内存，以 GB 为单位

--localcores 所需线程数

注：从方便核对结果的角度，id 和 sample 可以是相同的字符串；cellranger vdj 一般需要 30-50GB 内存，线程数给多少都可以，给多了跑得更快，一般给 40GB 内存+10 线程，可以在 1 小时以内跑完 cellranger 的比对。

如果运行了上述代码，当前结果由于 fastq 序列为示例所以显示如下

```
[error] Pipestance failed. Error log at:
Sub01/SC_VDJ_ASSEMBLER_CS/SC_MULTI_CORE/MULTI_CHEMISTRY_DETECTOR/VDJ_CHEMISTRY_DETECTOR/DETECT_VDJ_RECEPTOR/fork0/chnk0-u851e0f0431/_errors
Log message:
V(D)J Chain detection failed for Sample Sub01 in "/home/user50/scTCR_scBCR".

Total Reads      = 10
Reads mapped to TR = 3
Reads mapped to IG = 0

In order to distinguish between the TR and the IG chain the following conditions need to be satisfied:
- A minimum of 10000 total reads
- A minimum of 5.0% of the total reads needs to map to TR or IG
- The number of reads mapped to TR should be at least 3.0x compared to the number of reads mapped to IG or vice versa
Please check the input data and/or specify the chain via the --chain argument.

Waiting 6 seconds for UI to do final refresh.
Pipestance failed. Use --noexit option to keep UI running after failure.

2025-04-28 12:29:43 Shutting down.
Saving pipestance info to "Sub01/Sub01.mri.tgz"
For assistance, upload this file to 10x Genomics by running:
cellranger upload <your_email> "Sub01/Sub01.mri.tgz"
```

请返回家目录重新拷贝数据

```
cd
cp -r /data/biosoft/big/scTCR_scBCR/ .
cd scTCR_scBCR/
ll
```

1.4 运行完后，在当前目录[scTCR_scBCR 目录]下进行查看，可看到生成以下结果目录：

```
(base) [big@training scTCR_scBCR]$ ll
total 16
-rwxrwxr-x. 1 big big 250 Apr 21 11:57 1_cellranger.Sub01.sh
drwxr-xr-x. 3 big big 41 Nov 22 2022 refdata-cellranger-vdj-GRCh38-alts-ensembl-7.1.0
drwxrwxr-x. 5 big big 4096 Apr 21 11:57 Sub01
-rw-rw-r--. 1 big big 3350 Apr 21 11:45 Sub01_S1_L001_R1_001.fastq.gz
-rw-rw-r--. 1 big big 3350 Apr 21 11:45 Sub01_S1_L001_R2_001.fastq.gz
```

目录里的 outs 文件夹包含供下游分析使用的输出结果

```
cd Sub01/outs
ll
```

```
(base) [big@training scTCR_scBCR]$ ll Sub01/outs
total 724256
-rw-rw-r--. 1 big big      2704 Apr 21 11:52 airr_rearrangement.tsv
-rw-rw-r--. 1 big big    61380 Apr 21 11:52 all_contig_annotations.bed
-rw-rw-r--. 1 big big   63902 Apr 21 11:52 all_contig_annotations.csv
-rw-rw-r--. 1 big big 1605431 Apr 21 11:52 all_contig_annotations.json
-rw-rw-r--. 1 big big 732444785 Apr 21 11:52 all_contig.bam
-rw-rw-r--. 1 big big   29296 Apr 21 11:52 all_contig.bam.bai
-rw-rw-r--. 1 big big 175750 Apr 21 11:52 all_contig.fasta
-rw-rw-r--. 1 big big   16969 Apr 21 11:52 all_contig.fasta.fai
-rw-rw-r--. 1 big big   341618 Apr 21 11:52 all_contig.fastq
-rw-rw-r--. 1 big big     28 Apr 21 11:52 cell_barcodes.json
-rw-rw-r--. 1 big big    165 Apr 21 11:52 clonotypes.csv
-rw-rw-r--. 1 big big    735 Apr 21 11:52 concat_ref.bam
-rw-rw-r--. 1 big big     96 Apr 21 11:52 concat_ref.bam.bai
-rw-rw-r--. 1 big big   1022 Apr 21 11:52 concat_ref.fasta
-rw-rw-r--. 1 big big     39 Apr 21 11:52 concat_ref.fasta.fai
-rw-rw-r--. 1 big big   1013 Apr 21 11:52 consensus_annotations.csv
-rw-rw-r--. 1 big big    677 Apr 21 11:52 consensus.bam
-rw-rw-r--. 1 big big     96 Apr 21 11:52 consensus.bam.bai
-rw-rw-r--. 1 big big    504 Apr 21 11:52 consensus.fasta
-rw-rw-r--. 1 big big     38 Apr 21 11:52 consensus.fasta.fai
-rw-rw-r--. 1 big big      0 Apr 21 11:52 donor_regions.fa
-rw-rw-r--. 1 big big    891 Apr 21 11:52 filtered_contig_annotations.csv
-rw-rw-r--. 1 big big    509 Apr 21 11:52 filtered_contig.fasta
-rw-rw-r--. 1 big big    991 Apr 21 11:52 filtered_contig.fastq
-rw-rw-r--. 1 big big    931 Apr 21 11:52 metrics_summary.csv
-rw-rw-r--. 1 big big 2476194 Apr 21 11:52 vdj_contig_info.pb
drwxrwxr-x. 3 big big     41 Apr 21 11:52 vdj_reference
-rw-rw-r--. 1 big big   27365 Apr 21 11:52 vloupe.vloupe
-rw-rw-r--. 1 big big 4312114 Apr 21 11:52 web_summary.html
```

结果文件说明：

web_summary.html 是网页版的比对结果（可以直接用浏览器打开），包括 mapping 率，饱和度等一系列结果。

metrics_summary.csv 是表格版的比对结果（可以直接用 excel 打开），内容与网页版一致。

all_contig_annotations.csv 是供下游 scRepertoire 包分析 scTCR/BCR 用的结果，文件很小，只有 100KB 左右。

```
sample,barcode,is_cell,contig_id,high_confidence,length,chain,v_gene,d_gene,j_gene,c_gene,full_length,productive,fwr1,fwr1_nt,cdri,cdri_nt,fwr2,fwr2_nt,cdri2,cdri2_nt,fwr3,fwr3_nt,cdri3,cdri3_nt,fwr4,fwr4_nt,reads,umis,raw_consensus_id,exact_subclonotype_id
Sub01,AAACCCATCAGCATTG-1,false,AAACCCATCAGCATTG-1_contig_1,false,348,TRB,TRBV27,,TRBJ1-5,TRBC1,false,false,,,,,,,,,CASSFDLVGPQHF,TGTGCCAGCAG
TTTCGATTAGTAGGACCCAGCATTG-1,,76,1,,,
Sub01,AAACCCATCATTATCT-1,false,AAACCCATCATTATCT-1_contig_1,false,511,TRB,TRBV12-3,,TRBJ2-1,TRBC2,true,true,,,,,,,,,CASSLISGVNNEQFF,TGTGCCAGC
AGTTTAATAGCGGGGTGAACAATGAGCAGTTCTTC-1,,9340,1,,,
Sub01,AAACCGGAGATTTCAGT-1,false,AAACCGGAGATTTCAGT-1_contig_1,false,449,TRB,TRBV25-1,,TRBJ2-1,TRBC2,true,true,,,,,,,,,CASSEPLGEQFF,TGTGCCAGCAGT
GAACCGGGGCTTGAGCAGTTCTTC-1,,78,1,,,
Sub01,AAACGCTGTGTTTCGCT-1,false,AAACGCTGTGTTTCGCT-1_contig_1,false,512,TRB,TRBV7-9,,TRBJ2-3,TRBC2,true,true,,,,,,,,,CASRHPVRTDTQYF,TGTGCCAGCCG
GCACCCGATCAGGACAGATACGAGTATTTT-1,,10300,1,,,
Sub01,AAAGCCTGTAGTCGCA-1,false,AAAGCCTGTAGTCGCA-1_contig_1,false,362,TRB,TRBV7-3,TRBD1,TRBJ2-1,TRBC2,true,false,,,,,,,,,CASSLGGGRGEQFF,TGTGCC
AGCAGCTTAGCGGGGAGAGGGGAGCAGTTCTTC-1,,100,2,,,
```

2. scRepertoire 包解析 scTCR/BCR 数据 (运行非常快, 预计这部分的讲课用时 25min)

该部分可以在 windows 上进行, 操作更友好, 适合新手入门

2.1 下载并安装 R 和 Rstudio:

R 下载地址: <https://cloud.r-project.org/>

RStudio 下载地址: <https://posit.co/download/rstudio-desktop/>

1: Install R

RStudio requires R 3.6.0+. Choose a version of R that matches your computer's operating system.

R is not a Posit product. By clicking on the link below to download and install R, you are leaving the Posit website. Posit disclaims any obligations and all liability with respect to R and the R website.

DOWNLOAD AND INSTALL R

2: Install RStudio

DOWNLOAD RSTUDIO DESKTOP FOR WINDOWS

Size: 265.28 MB | [SHA-256: BB369743](#) | Version: 2024.12.1+563 | Released: 2025-02-13

2.2 Bioconductor 是 R 语言中专门为生物信息 R 包建立的管理网站, 可以在 Bioconductor 官网上搜索任何你想要学习的生信相关 R 包

Bioconductor 网站: <https://www.bioconductor.org/>

搜索 scRepertoire 后的结果: <https://www.bioconductor.org/packages/release/bioc/html/scRepertoire.html>

Installation

To install this package, start R (version "4.5") and enter:

```
if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")

BiocManager::install("scRepertoire")
```

只安装一次BiocManager即可一直使用

再用BiocManager安装任何Bioconductor上的R包

For older versions of R, please refer to the appropriate [Bioconductor release](#).

Documentation

To view documentation for the version of this package installed in your system, start R and enter:

```
browseVignettes("scRepertoire")
```

Using scRepertoire	HTML	R Script
Reference Manual	PDF	
NEWS	Text	
LICENSE	Text	

每个R包都是如此: 这里作者会给出详细的教学文档以及实现该文档的具体代码

这里是该R包里每个函数的详细帮助文档, 也可以直接在R里用问号+函数名的方式查看, 如"?combineTCR()"并回车

Details

biocViews	Annotation, Classification, ImmunoOncology, Sequencing, SingleCell, Software
Version	2.4.0
In Bioconductor since	BioC 3.12 (R-4.0) (4.5 years)
License	MIT + file LICENSE
Depends	ggplot2, R (>= 4.0)
Imports	assertthat, cubature, dplyr, evmix, ggalluvial, ggdendro, ggraph, grDevices, igraph, iNEXT, plyr, quantreg, Rcpp, reshape2, rjson, rlang, S4Vectors, SeuratObject, SingleCellExperiment, stringr, stringdist, SummarizedExperiment, tidygraph, truncdist, VGAM, purrr, lifecycle, methods
System Requirements	
URL	https://www.borch.dev/uploads/scRepertoire/ 有些优秀的R包会单独设置自己的教学网站，链接都放在这个位置，这个教程往往比上一页中的教程更好更新
Bug Reports	https://github.com/BorchLab/scRepertoire/issues

scRepertoire 2.3.4

Getting Started

Install

Vignettes

News/Changelog

Reference

FAQ

quick start or installation

scRepertoire

如何学习新包：读取教程的示例数据集，一步一步粘贴代码到自己的脚本里，运行，每一步都与教程结果进行对比无误后，再进行下一步。同时结合帮助文档，尝试修改函数参数

Introduction

Single-cell sequencing is an emerging technology in the field of immunology, enabling researchers to couple RNA quantification and other modalities at the level of an individual cell. A number of workflows and software packages have been developed to analyze this data. These packages allow users to take the vast dimensions of single-cell data into novel insights. Unlike the transcriptomic field, the field of immunology has not yet developed a standard workflow for analyzing single-cell data. Enabling users to easily combine RNA and immunology data, we have developed scRepertoire. It is compatible with single-cell data from MIXCR, Omniscope, TRUST4, and WAT3R single-cell clonality analysis pipelines.

Applying Deep Learning to VDJ data

scRepertoire is compatible and integrated with the R packages for T cell receptor and Ibex for the B cell receptor. If you are interested in applying deep learning to VDJ data, please see immApex.

Loading Data

Combining Contigs into Clones

Additional Processing

Basic Clonal Analysis

Visualizing Clonal Dynamics

Summarizing Repertoires

Clonal Diversity, Rarefaction, and Overlap

Clustering Sequences by Edit Distance

Combining Clones and Single-Cell Objects

Visualizations for Single-Cell Objects

Quantifying Clonal Bias

Making Deep Learning Models with immApex

Combining Deep Learning and TCRs with Trex

Combining Deep Learning and BCRs with Ibex

Single-cell Gene Set Enrichment Analysis



single-cell transcriptomic experiments and distill the results into a single-cell immune receptor repertoire. scRepertoire is compatible with 10x, AIRR, BD, and other single-cell data pipelines.

Decoding the T cell immune receptors, please see the vignettes.

Links

[View on Bioconductor](#)

[Browse source code](#)

[Report a bug](#)

License

[Full license](#)

[MIT + file LICENSE](#)

Citation

[Citing scRepertoire](#)

Developers

Nick Borchering

Author, maintainer

Qile Yang

Author

Ksenia Safina

用 RStudio 执行从教程网站粘贴来的代码：

RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function

Source

Run

Environment History Files Connections Packages Help Tutorial Viewer

Project: (None)

2_2_Seurat_with_split_donor.R 2_scissor.R Untitled5.R 8_subgroup_analysis.R scRepertoire.scTCR.R

```

39 name = "sample",
40 variables = c("P18L", "P18B")
41
42 head(subset1[[1]])
43
44 subset2 <- combined.TCR[c(3, 4)]
45 head(subset2[[1]])
46
47 clonalQuant(combined.TCR,
48             cloneCall = "strict",
49             chain = "both",
50             scale = TRUE)
51
52 clonalQuant(combined.TCR, cloneCall = "gene", group.by = "type", scale = TRUE)
53
54 clonalAbundance(combined.TCR,
55                 cloneCall = "gene",

```

R代码脚本区，可以用鼠标选中，并一次性执行多行代码

R语言交互区，类似单独的R语言打开的界面，一次性只能执行一行代码

用问号查看函数的帮助文档

帮助文档区

R Documentation

Quantify the unique clones by group or sample

Description

This function quantifies unique clones. The unique clones can be either reported as a raw output or scaled to the total number of clones recovered using the scale parameter.

Usage

```

clonalQuant(
  tcrseq_data

```

Plots Presentation

Zoom Export

绘图区，可放大查看，可导出成png文件，或者用代码直接保存高分辨率的图片文件。

Sample	Percent of Unique Clones
P17B	~25
P17L	~75
P18B	~95
P18L	~95
P19B	~80
P19L	~60
P20B	~70
P20L	~95

四、 补充：FileZilla 上传下载软件使用

FileZilla 是一个常用的上传下载软件，它可以远程登陆服务器，通过拖拽方式从服务器上下载资源到 pc 机，在有写入权限的情况下，也可以从本地上传文件到远程服务器。

FileZilla 下载链接为 <https://www.filezilla.cn/download/client>，下载并安装。

打开 FileZilla，进行如下操作链接我们的服务器：

1、打开 FileZilla，如下图：

FileZilla

文件(F) 编辑(E) 查看(V) 传输(T) 服务器(S) 书签(B) 帮助(H)

主机(H): 用户名(U): 密码(P): 端口(P): 快速连接(Q)

本地站点: C:\Users\steve\

远程站点:

文件名	文件大...	文件类型	最近修改
..		文件夹	2022/9/20...
android		文件夹	2022/9/20...
.config		文件夹	2024/3/23...
.MUMUVM		文件夹	2023/9/25...
.obs-browser...		文件夹	2023/11/9...
.oss-browser		文件夹	2023/11/9...
.spss		文件夹	2022/9/3...
.subversion		文件夹	2022/9/3...
.TBtools		文件夹	2024/12/1...
3D Objects		文件夹	2022/9/3...
86B3F2D6AC2...		文件夹	2024/2/6...
AppData		文件夹	2022/9/20...

16 个文件和 38 个目录。大小总计: 16,714,845 字节

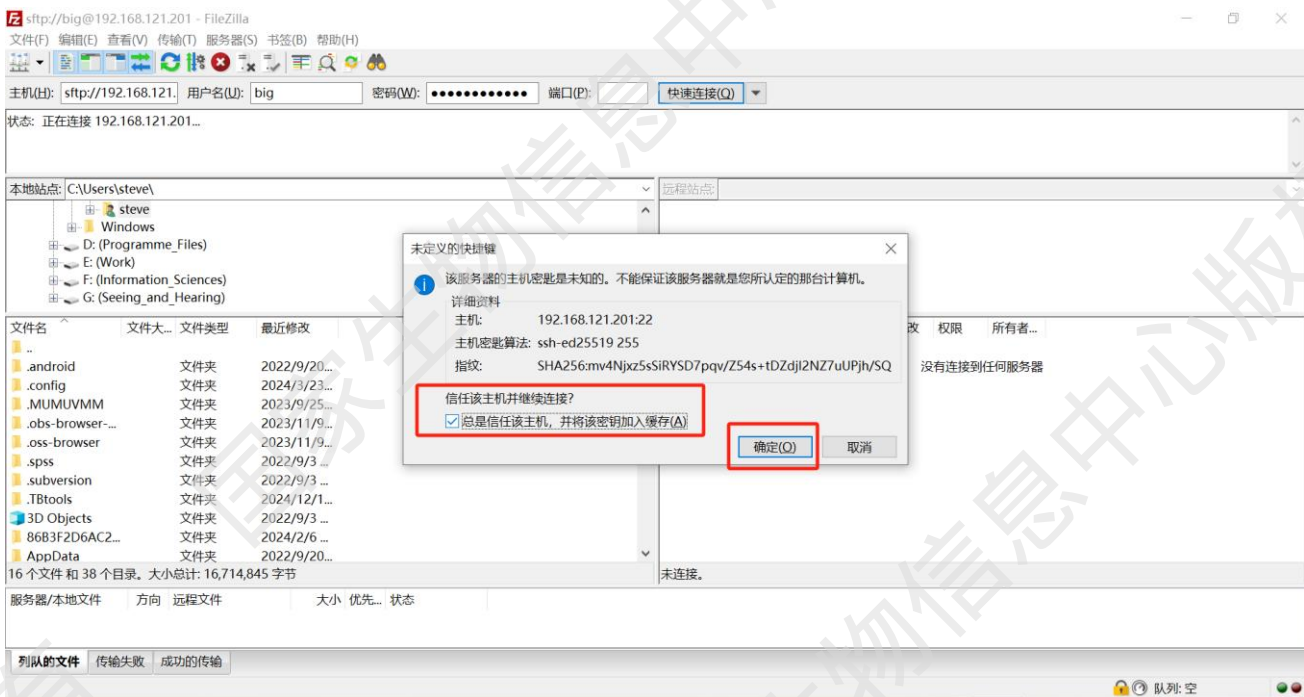
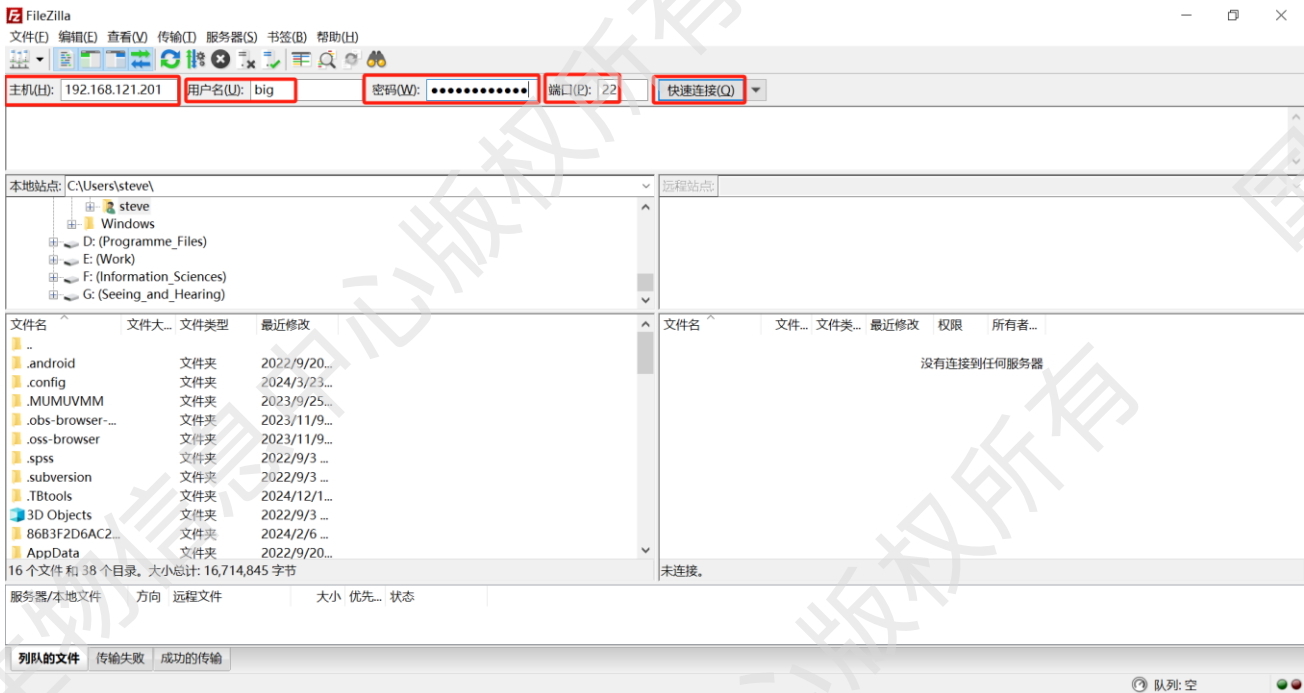
服务器/本地文件 方向 远程文件 大小 优先... 状态

文件(F) 文件... 文件类... 最近修改 权限 所有者...

没有连接到任何服务器

未连接。

2、点击新建站点，依次填入 “主机 ID: 192.168.121.201”，“端口: 22”， “用户名”，“密码”，点击 “快速连接”，即可以建立本地 pc 机与远程服务器的连接。



3、在左侧选择本地站点的路径(即 pc 文件要存放的路径)，用于存放将要下载的数据。在右侧输入服务器路径，比如 “/home/user1”，注意 user1 换成自己的 ID。就可以看到 WGS 文件夹，双击文件夹进入，选择自己需要下载的文件左右拖拽就可以开始上传下载。

