

Practical Session

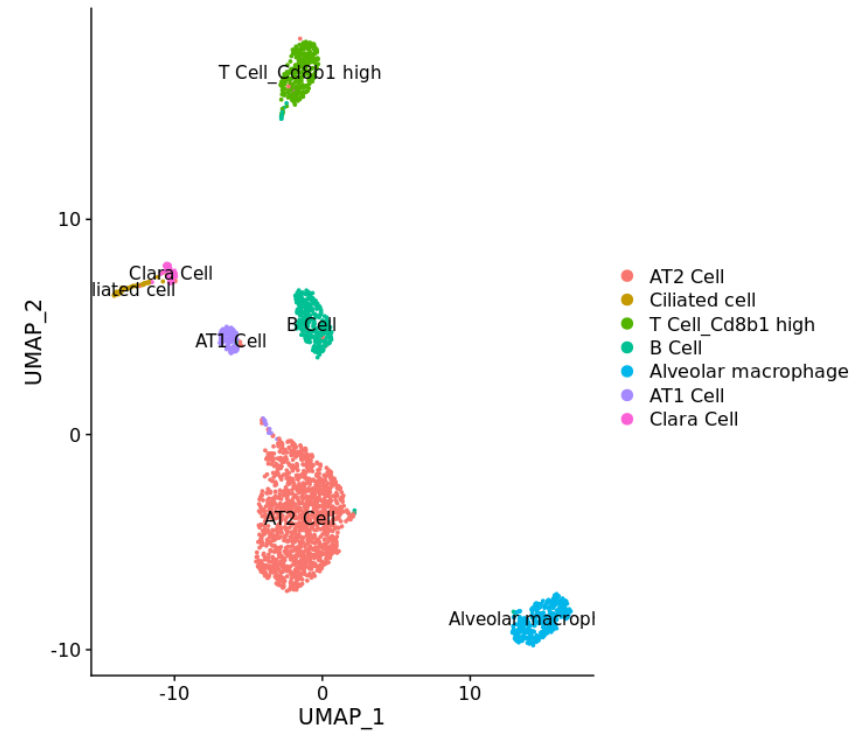
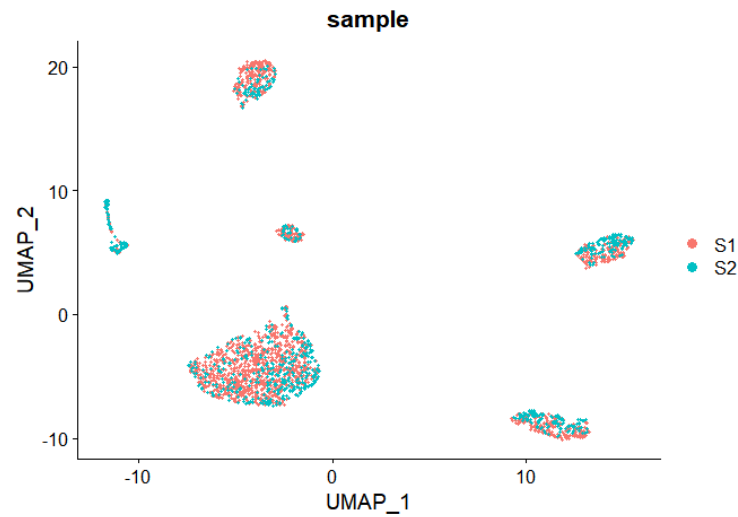
Cell type annotation

<https://rstudio-singlecell.sb-roscoff.fr>

Aim of the session

Exploratory Data Analysis and basic analysis pipeline (for open analysis)

– Mouse Lung Atlas dataset, 2 samples



• Annotation of the cells using SingleR

- Celldex reference
- You own reference
- Compare with Azimuth

Access to the data

Connect to the ABIMS cluster through SSH (or MobaXTerm, or CyberDuck).

The data and .Rmd file are in the folder:

`/shared/projects/sincellte_2022/Courses/Secondary_analyses/`

• In a bash terminal :

1) Create your working folder

```
> mkdir -p /shared/projects/sincellte_2022/${USER}/Secondary_analyses/
```

2) Copy scripts

```
> cp -r /shared/projects/sincellte_2022/Courses/Secondary_analyses/scripts  
/shared/projects/sincellte_2022/${USER}/Secondary_analyses/scripts
```

Log into Rstudio server: `rstudio-singlecell.sb-roscoff.fr`

Change the working directory:

```
> user.id <- Sys.getenv('USER')  
> setwd(paste0("/shared/projects/sincellte_2022/", user.id, "/Secondary_analyses/scripts"))
```

R code for the practical is in the **TP_Cell_annotation.Rmd** file