

Kevin Wang

2019 Semester 2 Progress

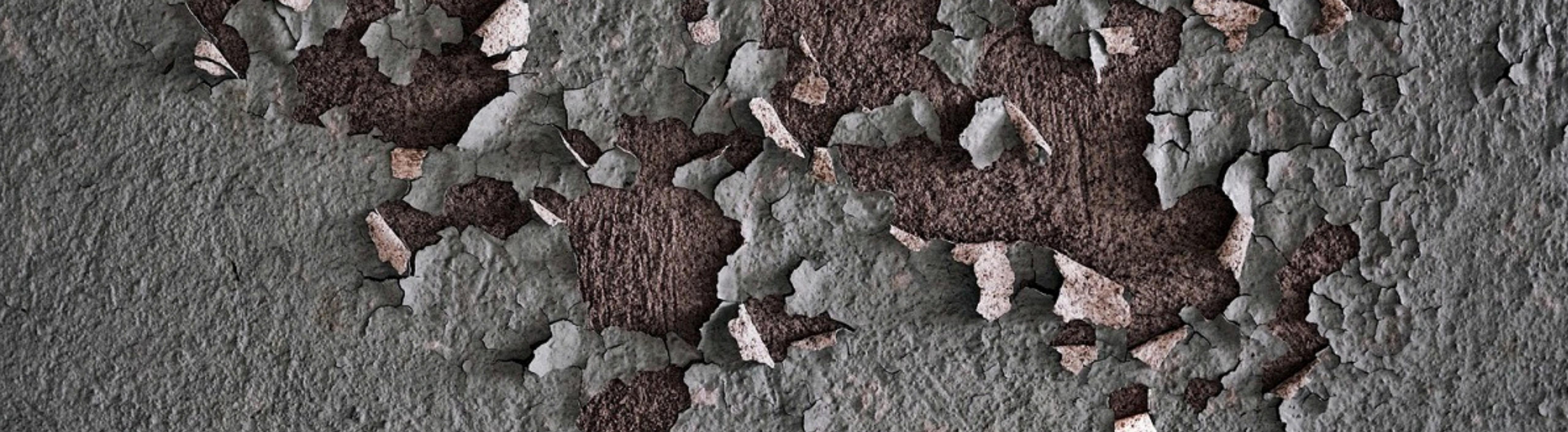


Hong Kong
Taipei
Taichung

Summary of the trip

- ▶ Good food and drinks
- ▶ SSAI Golden Jubilee Travel Grant
- ▶ APES was accepted as an invited ANZJS paper
- ▶ Submitted the mcvis paper with Samuel and Chen





Single Cell Plus @ HKU

Feedbacks

The workshop was well-received
by the attendees

Massive thanks to all the
contributors!



To be improved

- 1.Attendees did not install R 3.6 or packages
- 2.Download and installations can take up to 1.5 hours
- 3.Data file download was throttled
- 4.BiocParallel could not be installed on Windows

**R works differently on different OS
This reduces reproducibility**

Testing out Google Cloud

1. Go to <http://35.197.161.37/>
2. Type `setwd("/home/rstudio")` into your console
3. Click “Go to Working Directory” in the Files pane of RStudio
4. Type `source("test.R")` into your console



THE
END

Docker

1. `Dockerfile` script detailing how compilers and R packages should be installed
 2. Docker Engine builds an “image” using the script
 3. Because Docker is standardised across all OS, the image will run inside Docker identically on **any** machines
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- ▶ Docker is light-weight compare to VM
 - ▶ Community support (RStudio + BioC)

Upload Dockerfile to GC

**GC downloads R and data
files to
SYD cloud server**

**GC - SYD opens up a port for
us to access the Docker
running on the Cloud**

Testing out Google Cloud

1. Type `setwd("/home/rstudio")` into your console
2. Click "Go to Working Directory" in the Files pane of RStudio
3. Type `source("scMerge.R")` into your console