

# Shuyang XU

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I have 4 years work experience as **Bioinformatics Engineer** of Analysis and Development. I developed **scRNA-seq (Single Cell Sequence)** and **Iso-Seq (Full Length Transcriptome)** pipelines from beginning, which is my current and future focus.

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GitHub : <https://github.com/ShuyangXu>

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## EDUCATION

- 2011.09 - 2016.06, **Sun Yat-sen University**
  - 2015.09 - 2016.06, B.S. in **Information and Scientific Computation**, *School of Mathematics*
    - Thesis : *Modelling and Simulating Transcription Stochasticity of Eukaryotic Cells*
  - 2011.09 - 2015.06, B.S. in **Biotechnology**, *School of Life Science*
    - Thesis : *Functional Characterization of Monoclonal Antibody M3-85 against Trypanosoma brucei Cytoskeleton*

## WORK EXPERIENCE

- 2016.06 - now , **Bioinformatics Engineer**, *Guangzhou Genedenovo Biotechnology Co., Ltd*
  - 2018.12 - now, *member of Development Group*
    - Develop and maintain new pipelines : sc-VDJ, scATAC-seq, m6A RIP-seq, Visium Spatial, [scRNA-seq online tools](#), etc.
    - Deal with customized and/or intricate projects, for example, a COVID-19 VDJ project.
  - 2017.10 - 2018.12, *leader of Analysis Group*
    - Lead a 4 member analysis group, and mentor 2 new members.
    - Produce analysis results based on requires.
    - Develop and maintain new pipelines : Iso-Seq, scRNA-seq, Cell Trajectory, ceRNA, etc.
  - 2016.06 - 2017.10, *member of Analysis Group*
    - Produce analysis results based on requires.
    - Develop and maintain new pipelines : Prokaryotic RNAseq, GSEA, etc.

## SKILLS

- Highly skilled in **Perl, R**
- Work environments with **Linux, R (RStudio)**
- Familiar with **HTML, Markdown, git**

## ANALYSIS PROJECT

RNA-seq (124 cases)	LncRNA-seq (42 cases)
smallRNA-seq (27 cases)	Iso-Seq (27 cases)

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Single Cell Sequence (71 cases)    customized projects (42 cases)

## PIPELINE DEVELOPMENT

pipeline		release date	maintain	major tech
Prokaryotic RNA-seq		2017.09	to 2018.08	Rockhopper
Iso-Seq		2017.10	until now	smrtlink, CWL
m6A RIP-seq		2019.09	until now	samtools, bedtools, macs2, RiboDiff
10x Single Cell related	scRNA-seq	2018.05	until now	Cellranger, Seurat
	Cell Trajectory	2018.10	until now	monocle2
	scVDJ	2018.12	until now	Cellranger
	scATAC-seq	2019.04	until now	Cellranger, Signac
	scRNA-seq online tools backend program	2019.12	until now	Seurat
	Visium spatial	2020.05	until now	Space Ranger, Seurat
Other supplementary pipelines		ceRNA, GSEA, GSVA, SCIENIC ...		

## SOFTWARE COPYRIGHT

- *An interactive shell for Filter\_FQ*, Filter\_FQ的交互软件 (2017SR658807, all copyright transfers to company)
- *A plot software for gene's GO annotation and classification*, 一种绘制基因GO注释及分类图像软件 (2017SR658094, all copyright transfers to company)

## SHARING / TUTORIAL

- ggplot\_guts : [https://shuyangxu.github.io/ggplot\\_guts/Chapter1.index.html](https://shuyangxu.github.io/ggplot_guts/Chapter1.index.html) (2020.07)
- An inner study group about Single Cell Sequence (organizer, 2018.06)
- Introduction of Data Structure (2017.11)

## HONORS IN WORK

- **Best Employee** in 2018 (top 10%, Guangzhou Genedenovo Biotechnology Co., Ltd)
- **Best Employee** in 2017 (top 10%, Guangzhou Genedenovo Biotechnology Co., Ltd)
- **Best Freshman** in 2016 (top 10%, Guangzhou Genedenovo Biotechnology Co., Ltd)