Transcription at gene pairs in the convergent direction could cause RNAPII collision since RNA polymerase complex from both DNA strands are challenging to bypass, according to in vitro experiments in Yeast( Hobson et al., 2012). However, from NET-seq, we know antisense transcription is pervasive across both Eukaryotic and Prokaryotic genomes(Mellor et al., 2016). We ask if RNAPII collision occurs in the model plant species Arabidopsis thaliana. In our group, we combine bioinformatics analysis and smFISH methodology to investigate how transcription is coordinated at a single locus level in vivo and whether there is a common mechanism to avoid RNAPII collision. In addition to many other genome-wide analyses, we are curious about how gene pairs’ expression pattern is in different individual cells or cell types. Therefore, I need to understand scRNA-seq data and perform downstream analysis to interpret my postdoc project better.

I have been working tightly with single-cell technologies and feel fascinated by them. In the future, I would like to dedicate myself to single cell research.

On top of the requirement to analyze scRNA for the project, I am keen to understand the scRNA-seq technique more comprehensively.

I am grateful sci-life can provide this fantastic training program. It will be thrilling to be able to join this journey.