

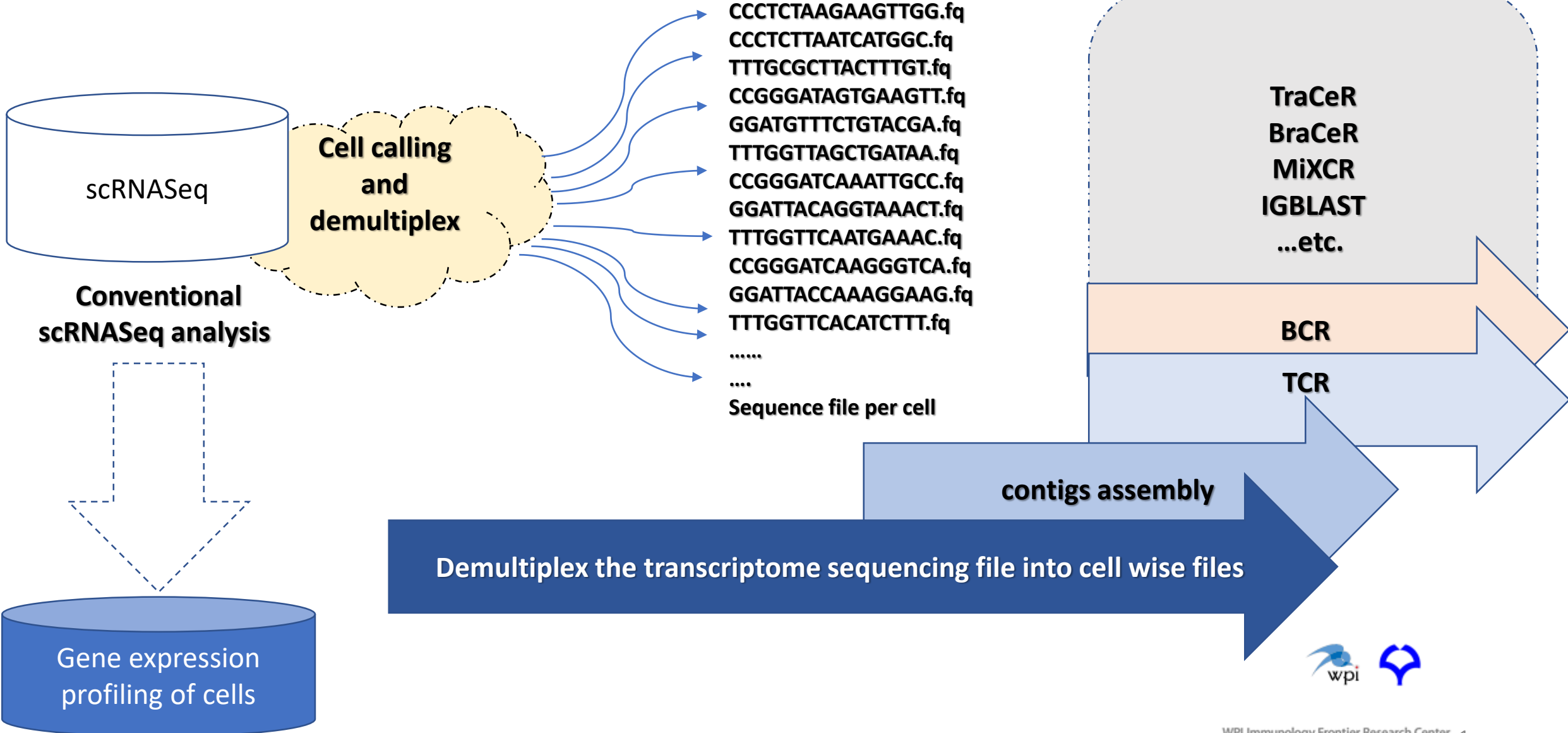
Reconstruction of immune phenotype from demultiplexed single cell transcriptome

Liu Yu-Chen, Ph.D.

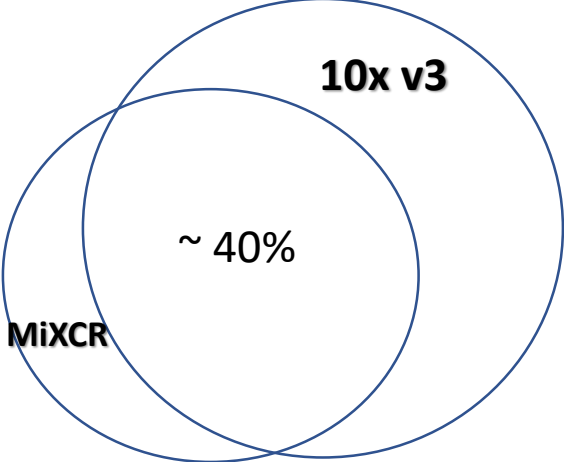
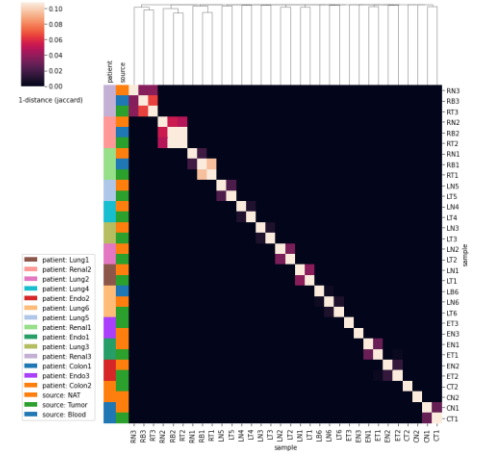
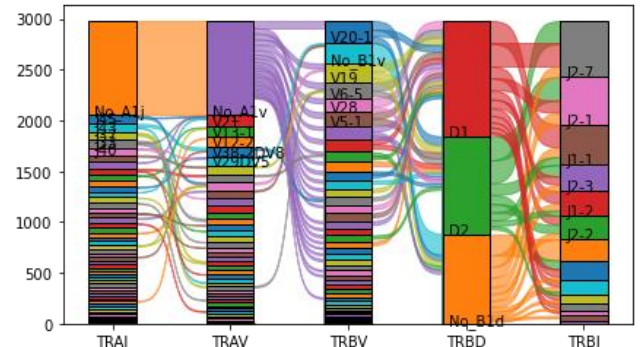
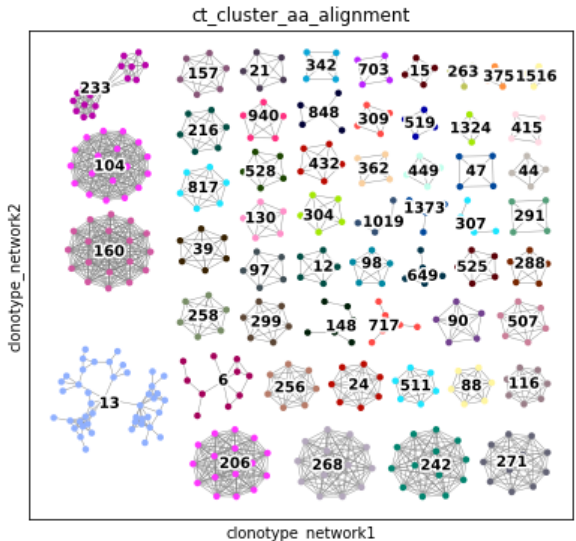
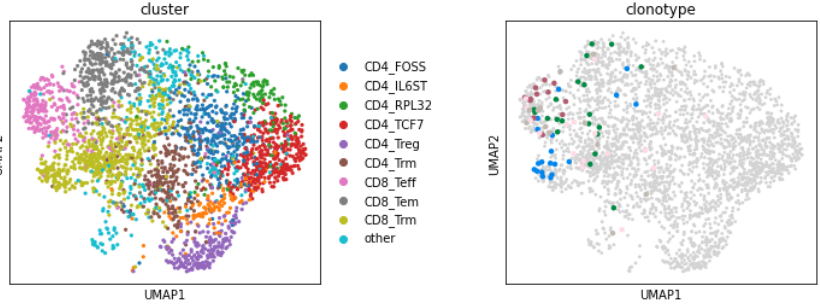
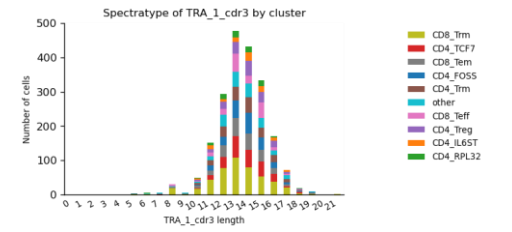
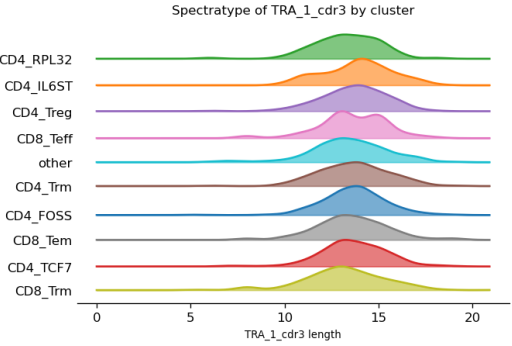
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Applied the lymphocyte receptor reconstruction algorithms designed for bulk RNASeq on single cell RNASeq data



Joint analysis of TCR and mRNA expression profiling can be conducted on the scRNASeq libraries without immune coupling.



~ 40% TCR can be assembled from RNASeq data with MiXCR (comparison done in assembly CDR3 sequences)

Within the currently available containing single cell RNA transcriptome data without application of barcode coupling lymphocyte receptor sequencing technology application, such analysis techniques provide a half as good insight into the immune phenotype diversity.

