	Thursday 23 February	Friday 24 February
9:30-10:00		Seurat/R/matrix overview
10:00-11:00		Seurat -matrix loading -> UMAP
11:00-12:00		
12:00-13:00		Lunch
13:00-14:00	Lecture overview: SPLiT-seq library construction	Doublet ID and removal
14:00-14:45	SPLiTseq - metadata prep	Markers/differential gene expression
14:45-15:00	Break	Break
15:00-16:00	SPLiTseq - processing of reads -> matrix	Chris Wicky - Parse kits, and what they can offer
16:00-17:00		Discussion, Review and Q+A