Approach to RNAseq for Collembolids:

1. Align and blast against two sister genomes (*Orchesella cincta* and *Folsomia candida*)
   1. Build a pipeline to map the .fastq files to O. cincta
   2. Build a pipeline to map the .fastq files to F. candida
2. Align and blast against the cap3 files provided from the dutch
   1. Build a pipeline to map the .fastq files for each species
3. Compile an assembly pipeline using the transcriptome
   1. Use transcriptome to build reference genome with Trinity
   2. Can do the above with Salmon (published 2017 to account for common biases) that does not require an assembled scaffold per se (sailfish is similar 2014).

STAR read aligner or (possibilities abound). The output from all three of these should be a little the same- something resembling a .bam which can be used to generate a count matrix/matrices.

From here:

A lot of the differential expression pipeline can be handled in R (edgeR, DESeq, etc)