Directory structure:

--[ROOT]

----[Kallisto] 50x bootstraped Kallisto-derived estimated counts

----[Library] transcript-to-gene mapping for tximport

----[Metabolomics] normalised metabolyte levels from service provider (Metabolon Inc.)

----[Proteomics] normalised protein levels from service provider (Francis Crick Institute)

----RNAseq.R, produce RNA-seq counts and abundances from Kallisto data

----Metabolomics.R, input + transform + QC metabolomics data

----Proteomics.R, input + QC proteomics da