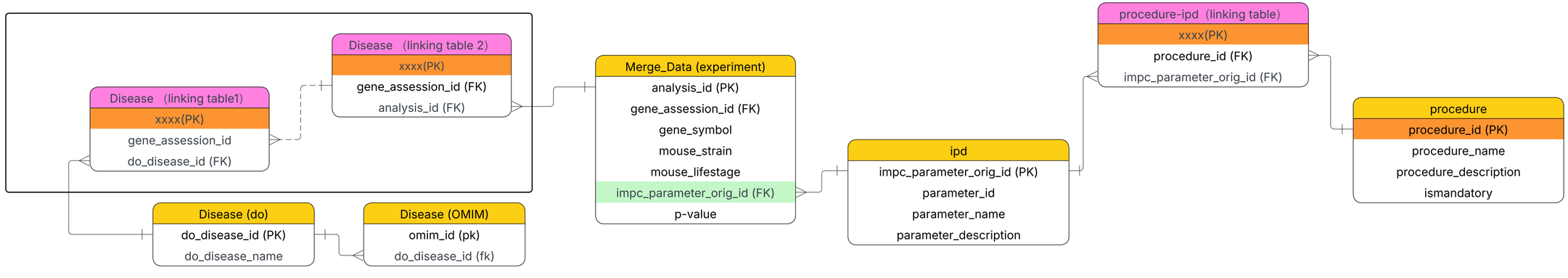
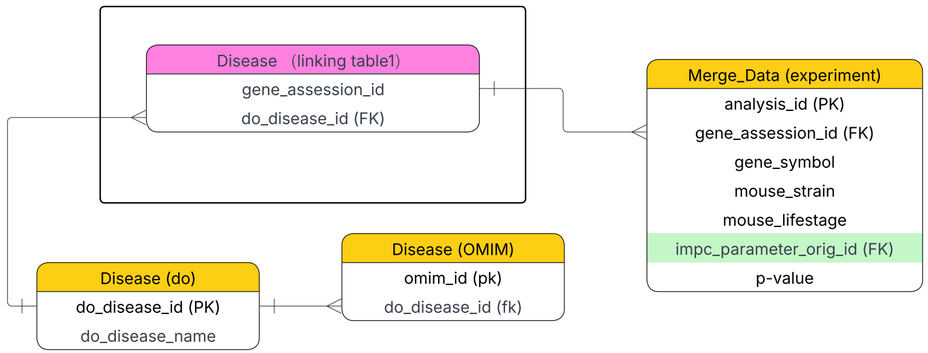
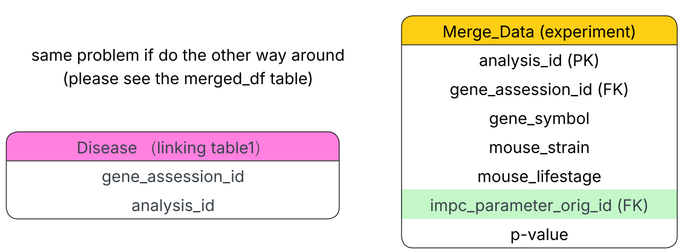
Version 6: (work in progress)



not work because same do_disease_id contains multiple gene_assession_id (please see the dis_inf table)



same problem if do the other way around (please see the merged_df table)