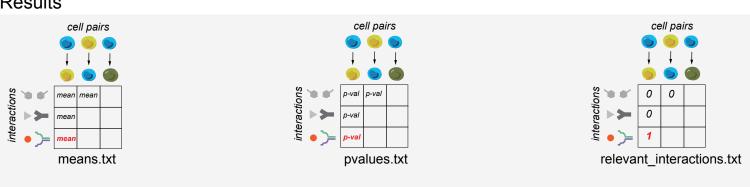
Input CellphoneDB database per celltype DEGs annotated scRNAseq cell types expression pre-computed by the user **Approaches** CellphoneDB tool method 3 **DEG_analysis** method 1 simple analysis method 2 statistical analysis significant DEGs Null distribution of the mean Random shuffle (R1-L1) in cluster1-cluster2 Ligand Sub.1 Receptor Observed mean (R1-L1) True observation Minimum in cluster1-cluster2 (Sub.1, Sub.2) mean RELEVANT (1) = all genes expressed & at least one gene is DEG p - value Results cell pairs cell pairs cell pairs



Important - interpreting results

