Hands-On session

Use of a genetic distance tool, SPIA

TASK 1 – to generate and observe the genetic distances obtained from n individuals' pairs, by using 143, 100, 80, 60, 40, and 20 high MAF SNPs;

TASK 2 – to generate and observe the genetic distances among m individuals using 100 unselected SNPs;

TASK 3 – to generate and observe the genetic distances among a set of samples that includes j normal/tumor pairs

TASK 4 – to change the *m value* (confidence) of (at least) one of the previous Tasks

See additional material: xxxcodexxx.R, SPIAssay.pdf, SPIA_input_genotype.tsv, SPIA_somatic_genotype.tsv, SPIA_selected_SNPs.txt