

# Use of a genetic distance tool, SPIA

TASK 1 – to observe genetic distances among  $n$  individuals using 143, 100, 80, 60, 40, 20 high MAF SNPs

TASK 2 – to observe genetic distances among  $m$  individuals using 100 from unselected SNPs

TASK 3 – to observe genetic distances among samples that include  $j$  pairs (normal and tumor DNA)

TASK 4 – to change confidence  $m$  in one of previous Tasks

See additional material: xxxcodexxx.R, SPIAssay.pdf, SPIA\_input\_genotype.tsv, SPIA\_somatic\_genotype.tsv, SPIA\_selected\_SNPs.txt