Assignment 1

- **Generate a matrix of pearson correlations between every pair columns (i.e, every pair of cancers shown) and show the results as a 12 x 12 matrix using matrix 1. (The actual files are available for download from oncourse)**

(The data shown comprises of RPKM values showing the miRNA expression across cancers for a particular patient group)

miRNA	bladder	breast_cancer	cervical	head n neck	KIRC	KIRP	LUAD	LUSC	PRAD	STAD	THCA	UCEC
hsa-mir-3128	0.0	0.0	0.0	0.51795	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
hsa-mir-3658	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
hsa-mir-217	8.15542	13.079703	1.292636		1.553849		22.170186		8.636935		11.046939	13.892229
hsa-mir-22	63975.513995		67989.751326	33975.331973		38610.030611		62109.621268		53628.721821		46660.234247
63806.452135												
hsa-mir-612	0.107308		0.0	0.430879		1.035899		0.0	0.0	0.0	0.414693	
hsa-mir-206	0.107308		0.0	0.10772	63.189844		0.312256		2.790394		0.0	1.86612

- **Now represent the correlations matrix (12 x 12 dimensions) as a heatmap using one of the publicly available tools such as matrix2png or cluster/java tree view or using R's heatmap tool so that similarity between cancers is revealed. Perform the same analysis as above with matrix 2 (also available for download) and finally compute a pearson correlation between the two original matrices (matrix 1 and matrix 2).**