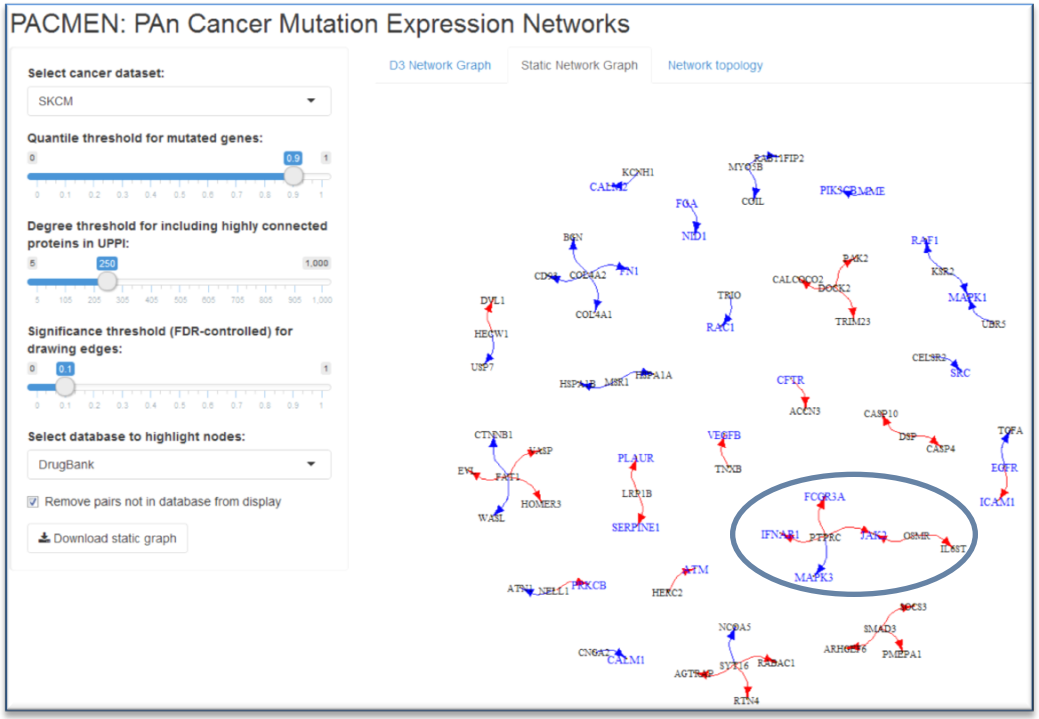
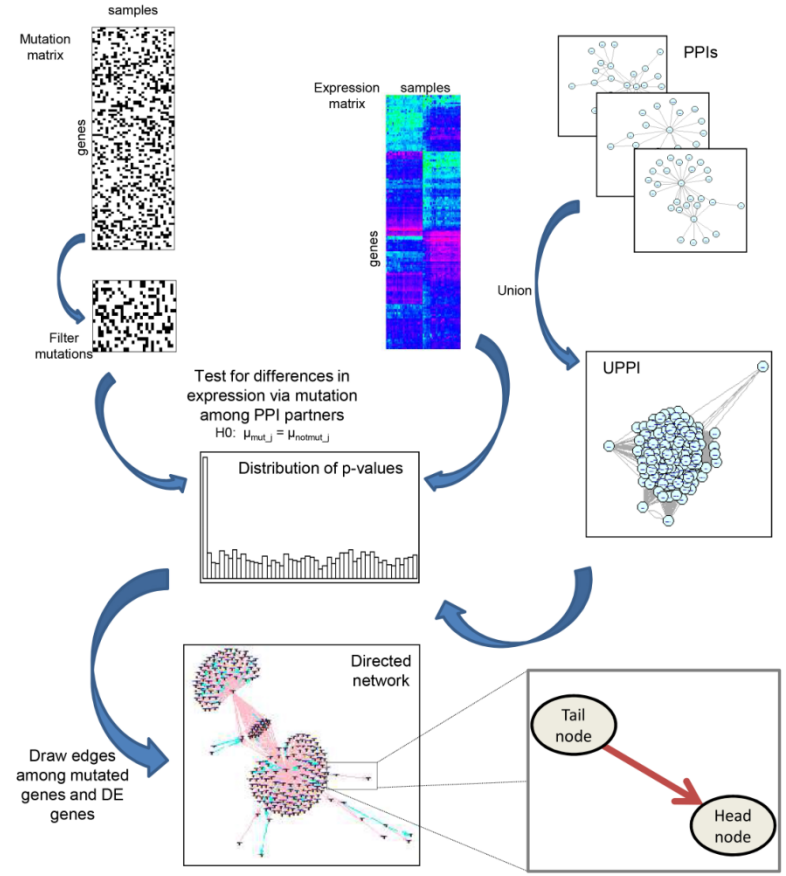
Characterizing mutation-expression networks in multiple cancers

Shila Ghazanfar and Jean Yee Hwa Yang

4,443 tumours analysed over **19** cancers from **TCGA**
R Shiny app to explore results among different parameters
Available to download at
www.maths.usyd.edu.au/u/sheilag/pacmen.zip



Network construction



Overlap with known cancer genes

	KICH	OV	LAML	GBM	KIRP	PRAD	LGG	BRCA	READ	KIRC	STAD	UCEC	COAD	HNSC	BLCA	LUSC	LIHC	LUAD	SKCM
NCG all Nodes								0		0.09		0	0.09	0		0.02		0.01	0.06
NCG tail Nodes								0			0.03	0	0.02	0		0.02		0	0
NCG head Nodes								0.02		0.02									