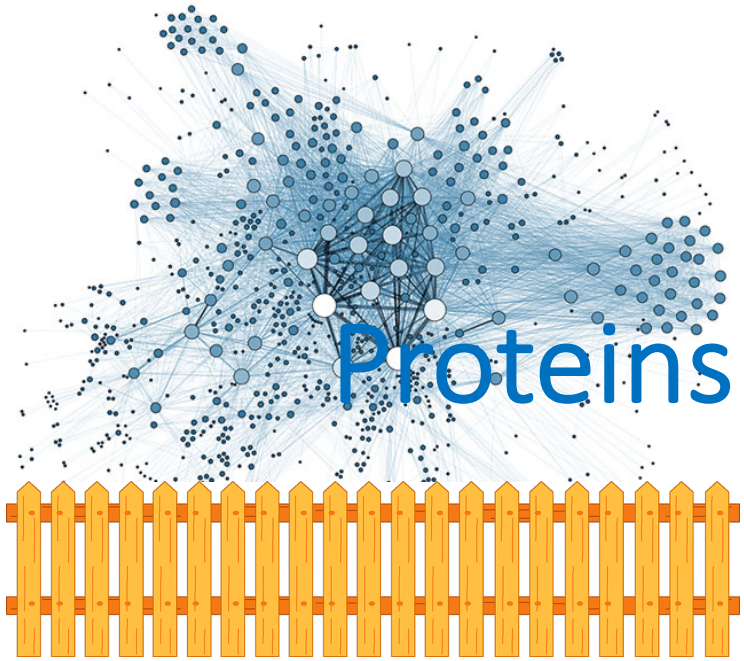
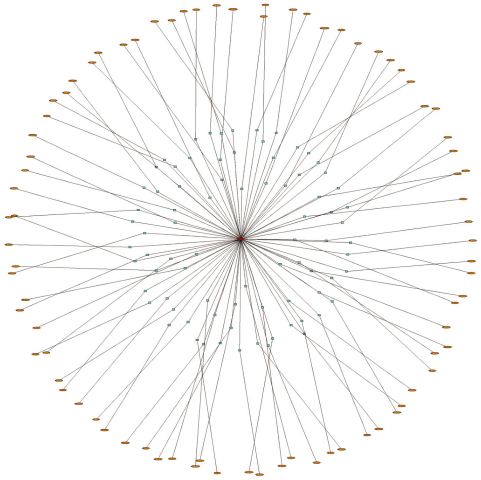


Proteins are part of a biological system

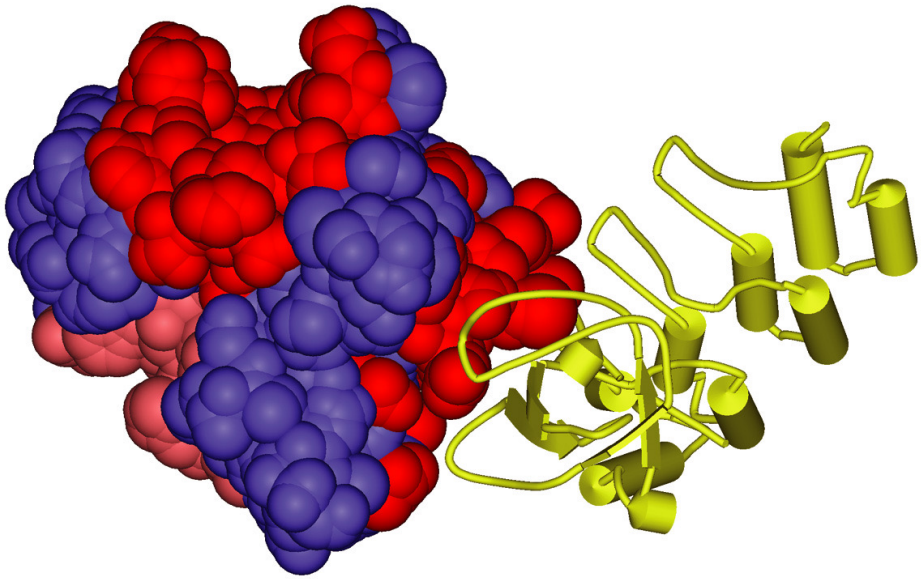


Episode in the series on protein bioinformatics

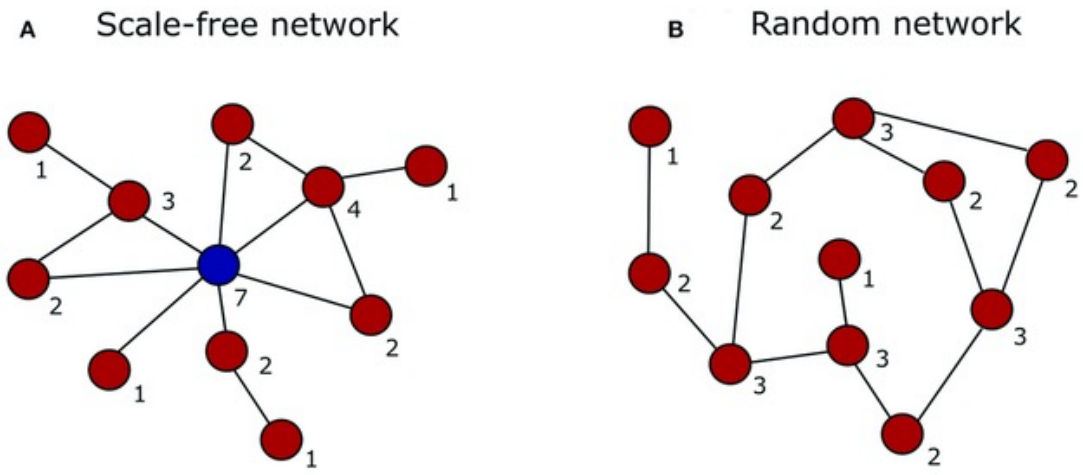
Function, interaction, localisation and systems of proteins

- interpreting sites in protein sequence and structure that are relevant to system role,
- connecting components in ways that biological evidence indicate, and
- analysing patterns of connectivity—biological networks and pathways

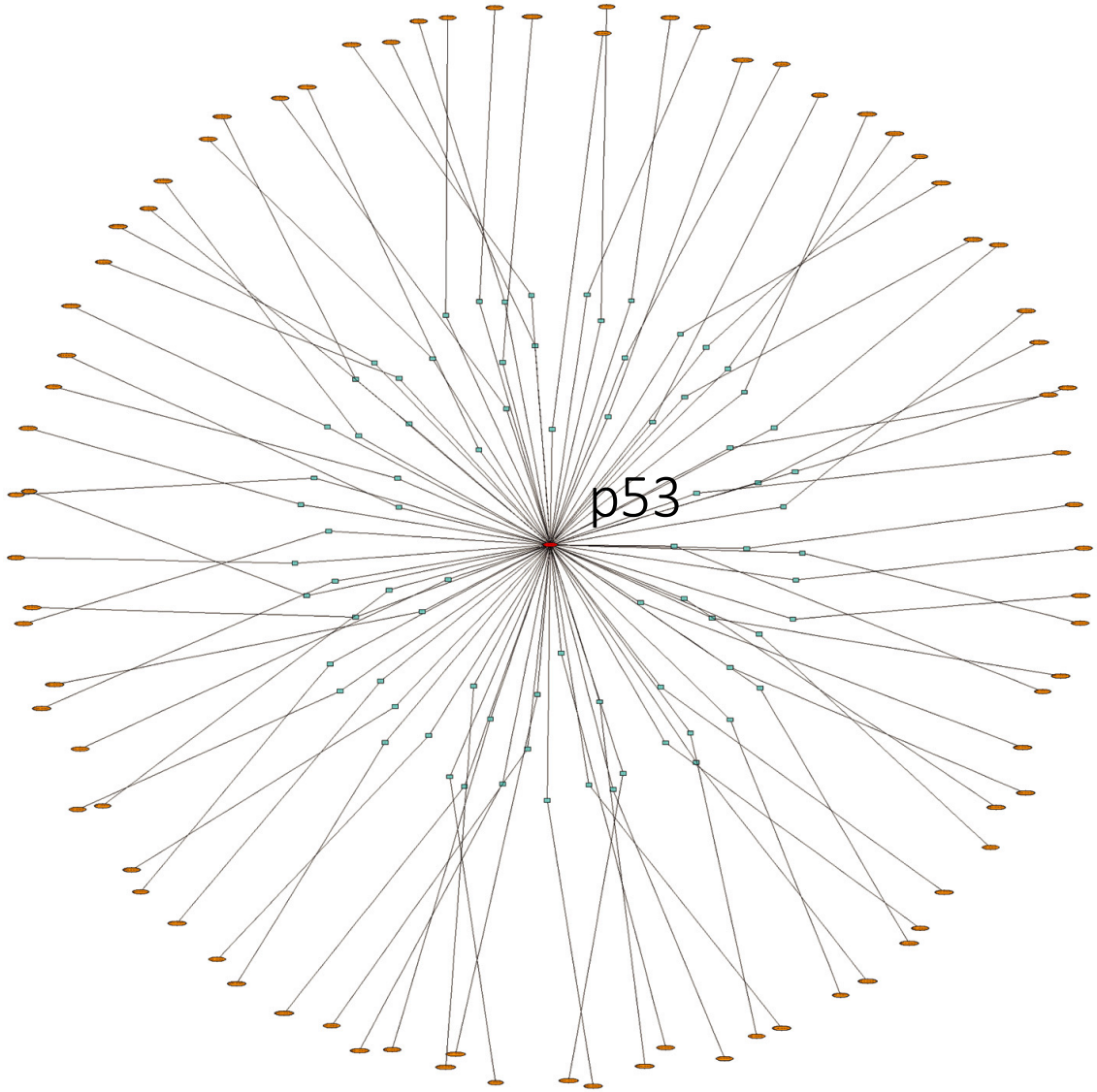
Example: p53 and its binding domains

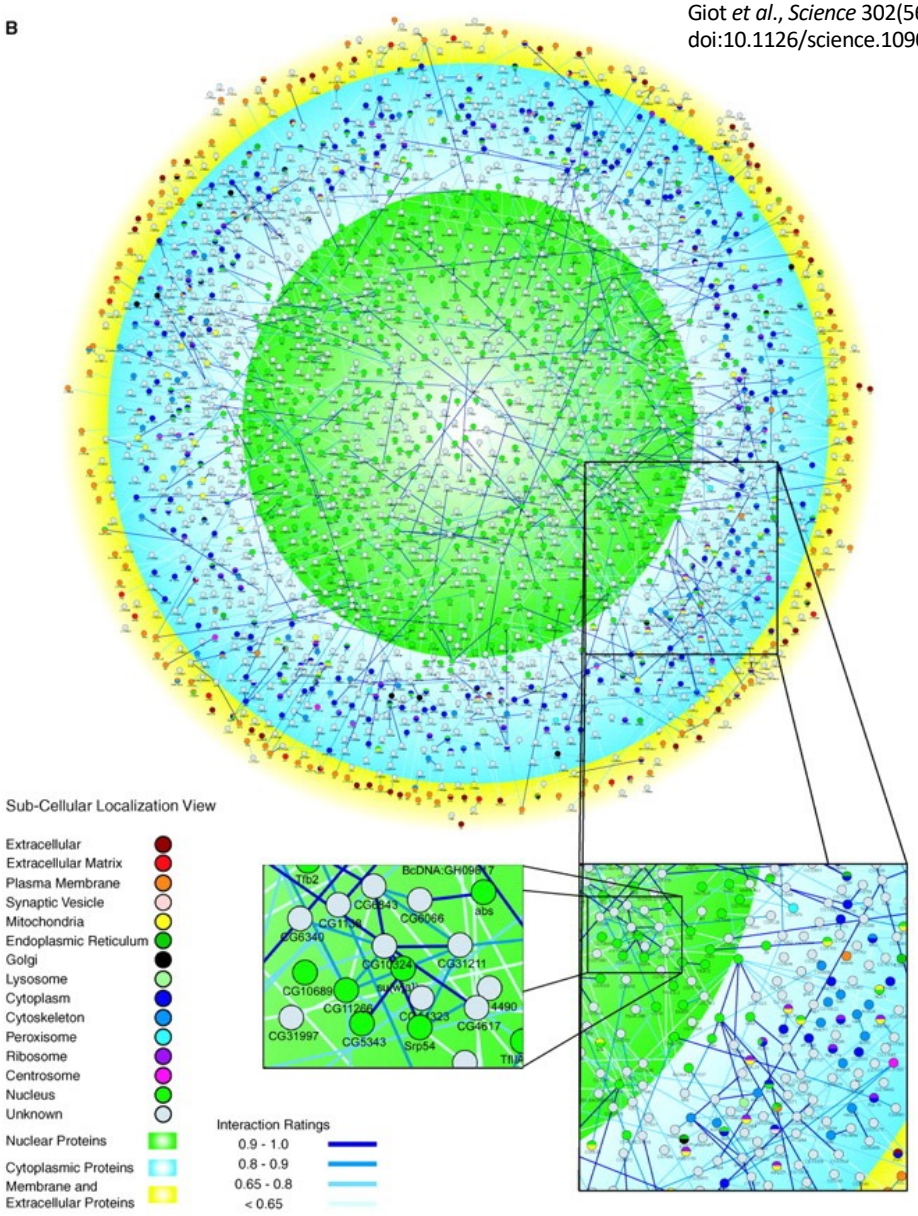


Biological networks are not random



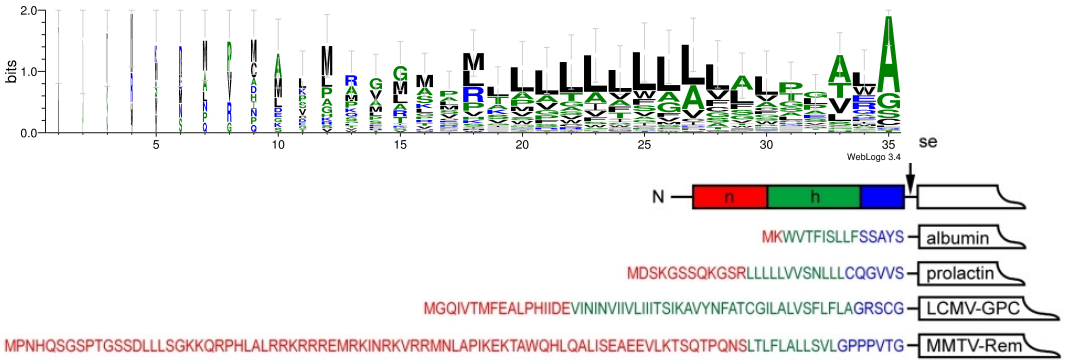
Networks are an abstraction but have properties


p53

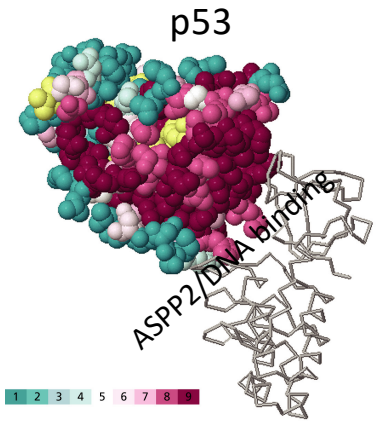


Giot *et al.*, *Science* 302(5651)
doi:10.1126/science.1090289

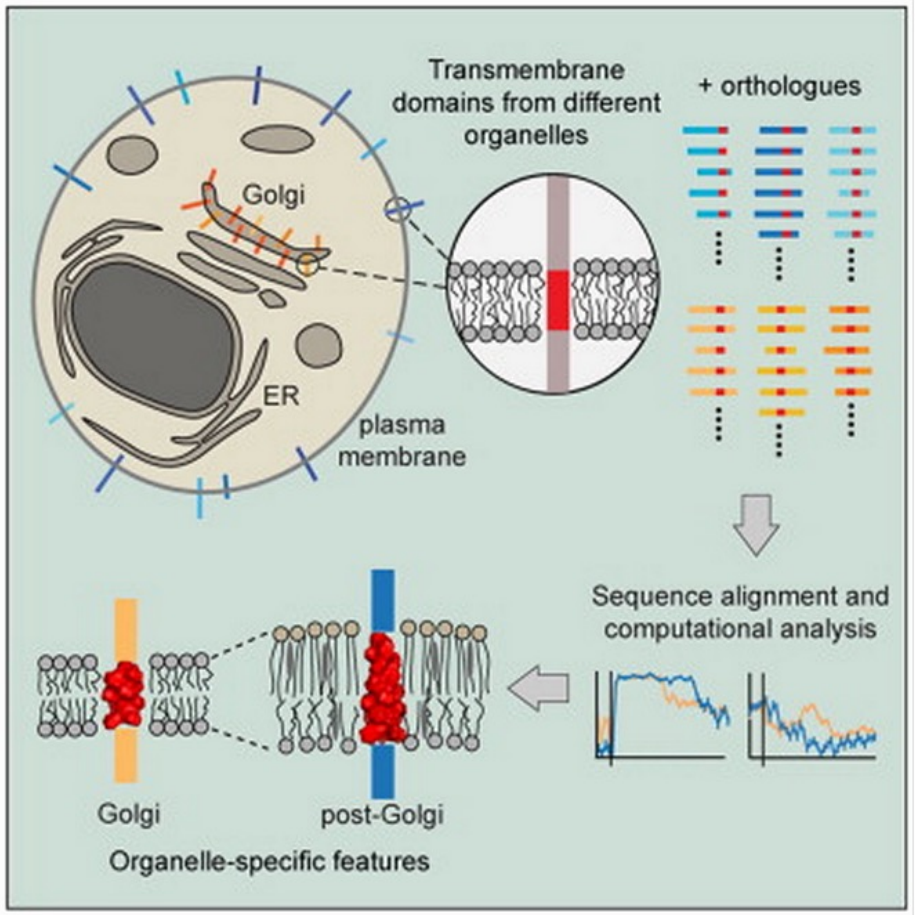
- Most analyses are focused on individual components and their properties—in spatial and temporal isolation
- Molecular function is often determined from properties of *multiple* components
- Biological processes are supported by the *interaction* and *abundance* of components
- How do we bring this information together?



Protein localisation signals
(here signal peptides)



- Conservation (maybe spread in sequence but come together in structure)
- Many same-charged residues (electro-static interaction)
- Hydrophobic patch (unusual at surface; interaction by hydrophobic forces)
- Aromatic residues
- Mainly β sheets or long loops



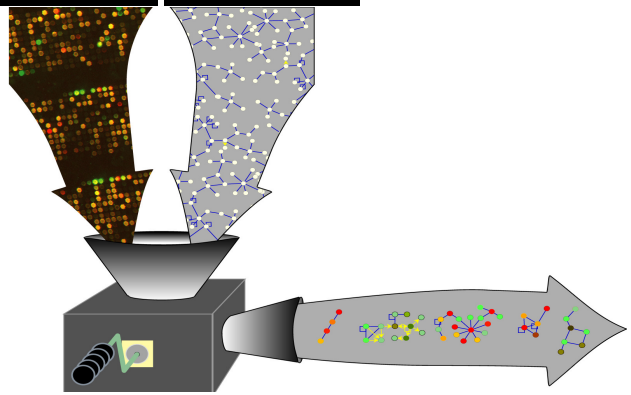
Expression @ condition

	X_1	X_2	...	X_m
G_1	+			+
G_2	+	+		
G_3		+		
G_4	+	+		
...	...			
G_n				

Co-expression

	G_1	G_2	...	G_n
G_1	+			
G_2	+	+		
G_3		+	+	
G_4	+	+		+
...	...			
G_n				

Expression **Interaction**



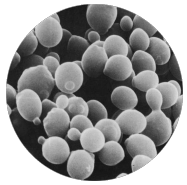
Biological system

Interaction

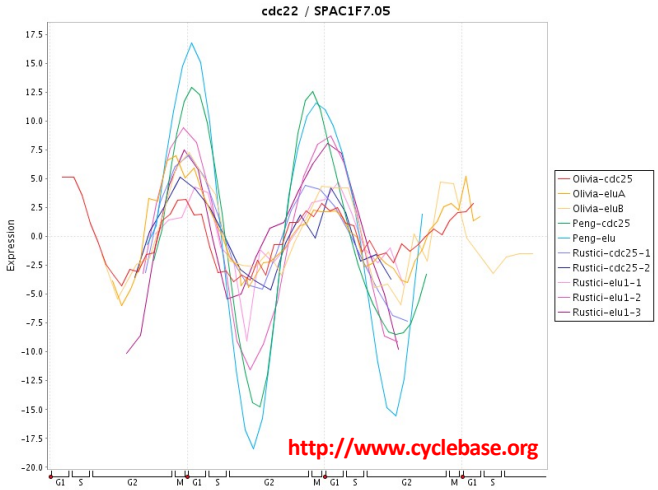
	G_1	G_2	...	G_n
G_1				
G_2	Yes			
G_3				
G_4		Yes		
...	...			
G_n				

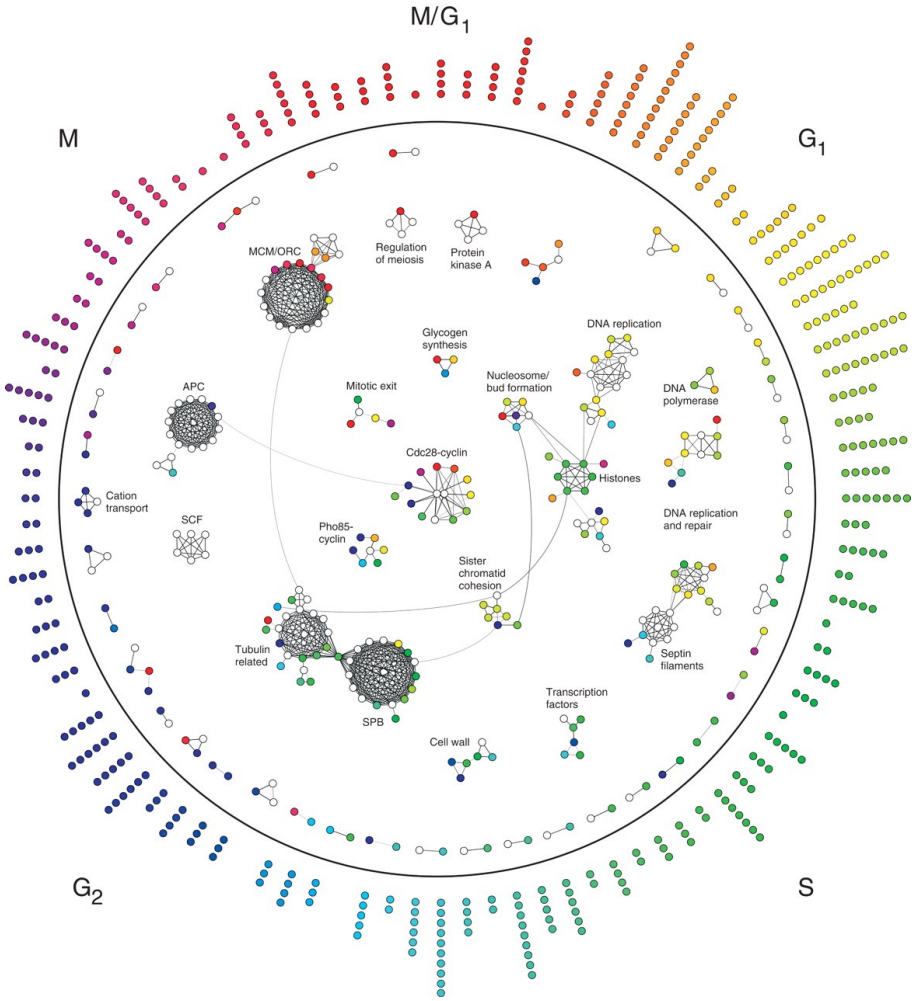
Creating a yeast cell cycle interactome

Synchronized cell culture



Micro arrays





Qi and Ge, *PLoS Comp Biol, 2:e174, 2006.*