Online material 2. Error analysis

Network	**Exponential fitting**			**Poisson fitting**	
	$\mathbf{P_0}$	**A**	$\mathbf{R^2}$	$\boldsymbol{\chi^2}$	**p-value**
Polarity	0.233 ± 0.020	0.132 ± 0.046	0.932	115.6	1.08×10^{-20}
Polarity + 20%	0.188 ± 0.018	0.129 ± 0.042	0.878	1,197	6.33×10^{-251}
Polarity - 20%	0.270 ±0.0146	0.209 ±0.033	0.971	56.9	1.88×10^{-10}
Random	-	-	-	1.2	0.99

To evaluate the possible effects of false positives in the initial data sets, 20% of proteins (i.e., direct neighbours of randomly chosen polarity proteins) were added to the polarity network ('Polarity + 20%'). Similarly, to evaluate the possible effects of false negatives, 20% of proteins were removed from the polarity network ('Polarity - 20%'). Then, the $P(k)$ curves of the two artificially altered networks were fitted either by the exponential function $P(k) = P_0\, e^{-Ak}$ (*left side*) or to a Poisson distribution (*right side*). Results indicate that the exponential distribution remains unaffected, with just minor changes in the values of the P_0 and A coefficients. Furthermore, no significant chi-squared values were obtained in the Poisson fitting (unlike the random network). Thus, even extremely high error rates (either false positives or false negatives) would not invalidate the major conclusions on the exponential (yet non-random) nature of the polarity network.