

Performance of alternative simple imputation methods, as measured by correlation

	Pombe	Signalling	Chromosome	ESP	RNA
Zeros	0.00	0.00	0.00	0.00	0.00
Medians	0.34	0.19	0.25	0.36	0.19
Means	0.33	0.24	0.27	0.18	0.26

Performance of alternative simple imputation methods, as measured by NRMSE

	Pombe	Signalling	Chromosome	ESP	RNA
Zeros	1.01	1.00	1.01	1.00	1.00
Medians	0.97	0.99	0.99	0.94	0.99
Means	0.96	0.98	0.97	0.99	0.97

Method: Gene Means

This is a naive global technique and represents a simple improvement on filling in with dataset means. For each missing interaction (i,j) we calculate an estimate by averaging the mean interaction score for i and j across all other genes. This is used as an initial estimate for LLS.

Method: Medians

It has been previously observed that there is a relationship between the measured interaction of two genes, and the correlation between their interaction profiles. See Schuldiner *et al* [14] for full details.

Collins *et al* [3] suggested that this could be used as a way to estimate missing genetic interactions by finding the median interaction score for interactions between gene pairs with similar correlations between their interaction profiles.

We implemented this approach as follows : for the missing value (i,j), we calculate the correlation (r) between the interaction profiles of i and j. We then identify gene pairs with a similar interaction profile correlation, and find the median interaction score between them. A sliding window of size 0.1 was used to implement this – so for a correlation of 0.65, gene pairs which had a correlation between 0.6 and 0.7 would be used to calculate the median.