supplementary figures

supplementary figure 6

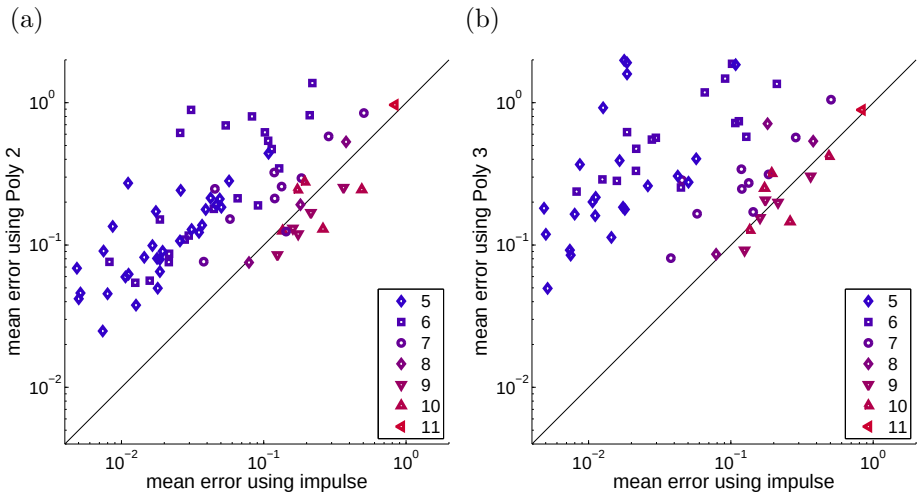

Figure 1: **(a)** Scatter plot of the mean error for each condition using the impulse model and polynomials. **(a)** 2^{nd} . **(b)** 3^{rd} order Polynomial.

supplementary figure 7

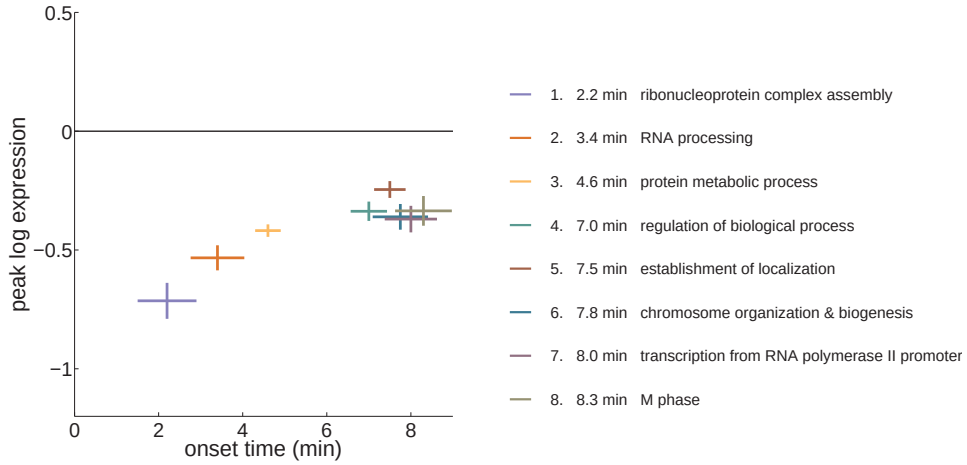

Figure 2: **A timeline of responses to gamma irradiation, *biological processes*.** Each cross denotes the median peak and onset time of all genes in the relevant GO category (Gasch, 2001). Length of bars denote the standard error of the mean (s.e.m.) across genes associated with the category.

supplementary figure 8

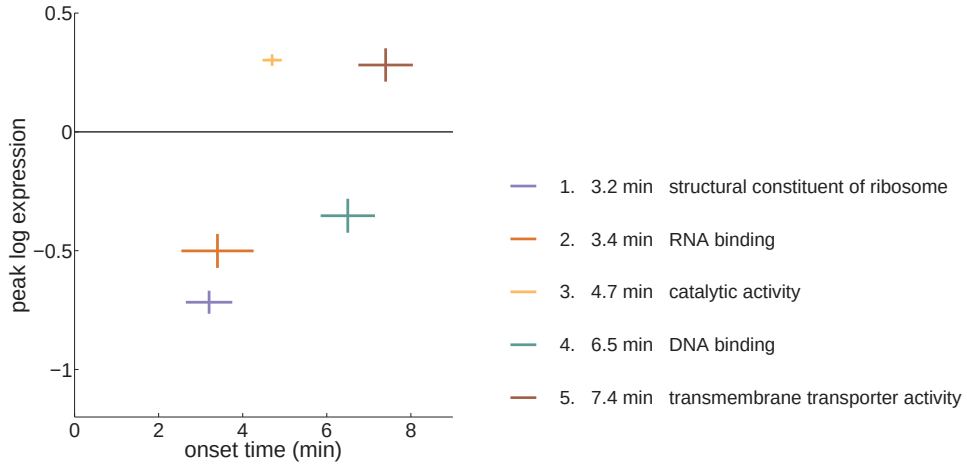

Figure 3: **A timeline of responses to gamma irradiation, *molecular function*.** Each cross denotes the median peak and onset time of all genes in the relevant GO category (Gasch, 2001). Length of bars denote the standard error of the mean (s.e.m.) .

supplementary figure 9

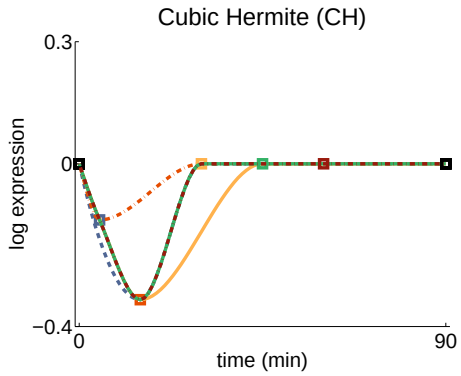

Figure 4: **Comparison of leave-one-out fits to a gene expression profile**. Same analysis as in Fig 2 but for cubic Hermite interpolation (CH). CH interpolation is often heavily local: in this example, it is close to a piece-wise linear interpolation. Fig 2(a) shows that, on average, this type of fit yields poor approximations in comparison with the impulse model. Each curve corresponds to a fit performed with a different single measurement that was left out during the fit. The color of each curve corresponds to the color of the hidden value (square marker).

supplementary figure 10

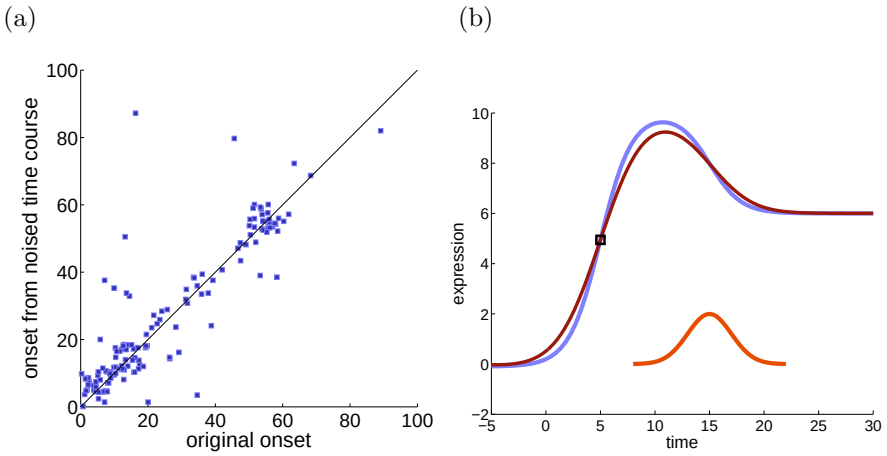

Figure 5: **(a) Robustness to expression level noise:** Onset extracted from corrupted time courses is highly correlated with the original onset (correlation coefficient is $\rho = 0.89$). Time courses were corrupted by additive Gaussian noise $N(0, 0.1)$. Each point corresponds to a gene; shown are differentially expressed genes (log expression > 1) under exposure to peroxide (Gasch, 2000).**(b) Robustness to timing noise:** Convolution of an impulse model (blue curve) that has an onset at 5 minutes (black square), with a Gaussian (red curve, 2 minutes standard deviation). The resulting convolution (purple curve), has essentially the same onset as the original impulse blue curve.

supplementary figure 11

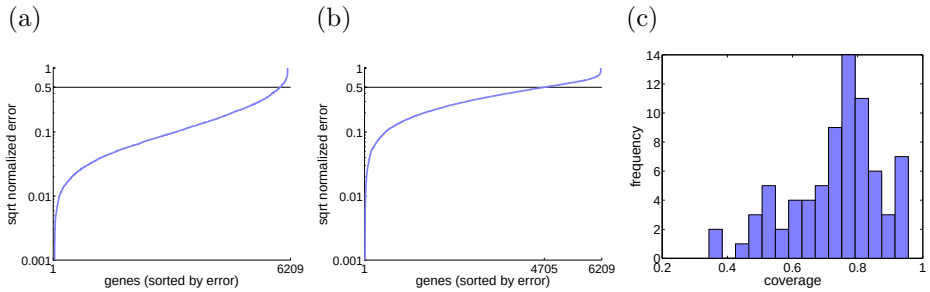

Figure 6: **Distribution of normalized error across all genes. (a)** The condition with largest number of genes with low error, adenine starvation (Gasch, 2000); more than 95% of the genes (5934) have a normalized error below half a standard deviation of the expression. **(b)** A condition with typical error profile (synthetic complete media with Ethanol and inositol). Condition was chosen as the median across conditions; 4705 genes (78%) had normalized variance below half a standard deviation. **(c)** Distribution of coverage (fraction of genes with error below cutoff) across conditions.

supplementary figure 12

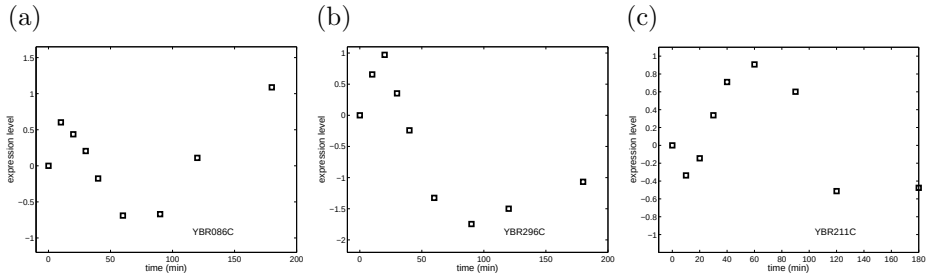

Figure 7: **Non-impulse responses to exposure to 1M KCl (ORourke, 2002).** These genes follow at least three transitions.

supplementary figure 13

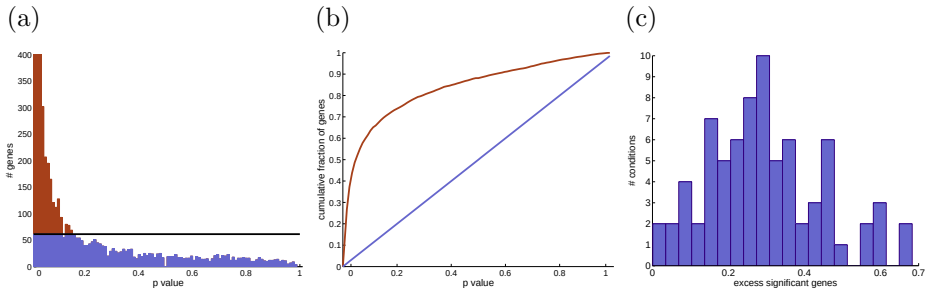

Figure 8: **Impulseness. (a)** Distribution of p-values for impulse model fitting for responses of yeast genes to diamide. The expected distribution of p-values (flat) is plotted as a black line, and the excess of significant genes over random is colored in red. **(b)** Cumulative distribution of the p-values (red) vs the expected in random (blue). **(c)** Distribution of the excess of significant genes across 76 stress conditions. It shows that the impulse model fits on average about 35% of the yeast genome above the baseline level.