The symphony of gene regulation

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Chapter 4 Promoter sequence determines the relationship between expression level and noise.

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4.1 Summary

The ability of cells to accurately control gene expression levels in response to extracellular cues is limited by the inherently stochastic nature of transcriptional regulation. A change in TF activity results in changes in the expression of its targets, but the way in which cell-to-cell variability in expression (noise) changes as a function of TF activity, and whether targets of the same TF behave similarly, is not known. Here, we measure expression and noise as a function of TF activity for sixteen native targets of the transcription factor Zap1 that are regulated by it through diverse mechanisms. For most activated and repressed Zap1 targets, noise decreases as expression increases. Kinetic modeling suggests that this is due to two distinct Zap1-mediated mechanisms that both change the frequency of transcriptional bursts. Notably, we found that another mechanism of repression by Zap1, which is encoded in the promoter DNA, likely decreases the size of transcriptional bursts, producing a unique transcriptional state characterized by low expression and low noise. In addition, we find that further reduction in noise is achieved when a single TF both activates and represses a single target promoter. Our results suggest a global principle whereby at low TF concentrations, the dominant source of differences in expression between promoters stems from differences in burst frequency, whereas at high TF concentrations differences in burst size dominate. Taken together, we show that the precise amount by which noise changes with expression is specific to the regulatory mechanism of transcription and translation that acts at each gene.

4.2 Introduction

The cellular response to environmental changes is mediated through activation of TFs and subsequent coordinated activation and repression of dozens of target genes. However, gene expression is noisy\(^{20}\), and this limits the precision with which cells can regulate protein levels. Genome-wide, noise (\(\sigma^2/\mu^2\), variance/mean\(^2\)) decreases as expression increases\(^{21\text{-}23}\). Along this global trend, individual genes with the same average expression in the population differ in their amount of noise. The level of noise for each gene is related to its function and is determined by the mechanisms of regulation\(^{24}\). However, the precise mechanisms by which control of noise is accomplished for native genes are not known.

Two quantities that describe the dynamics of gene expression, and have been related to the distribution of protein abundances, are burst size and burst frequency. Burst frequency is the rate at which the promoter switches from an inactive to an active transcriptional state due to TF binding and subsequent PolII recruitment (promoter on-switching). Burst size is the number of proteins produced during each promoter on-event\(^{25\text{-}27}\). Native genes differ in the relative contribution of burst frequency and size to expression\(^{23,28,29}\), suggesting that evolution can tune both parameters in order to reach an optimal level of expression and noise for each gene\(^{30}\).
When an increase in gene expression is caused by an increase the rate of promoter on-switching (burst frequency), noise ($\sigma^2/\mu^2$) decreases monotonically with expression\textsuperscript{31}. In contrast, an increase in burst size (due to a decrease in promoter off-switching rate or an increase in the transcription or translation rate) results in an increase in expression and in noise strength ($\sigma^2/\mu$), and no change in noise\textsuperscript{31}. Mutations in the TATA box in yeast\textsuperscript{32} or in the ribosome binding site in \textit{E. coli}\textsuperscript{33} both affect noise strength, but not noise. The former is thought to be involved in transcription re-initiation\textsuperscript{34}, thus extending the time of each active state of the promoter, while the latter affects the number of proteins produced from each mRNA molecule. These observations strengthen the claim that changes in mean expression but not noise stem from molecular mechanisms that affect the number of proteins produced during each transcriptional event, but not the frequency of such events. Taken together, these data support a model of gene expression in which changes in promoter dynamics, such as changes in on-switching rates and transcription and translation rates can be deduced by measuring how noise changes with expression\textsuperscript{23,26,27}.

Since most genes are regulated through multiple mechanisms, each of which can affect burst size and burst frequently differently, different genes should exhibit different relationships between mean expression and noise. However, measurements of a set of seven different promoters in \textit{E. coli} all showed similar changes in expression and noise throughout induction\textsuperscript{35}. Gene regulation in eukaryotes is more complex, and we thus hypothesize that burst frequency and burst size will be differentially regulated for each gene, and as a consequence, that the relationship between noise and expression will be different for different genes.

To characterize the relationship between mean expression and noise for native promoters in response to environmentally stimulated changes in TF activity, we generated a set of sixteen strains in which distinct promoters were fused upstream of a yellow fluorescent protein reporter (YFP). In each strain, we extracted a different Zap1 binding-site containing promoter from its native locus, integrated it into the \textit{his3} locus, and measured its expression and noise at 12 different zinc concentrations (induction levels). Decreasing zinc concentration increases the activity and expression of Zap1 and changes the expression of Zap1 target promoters. The resulting Zap1 dose-response curves of these targets show activation, repression, and a combination of activation and repression, consistent with previous observations\textsuperscript{36}.

We found that for Zap1-activated targets, an increase in Zap1 causes an increase in expression and a decrease in noise. Similarly, Zap1-repressed targets exhibit the same relationship between expression and noise, whereby an increase in Zap1 causes a decrease in expression and an increase in noise. Despite this general trend that has previously been reported\textsuperscript{21-23}, we found that the slope of noise versus expression is unique for each promoter, showing that noise is not determined by expression level alone. The most notable exception to expression determined noise is the ZRT2 promoter, which is both activated and repressed by Zap1\textsuperscript{37}, where we
found a different and novel relationship between mean expression level and the distribution of expression. We found that repression of ZRT2 by Zap1 results in a decrease in both expression and noise, leading to a transcriptional state of low expression and low noise that is unique among the sixteen tested promoters. This behavior is predicted by a kinetic model in which repression is due to a secondary binding event near the TATA that causes a decrease in transcription rate (burst size), thereby preventing the typical increase in noise that accompanies repression that is due to a reduction in burst frequency. These results suggest that the relationship between noise and expression is unique to each promoter and is determined by the regulatory mechanism encoded in the promoter DNA sequence and not by mean expression level alone.

Next, we hypothesized that further noise reduction will occur when activator and repressor are performed by the same TF. Using a model of noise that takes into account the sensitivity to TF level fluctuations and an experiment in which we decouple activator from repressor, we find strong evidence supporting our hypothesis that coupling between activator and repressor is a mechanism for noise reduction.

Finally, analysis of the data from all measured Zap1 targets brings forward a global principle of regulation in which the major source of differences in expression between promoters changes with induction. Our results strongly support a model in which at low Zap1 activity, differences in expression between Zap1 targets are due to variability in the frequency of transcriptional bursts, while at high Zap1 activity, differences are due to variability in the number of proteins produced during each transcriptional burst. This model suggests that such behavior is a general property of transcriptional regulation.

4.3 Results

4.3.1 Each target of a single transcription factor exhibits a unique gene-specific scaling of expression and noise in response to changes in TF activity

To study how expression of different native promoters is regulated by environmental-induced changes in TF activity, we measured promoter-driven expression in single cells for sixteen targets of the transcription factor Zap1 in response to changes in extracellular zinc. To do this we used an experimental system that we previously developed in which a promoter of interest drives YFP expression from the genomic his3 locus (Figure 4.1A) 38. We generated a set of sixteen promoter-YFP fusion strains and used flow-cytometry to perform quantitative single-cell measurements of promoter-driven expression at 12 induction points (Figure 4.1C). These promoters (Figure 4.1B) have diverse activation curves (Figure 4.1D, Figure 4.8) and, while the response of each promoter correlates with the predicted Zap1 occupancy along the promoter (Figure 4.9), the diversity of responses suggests that the way in which Zap1 alters expression is different for different promoters. In addition, we examined the
changes in noise and noise strength along the induction curves (Figure 4.1G). For most activated (11/13) and repressed (2/3) promoters, noise decreases as expression increases (Figure 4.1E, average Pearson correlation for all promoter of -0.73, Figure 4.10A), consistent with observed genome-wide trends. In contrast, noise strength changes less consistently across Zap1 targets (Figure 4.1, average Pearson of -0.09, Figure 4.10B). Surprisingly, not only do different promoters exhibit different amounts of noise at the same level of expression (Figure 4.1C), but also the way in which noise and noise strength change with expression is unique to each promoter (Figure 4.1E,G, Figure 4.11). Interestingly, a single promoter (ZRT2) that is both activated and repressed by Zap1, shows very different amounts of noise at the same mean expression (Figure 4.1F). Because different molecular mechanisms of gene regulation can lead to the same change in mean expression but different changes in noise, these results suggest that the precise molecular mechanism by which a change in Zap1 activity causes a change in expression may be different at each promoter.
Figure 4.1: Measuring mean promoter activity and cell-to-cell variability for a library of Zap1 target promoters. (a) The transcription factor Zap1 is induced by decreasing the concentration of zinc in the growth medium. A schematic of the site of chromosomal integration for measuring promoter-driven expression is shown. Each yeast strain has a single promoter inserted upstream of the YFP coding sequence. At the same locus a constitutively expressed mCherry is also integrated, which is used to normalize the YFP signal and correct for extrinsic cell-to-cell variability. (b) For each Zap1 target promoter the predicted locations of the major architectural features are shown. Promoters are aligned by the transcription start site (TSS) (cyan). PSSMs for the TATA box (purple) [36] and Zap1 (green) [17] were used to predict binding sites for TBP and Zap1, respectively. The width of the green bars is proportional to the predicted affinity of each
Zap1 binding site. Darker shades of grey show regions with higher predicted nucleosome occupancy. Blue lines show translation start sites. (C) Zap1 activates its own transcription, in addition to other target promoters, such as Zrt1. Shown is the measured expression (the ratio between YFP and mCherry fluorescence) of the ZAPI promoter and the activated target ZRT1, graphed against the concentration of zinc added to the growth media. The inset shows the single-cell distribution of measured fluorescence intensities for ZAP1 and ZRT1 at two zinc levels obtained from flow-cytometry. (D) Measured promoter driven expression (quantified as the ratio between YFP and mCherry fluorescence) throughout the Zap1 induction is shown for each measured promoter. Each point shows the average of at least four biological replicates. (E & G) Noise and noise strength graphed against mean expression for each promoter that changes expression by more than two-fold. The line $\eta=\mu^{2}$ was fit (solid lines) to the induction data per promoter, showing that different promoters show different scalings of noise and mean expression. (G) The measured expression distribution for the ZRT2 promoter at two different zinc induction levels (50.4 uM and 648 uM zinc, blue and red points in E & G) with the same mean expression level but different distributions. The mean expression level for each distribution is marked with a dashed line.

### 4.3.2 A kinetic model of promoter switching replicates the experimentally observed changes in expression and noise for the ZRT1 promoter

To better understand what determines the relationship between expression and noise we used an analytical model of gene regulation (Figure 4.2A) to predict changes in expression and noise in response to changes in TF activity (see Methods). We fit this model to measurements of ZRT1 expression and noise and find that the model replicates our experimental results when an increase Zap1 activity causes an increase in the promoter on-switching rate ($K_{on}$) (Figure 4.2B,C). To further challenge the model we created a set of seven start codon context mutants of the ZRT1 promoter (NNNNATG) and measured the expression distribution of these variants at twelve different levels of TF activity (Figure 4.2D-F) (only three are shown for clarity). These mutations to change translational efficiency and therefore the number of proteins produced per mRNA ($b$), without affecting promoter dynamics (Figure 4.12). We find that ATG context variants at a single induction point differ in expression but not in noise, consistent with similar experiments in *E. coli* 

In support of the above hypothesis, we obtain the best fit of the model to our data when the TF induction is modeled as changing $K_{on}$ while the ATG context variants change $b$ (Figure 4.13 and Figure 4.14). Furthermore, when fitting our model to data we find that the optimal rate constants are on the order of experimentally measured promoter switching rates\(^{28,40,41}\) and not TF binding/unbinding rates\(^{42}\). This suggests that promoter-switching rates probably correlate with, and are partially determined by, TF concentration and binding kinetics. However, each TF binding event does not necessarily lead to transcription initiation. These results suggest that increases in TF activity increase the frequency of transcriptional bursts, while increases in translational efficiency cause an increase in the size (number of proteins produced) of each burst. We note that this
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is in contrast to observations in *E. coli* 35 and in yeast at the *GAL1* promoter13, in which TF induction appears to change the promoter off-switching rate (Koff) but consistent with measurements of the *PHOS* promoter 16.

Figure 4.2: Measured and modeled gene expression of ZRT1. (a) ZRT1 expression is modeled with a kinetic scheme in which the promoter switches between a transcriptionally active [on] and inactive state [off] as a result of Zap1 (red oval) binding and unbinding. (b) Experimentally measured ZRT1 promoter driven expression changes as a function of zinc concentration (triangles). The kinetic model in (a) fits (line) the data (triangles) when zinc is assumed to change *Kon* (inset). (c) Noise graphed as a function of expression for the data and model from (b). (d) A schematic of the experimental system used to change translation efficiency through mutations of the ATG context. (e) Measured expression distributions for two ATG context variants at three zinc induction levels shows that changing expression via induction or ATG context has a different effect on the shape of the expression distribution. Measured (f, squares) and fit (f, solid lines) of noise as a function of mean expression for three ZRT1 promoter mutants (f, colors) that each has a unique 4 base-pair sequence immediately upstream of the ATG. A model (f, solid lines) in which the only difference between ATG context variants (different colors) is in the number of proteins produced per mRNA (f) fits the experimental data (squares) better than any alternative model.
4.3.3 Repression of ADH1 and ADH3 by Zap1 is likely due to a decrease in the frequency of transcriptional bursts

In addition to increasing expression of target genes, Zap1 can also act as a repressor. Zap1 represses two targets (ADH1 and ADH3) by binding upstream of the core promoter and inducing intergenic transcription through the core promoter, probably promoting dissociation of the activating transcription factor Rap1. Two mechanisms have been proposed for repression by transcriptional interference: dislodgement of TFs and the Pol II pre-initiation complex by RNA Polymerase, and competitive binding, one form of which is deposition of nucleosomes in the otherwise nucleosome free region where the activating TFs and Pol II bind. We hypothesized that deposition of nucleosomes would result in occlusion of the activating binding site, the TATA box, and PolII binding, thus reducing the effective TF concentration and lowering the frequency of transcriptional activation. We model this mechanism as a reduction in Kon. Alternatively, passage of RNA polymerase may dislodge already bound Rap1, TBP, and/or the RNA polymerase pre-Initiation Complex. This would shift the promoter from the ‘on’ into the ‘off’ state, thus reducing the length of each transcriptional on state and therefore the number of mRNA molecules produced during each transcriptional burst (Figure 4.3C). We model this mechanism as an increase in Koff. To determine the ability of dislodgement by Pol II (TD) or occlusion of TF binding by nucleosomes (NO) to explain our experimental data we fit each model to our data. We find that the NO model fits our data better than the TD model (Figure 4.3D) (see Methods). Furthermore, the NO model consistently fits the data better in the case in which we vary each parameter by up to two-fold. The increased robustness (Figure 4.3E) and decreased sensitivity (Figure 4.15) of the NO model gives us further reason to favor a model in which repression by Zap1 at the ADH1 and ADH3 promoters occurs by inducing intergenic transcription and nucleosome deposition over the core promoter and/or Rap1 binding site.
Figure 4.3: Measured and modeled gene expression for ADH1. We model ADH1 expression using a two-state kinetic scheme (a) in which Kon and Koff are determined by the binding of transcriptional activators (blue circle) or a repressor (red circle). (b) Two mechanisms have been proposed for repression by upstream interfering transcription: TF dislodgment, in which an alternative transcript dislodges the bound activator, and nucleosome occlusion, where transcription through the promoter results in an occluding nucleosome that prevents binding of the activator. Hence, we assume that TF dislodgment increases the dissociation rate of the activator and that nucleosome occlusion results in a decrease in the binding rate of the activator. (c) We fit the model such that either Kon (black) for nucleosome occlusion or Koff (blue) for TF dislodgment changes as a function of [zinc]. (d) Measured mean expression versus noise (triangles) and fits (lines) of both model variants show that the nucleosome occlusion model has a better fit to the data (\( \Delta \) is distance of fit to data). (e) To compare the robustness of each model, each parameter was independently perturbed 50 times over a two-fold change from the fit value, and the distance of each model to the data was computed. Shown are the cumulative distributions of these distances. The narrower distribution of the nucleosome occlusion model (black) shows that it is significantly more robust to parameter variation than the TF dislodgment model (blue).
4.3.4 ZRT2 achieves a state of low expression and low noise due to a repression mediated mechanism of intrinsic noise reduction

Uniquely among Zap1 target promoters, ZRT2 responds non-monotonically to an increase in Zap1 activity, whereby its expression first increases then decreases in response to increasing Zap1 activity [37]. In the activating regime of ZRT2, noise decreases as expression increases, suggesting a Kon (burst frequency) dominated change that is similar to the purely activated targets. However, in contrast to the repressed targets ADH1 and ADH3, where noise increases with the decrease in expression, in the regime where ZRT2 expression decreases noise remains constant. These results suggest that the decrease in ZRT2 expression is a result of a decrease in burst size (see below), with the consequence of having induction points that have the same mean expression level but different expression distributions (Figure 4.1F). At high induction, the distribution is less noisy (Figure 4.1F, blue) than at low induction (Figure 4.1F, red). Thus, the ZRT2 promoter reaches a state that is unique amongst Zap1 targets that is characterized by both low expression and low noise. Taken together, these findings suggest that although ADH1, ADH3 and ZRT2 are all repressed by Zap1, the mechanism by which ZRT2 is repressed is unique.

4.3.5 A Zap1 binding site near the TATA box is both necessary and sufficient for repression through Zap1 mediated burst size reduction

In response to increasing Zap1, ZRT2 expression first increases and then decreases. The activation by Zap1 is a result of Zap1 binding at activating binding sites 250-300bp upstream of the start codon, while the repression is due to the presence of repressive Zap1 binding sites near the TATA box (between -90 and -112) [37]. In addition we made a variant (ZRT2-zre) of the ZRT2 promoter that lacks the repressive binding sites (Figure 4.4B). We hypothesized that a model of the ZRT2 promoter should include promoter states in which Zap1 is bound as an activator, as a repressor and both as activator and repressor (Figure 4.4A). Based on experimental evidence [37], we model the binding site affinity for the repressive site as weaker than that of the activating site. We assume that binding of Zap1 to the repressive site turns off the promoter but does not affect the transition probabilities between states. When the model was simultaneously fit to both the ZRT2-WT and ZRT2-zre experimental data, we find that the model obtains a good fit to data when, like with ZRT1, an increase in Zap1 activity increases Kon and does not affect any other parameters. Interestingly, we find that the repressed state (state 4, Figure 4.4A) is not fully off, but has a small, but not insignificant, transcription rate relative to the transcription rate of the active state (state 2, Figure 4.4A). Notably, the only parameter change required to change from ZRT2-WT to ZRT2-zre is setting Koff to be very high, mimicking the mutation of the repressive binding sites (Figure 4.4C,D). These experimental and modeling results suggest that binding of the transcriptional activator Zap1 to a binding site between the TATA box and TSS is necessary to generate a promoter state with low transcriptional activity. Notably, a very simple promoter model is able to replicate a
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non-monotonic response to changes in TF activity. Furthermore, it suggests that the reason that the ZRT2 promoter is able to reach a state of low expression and low noise purely through transcriptional regulation is due to a promoter state with high burst frequency (due to binding of activating Zap1) and low burst size (due to binding of repressive Zap1).

These results suggest that in the ZRT2 promoter, an increase in Zap1 both increases the frequency and decreases the size of transcriptional bursts. Therefore, our simple kinetic model shows that adding a repressive binding site for the activating TF is sufficient for explaining both ZRT2 expression and noise as a function of induction.

Repression of ZRT2 is accompanied by a decrease in noise strength, suggesting that repression occurs via a decrease in burst size. We therefore hypothesized that addition of a repressive Zap1 binding site to a native Zap1 target that lacks repression would cause a decrease in expression and burst size. To test this hypothesis, we added a consensus Zap1 binding site (ACCTTAAGGT) upstream of the transcription start site of ZRT1 (Figure 4.4E, ZRT1pr+ZRE). Consistent with our hypothesis that this repressive site reduces expression through a decrease in burst size, this additional site results in a constant ~2 fold decrease in expression, a decrease in noise strength and no change in noise (Figure 4.4F). A model identical to the ZRT2 model (Figure 4.4A), except that the repressive site has a higher affinity to Zap1 than the activating site, replicates the experimental data (Figure 4.4F). Interestingly, we find that while both models require the repressed state to be partially active, the repressed state of the ZRT1 promoter has higher activity (in model and data) than for the ZRT2 promoter. This may be because ZRT2 has at least two repressive Zap1 binding sites, while we only introduced a single repressive binding site into ZRT1. Nevertheless, these results show that the presence of a Zap1 binding site between the TATA box and transcription start site is both necessary and sufficient for repression mediated by a decrease in burst size.
Figure 4.4: A repressive Zap1 binding site is both necessary and sufficient for repression in ZRT2. (a) We model ZRT2 expression with a 4-state kinetic scheme that represents four promoter configurations as a result of binding and unbinding of Zap1 to two different binding sites. One binding site is activating (blue square) and as a result we assume that each configuration can have different transcriptional activity (see Methods for a detailed description of the model). (b) Promoter architectures are shown in terms of Zap1 binding sites (green), TATA box (purple), TSS (light blue) and nucleosome occupancy (white to grey for increasing occupancy) for wild-type ZRT2 and a ZRT2 mutant (+zre) in which the repressive Zap1 binding site was removed (at the arrow). (c) Measured (triangles and squares) and modeled (lines) mean expression as a function of [zinc] for wild-type ZRT2 (black) and the +zre mutant (blue). (d) The same measured data and model from (c) are shown for mean expression versus noise. The ZRT2 model was simultaneously fitted to the wild-type (c,d, black line) and the mutant (c,d, blue line) with the assumption that the only difference between wild-type and mutant is that the Kd of the mutant is infinite, to model the removal of the repressive binding site. Intrinsic noise (d, inset) measured in a dual reporter assay shows the same mean to noise scaling. (e) The promoter architectures are shown for the wild-type ZRT1 promoter and a +zre mutant in which a repressive Zap1 binding site was added around the TSS/TATA (at the arrow). (f) Measured mean expression and noise for the ZRT1 wild-type (green circles) and the +zre mutant (red triangles), and mean expression versus noise strength (inset). The ZRT2 model was simultaneously fitted to both wild-type ZRT1 (green line) and +zre
mutant (red line) again with the assumption that only $K_d$ changes as a result of the addition of a repressive binding site. The black bar and inset indicate that a shift in expression occurred without a change in noise consistent with the assumption that the repressive binding site changes the apparent ‘off’ rate and not the ‘on’ rate.

4.3.6 Mutation of additional repressive Zap1 binding sites suggests that a combination of activation and repression may be common

A computational search for Zap1 binding sites between the TATA box and the transcription start site identified three weak Zap1 binding sites in the ZRT3 promoter (Figure 4.5A). A closer look at the ZRT3 induction curve at very low zinc concentrations showed that expression of ZRT3 decreases slightly at high Zap1 induction (Figure 4.5B, inset). To determine if these weak Zap1 sites were functional, we mutated them and measured expression of the wild-type and mutant ZRT3 promoters. Consistent with our hypothesis that Zap1 binding sites around the TSS are repressive, removal of the presumptive Zap1 binding sites increased expression (Figure 4.5B), in particular at higher induction, consistent with our model in which repression is a function of repressor activity. This suggests that low-affinity binding sites may be functional at high TF concentration, perhaps mostly at promoters that have additional high-affinity binding sites.

![Figure 4.5: Removal of a predicted repressive Zap1 binding site increases expression of ZRT3. (a) Promoter architectures are shown for wild-type ZRT3 (wt) and a ZRT3 mutant (-zre) in which a potential repressive Zap1 binding site was removed (at the arrow).]
4.3.7 Activation and repression by the same TF as a mechanism for reduction of extrinsic noise due to fluctuating TF levels

The ZRT2 promoter presents a case in which the activator and repressor are the same TF. We were intrigued by this mechanism and wondered whether this affects the noise properties. Many promoters in yeast are regulated by the binding of both activators and repressors to different binding sites in the promoter. The activator and repressor can be different proteins (e.g., ADH1 is activated by Gcr1 and Rap1 and repressed by Zap1) or the same protein (such as ZRT2 that is both activated and repressed by Zap1) (Figure 4.6A). We hypothesized that the sensitivity to TF fluctuations for a promoter that is both activated and repressed depends on the coupling between activator and repressor. For example, we expect that when activator and repressor are done by the same TF, in a regime where a change in activator binding has the exact opposite result on expression as the same change in repressor binding, the promoter is insensitive to any fluctuations in TF levels. To study this hypothesized phenomenon, we used our kinetic model of ZRT2 and simulated the case where activator and repressor are different (decoupled) and where they are the same TF (coupled). We then calculated the contribution of TF fluctuations to expression noise throughout the induction (Figure 4.6B) (See section Materials and Methods for a detailed description of the model). Coupling of the activator and repressor reduces the sensitivity to TF fluctuations throughout induction and places the point of minimal sensitivity to TF fluctuations at the point of maximum target gene expression (Figure 4.6B blue line).

Our model predicts that the total sensitivity to TF fluctuations is reduced throughout the induction curve, and that this reduction is greatest at maximal promoter expression (Figure 4.6B, point 1). To test this we measured extrinsic noise (the contribution of variance in all factors, e.g. ribosomes, Zap1, PolII) for the native ZRT2 promoter using a dual-reporter. We find that extrinsic noise is constant across the induction (Figure 4.6D, purple). However, when we remove as much global extrinsic noise as possible using a very narrow forward and side scatter gate (Figure 4.16) we hypothesize that we are left with mostly pathway-specific noise, e.g. noise due to TF level fluctuations. In support of this hypothesis, we find that pathway-specific noise is not constant, but rather varies greatly (around 10 fold) with induction. We find that this signal, which we expect to be dominated by
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changes in TF sensitivity, does indeed drop around the point of maximal expression (Figure 4.6D, blue), consistent with our model. In fact, the extrinsic noise replicates quite well the general predicted change in TF sensitivity with induction.

Finally, our model predicts that decoupling of activator and repressor will increase total noise as the sensitivity to TF fluctuations is increased. To test this we replaced the two activating Zap1 binding sites of ZRT2 with two Gal4 binding sites (Figure 4.6A) and measured expression and noise throughout the repressive regime (at high Gal4 induction as to reduce its noise and remove any bias for comparison with native ZRT2). Consistent with our model, the Gal4-Zap1 regulated ZRT2pr variant has higher noise than the wild-type promoter (Figure 4.6C). These results show that, while repression is able to reduce expression and keep noise constant a transcriptional regulatory motif, in which the activator and repressor are the same protein, is capable of reducing noise even further. This suggests that the coupling of activator and repressor can be a mechanism to regulate gene expression with less variability.

Figure 4.6: Activation and repression by the same TF as a mechanism for noise reduction. (a) A promoter that is both activated and repressed can be regulated by two different TFs (decoupled, e.g. Gal4-act and Zap1-rep) or one TF (coupled, e.g. Zap1) that functions as both an activator and repressor. (b) A simulation of noise as a result of fluctuations in TF concentration is shown for a coupled (blue) and decoupled (red)
system. The Y-axis shows noise as a result of TF fluctuations as a function of promoter induction (mean on-switching rate, \(K_{on}\)) for the coupled (blue) and decoupled (red) system. In addition, the mean expression at each induction level is shown (dashed line). Noise from TF fluctuations was quantified by sampling the model at different TF concentrations (i.e. \(K_{on}\) values) that were drawn from a gamma distribution (See Methods for a detailed description of the model). The model predicts that coupling of activator and repressor (e.g. if they are the same molecule) reduces noise. Notably, reduction is maximal where mean expression peaks (arrow 1). (c) Noise measurements, at various zinc induction levels, of native ZRT2 (blue) and a mutant that has two Gal4 UASs upstream of a repressive Zap1 site (red). The coupled system (wild-type Zrt2) has consistently lower noise than the decoupled system (Gal4-act Zap1-repr), as is predicted by our model. (d) Measurement of extrinsic noise from a dual-reporter assay is shown as a function of zinc induction. Non-stringent gating on cell-size (through forward and side scatter) shows an extrinsic noise that is constant with induction (purple). However, strict gating (through a small forward and side scatter gate) significantly reduces the extrinsic noise and reveals a signal that changes with zinc induction (blue). We hypothesize that this signal is determined by noise from TF fluctuations, which according to our model has specific behavior as a function of induction. As predicted by our model we find a reduced noise where mean expression (dashed line) is maximal and sensitivity to TF changes is minimal (b,d, arrow 1), and minimal reduction (maximal extrinsic noise) where mean expression is most sensitive to changes in TF concentration (b,d, arrow 2).

4.3.8 The dominant source of differences between promoters in expression and noise changes with TF concentration

We hypothesized that the source of differences in expression between genes might change with TF concentration. At low TF concentrations, promoters will be inactive most of the time, and differences in expression may depend mostly on differential recruitment of the TF. In this case, the major source of differences in expression between promoters should stem from the frequency with which transcriptional bursts occur. Alternatively, at saturating concentrations of activating TF, the promoter should be ‘on’ most of the time and the major difference in expression between promoters should arise from the transcription and translation rates of each promoter. Thus, as the concentration of TF changes from negligible to saturating, we expect the transcription and translation rates of each promoter to become more important in determining expression differences between genes.

To determine whether burst frequency or burst size dominate the differences in expression between promoters, for each induction level, we measured the correlation between expression and noise or noise strength across promoters. Consistent with the above hypothesis, across all promoters, noise is highly correlated with expression at low levels of Zap1 activity (R= -0.66, P<0.01), while noise strength is uncorrelated (R= -0.02, P<0.94) (Figure 4.7A). This suggests that at low TF concentration, burst frequency determines the differences in expression across promoters. Conversely, at high levels of Zap1 activity, noise strength is
Promoter sequence determines the relationship between expression level and noise

correlated with expression \( (R=0.63, p=0.01) \), and noise is slightly less correlated \( (R=-0.55, p=0.04) \) (Figure 4.7A). Overall, we found a continual increase in the correlation between noise strength and expression with increasing TF activity (data not shown). To test the hypothesis that these differences are due to a change in the dominant source of expression difference between promoters, we generated 50 random genes \textit{in-silico} that differ only in their rates of promoter on-switching \( (K_{on}) \) and translation \( (K_{tl}) \). We then performed an induction by increasing \( K_{on} \) for each promoter to 20 times its original value. This results in a mean to noise and mean to noise strength scaling that is strikingly similar to what we observed for the native Zap1 targets (Figure 4.7B). Taken together, our results suggest that as a set of targets of the same TF are induced, the major source of expression differences between them changes from being dominated by burst frequency to a combination of burst frequency and burst size.

Figure 4.7: The correlation of noise and noise strength with expression changes with TF concentration. (A) Scatter plots of noise (top) and noise strength (bottom) graphed against expression for each promoter at low (left side) and high (right side) Zap1 induction points. A line fit to each set of points using linear regression shows that, across promoters, noise strength is uncorrelated with expression at low TF concentration, but...
is positively correlated with expression at high TF concentration. (B) Noise and noise strength graphed against expression for high and low TF as in (A) but for in-silico promoters that differ in both KON and KTL. The change from low to high TF was simulated by multiplying the initial KON of each promoter by 20.

4.4 Discussion
We have measured the dose response curve, in terms of expression and noise, for a set of native yeast promoters that are all targets of the same TF, yet are regulated by that TF via at least three distinct transcriptional mechanisms: activation, repression by binding between the TATA box and TSS, and repression by induction of an upstream interfering transcript. Although noise generally decreases with increased expression, the quantitative scaling of noise with expression is specific to each promoter and depends on the mechanism by which the TF regulates the promoter.

4.4.1 The promoter sequence determines how activation by Zap1 affects noise and expression
As in the global trend seen in expression, our data suggests that changes in expression of individual promoters are dominated by differences in burst frequency. This is consistent with Zap1 binding to promoters being limiting for transcriptional activation, especially at low Zap1 concentrations, and with the proposal that the rate-limiting step in transcription for yeast is promoter firing rate, which is determined by TF search times. However, the observation that different activated targets have different scaling between noise and expression suggests that while activation by Zap1 acts only through burst frequency at most activated promoters, it may act partially or even completely through burst size at other activated promoters. This is entirely reasonable; Zap1 is not the only TF acting at these promoters, and the promoters differ in both nucleosome organization and the presence and location of TATA boxes. Experiments that placed a tetO sequence at different locations within the FLO11 promoter suggest that the same TF can have different effects on promoter dynamics, depending on the location of binding sites within the promoter. Unfortunately, there are not enough strongly induced Zap1 targets in S. cerevisiae to identify the promoter architecture features that determine the source of the promoter-specific slope. It will be interesting to perform dose-response curves for a larger set of promoters from other yeasts, or on synthetic promoters, in order to identify promoter architecture that determine the promoter-specific slope.

4.4.2 Different mechanisms of regulation by the same TF can cause similar changes in expression but different changes in noise
Our observation that repression by production of an upstream interfering transcript causes an increase in noise, while repression when the TF binds near the TATA box causes a decrease in noise, suggests that different dynamics occur at each
promoter during repression. This, along with previous observations, suggests that the mechanism of regulation by any TF is determined in cis by the promoter architecture. Binding sites between the TATA box and TSS decrease burst size, binding sites within a few hundred bases upstream of the TATA box increase burst frequency, and binding sites further upstream, with a nearby downstream TATA box, repress through a reduction in burst frequency. These data show for the first time that different promoter architectures can cause a similar change in expression in response to changes in TF activity, but exhibit different changes in noise.

4.4.3 High burst frequency and low burst size is a strategy to produce low abundance proteins with low noise

If the genome-wide scaling of expression and noise extends to proteins with very low expression, then a large fraction of cells will have zero molecules of protein\textsuperscript{51}. Single-molecule studies have confirmed this: many cells have zero molecules of proteins with low levels of expression\textsuperscript{23}. However, many proteins expressed at low levels are essential. This raises the question: how does the cell maintain a low level of both expression and noise for essential proteins, so that all cells have the minimum number of proteins. Our results showing that burst size regulation can reduce expression without increasing noise suggest a way out of this trap. Lowly expressed genes tend to be bound by many transcriptional regulators, both activators and repressors\textsuperscript{48}. Low levels of an activating TF result in low expression and high noise. Notably, a motif in which weak transcription but efficient translation generates high noise may exist at the \textit{comK} gene in \textit{B. subtilis}\textsuperscript{52}. In contrast, combinatorial regulation that results in high burst frequency and low burst size (approaching the Poisson limit\textsuperscript{20}) provides a regulatory motif through which cells can produce low levels of protein with low cell-to-cell variability. Our identification of this same regulatory motif in the \textit{ZRT3} promoter suggests that this motif may be common. This regulatory strategy may be used to prevent some cells from having zero molecules of protein when expression is low.

4.4.4 Coupling of activator and repressor as a mechanism for reducing extrinsic noise

The concentrations of TFs, like those of all other proteins, vary greatly from cell to cell. We therefore expect that these variations have a significant impact on the cell-to-cell variability of target gene expression\textsuperscript{23}, and therefore wondered how cells deal with this source of noise. Interestingly, we find that \textit{ZRT2} is able to reduce noise through its reduced sensitivity to fluctuations in TF levels, as a result of activator and repressor being the same molecule. Mechanisms for extrinsic noise reduction have been previously reported\textsuperscript{39}. However, to the best of our knowledge, we are the first to propose theoretically and confirm experimentally a mechanism for desensitizing promoters to TF noise. Noise as a result of TF fluctuations has been proposed theoretically in several studies\textsuperscript{23,51}. In fact, Bai et al. propose a dual-reporter experiment to investigate extrinsic noise resulting from TF fluctuations, which we have performed in this work (Figure 4.6D). We note that noise from TF fluctuations is a special case of noise propagation in a gene network, where the
noise of a downstream gene is a function of its intrinsic noise and the noise from any upstream genes\textsuperscript{54}. An alternative mechanism for a similar reduction in sensitivity would be the regulation by multiple different decoupled TFs. We hypothesize that as the number of different TFs increases, target sensitivity (and therefore noise) decreases, if the TFs are sufficiently de-correlated. This potential mechanism, as well as the general characterization of the effect of TF noise on target noise, would make the subject of a meaningful follow up study.

4.4.5 The dominant type of noise changes with TF concentration

The observed change in the scaling between noise and expression throughout the increase in TF concentration suggests that variability between promoters in burst size (transcription efficiency, translation efficiency, and promoter off-switching rate) becomes more important as TF concentration is increased. This suggests that differences in promoter architecture play different roles at low and high TF concentrations. In the presence of limiting TF, promoter architecture may determine expression by determining TF search time, through the number of accessible TF binding sites. However, at high TF concentration, promoters are mostly bound by TFs, and the transcription and translation efficiency of each gene may play a greater role in determining expression. This idea is supported by the positive correlation between noise strength and expression at high TF concentration, as would be expected from theory\textsuperscript{16}. In addition, differences in burst frequency cannot account for the measured single-cell expression distributions at high TF concentration. These data suggest that the dominant sources of gene-to-gene variability in expression change with TF concentration: at low TF concentration burst frequency (the ability of the promoter to recruit TF) differences dominate, whereas at high TF concentration burst size (transcriptional and translational efficiency) differences dominate.

Overall, our results show that the relationship between expression and noise is highly dependent on the promoter architecture. One implication of this finding is that using only a single TF, evolution can implement diverse expression profiles with unique noise properties. The fact that repression of ZRT2 by Zap1 is evolutionarily conserved suggests that there is an advantage to this ability.

4.5 Materials and Methods

4.5.1 Yeast strains

Construction of promoter-YFP strains was performed as described previously\textsuperscript{38}. In brief, a master strain, his3::TEF2pr-mCherry-YFP-NatMX4 was created in the background strain Y8205\textsuperscript{55} by homologous recombination. Each promoter-YFP strain was created by integration of a PCR product containing the native promoter along with URA3 as a selection marker. Integration by homologous recombination upstream of YFP was confirmed by DNA sequencing and by identical expression and growth of multiple independent transformants.
4.5.2 Creation of promoter variants
To introduce, alter and remove elements within ~150bp of the ATG we developed a method in which an existing URA3-promoter-YFP cassette is amplified over multiple rounds of PCR. In each subsequent round a new primer is used that further extends the product towards the YFP and optionally introduces designed mutations. Thus multiple site-directed mutations can be tiled onto the 3’ end of the promoter. All promoter variants were confirmed by DNA sequencing.

4.5.3 Yeast growth and expression and noise measurements
Yeast strains were grown overnight to saturation in YPD, resuspended in low zinc medium, and grown overnight to saturation in media lacking zinc. Cultures were then diluted 1:40 in water and 6ul of this dilution was inoculated in 130ul of low zinc media supplemented with various concentrations of zinc. Cells were grown in round-bottom 96well plates shaking at 30°C a minimum of 12 hours, to approximately 5*10^6 cells / ml prior to expression measurements. Flow cytometry was performed on a BD LSRII. YFP and mCherry were excited using 488nm and 561nm lasers and emitted light was collected with 525/50nm and 610/20nm band-pass filters, respectively. There is no detectable spillover of YPF or mCherry into the other channel using these filters and lasers. Expression and noise measurements were collected calculated using the ratio of YFP over mCherry for each cell. To obtain expression and noise measurements from each well a relatively homogenous subpopulation of mostly G1 cells was chosen by gating on forward and side scattering. Wells containing fewer than 500 cells after gating or with obvious contamination were excluded from further analysis. Noise was quantified as the variance over the mean squared and noise strength as the variance over the mean.

4.5.4 Kinetic model of activation and repression
We model stochastic promoter state switching, transcription and translation using the master equation following the approach described by Sanchez et al., which in turn is an adaptation of previous derivations of the master equation for gene regulation.

In this description of promoter regulation, transcription factor (TF) binding and unbinding events determine the transitions between promoter states. A change in transcriptional activity occurs when a transition is made to a state with differing transcription rate. Each promoter state is modeled to have a low (including zero) or relatively high transcription rate to describe in-active (“off”) or active (“on”) states respectively. Translation occurs in bursts with the probability of a burst described by a geometric distribution. The master equation (in matrix notation) takes the form:

$$\frac{d}{dt} \hat{p}(n) = \left[ \hat{K} \frac{R}{1+b} \hat{R} - n\hat{I} \right] \hat{p}(n) + \hat{R} \sum_{\beta=1}^{n} h(\beta) \hat{p}(n-\beta) + (n+1)\hat{I} \hat{p}(n+1)$$

(1)
Where \( \bar{P} \) is the vector of probabilities of having \( n \) proteins in the cell for each promoter state. \( d/dt \bar{p}(n) \) describes the time evolution of these probabilities. \( \hat{K} \) is the matrix of promoter state transition rates, where \( \hat{K}_{ij} \) is the rate of transitioning from state \( j \) to state \( i \) and \( \hat{K}_{ii} \) is the sum over all outgoing rates from \( i \) times \(-1\). \( \hat{R} \) is the diagonal matrix of transcription rates with \( \hat{r} \) on the diagonal (\( \hat{R}_{ii} = \hat{r}_i \)), where \( \hat{r}_i \) is the transcription rate of state \( i \). \( \hat{I} \) is the identity matrix. \( b \) is the average burst size (proteins produced per mRNA). \( \delta \) is the protein degradation rate. \( h(\beta) \) describes a geometric distribution and is the probability of producing a burst of size \( \beta \).

To derive the mean protein abundance and variance we solve this system at steady state, thus for \( d/dt \bar{p}(n) = 0 \). We get mean protein abundance:

\[
\langle n \rangle = \frac{b \hat{r} \bar{m}_0}{\delta}
\]

(2)

Where \( \bar{m}_0 \) is the zeroth partial moment of the distribution of mRNA abundance and is the solution to:

\[
0 = \hat{K} \bar{m}_0
\]

(3)

We can get noise \( (\sigma^2/\mu^2) \) and noise strength \( (\sigma^2/\mu) \) by deriving:

\[
\langle n^2 \rangle = (1 + b)\langle n \rangle + \frac{b \hat{r} \bar{n}_1}{\delta}
\]

(4)

Where \( \bar{n}_1 \) is the first partial moment of the distribution of protein abundance and is the solution to:

\[
0 = (\hat{K} - \delta \hat{I}) \bar{n}_1 + b \hat{R} \bar{m}_0
\]

(5)

Variance \( (\sigma^2) \) is:
Promoter sequence determines the relationship between expression level and noise

\[ Var(n) = \langle n^2 \rangle - \langle n \rangle^2 \]  

(6)

Therefore noise \((\sigma^2/\mu^2)\) becomes:

\[ \langle \eta^2 \rangle = \frac{(1+b)\langle n \rangle - \langle n \rangle^2 + b \bar{r} \bar{n}_{(1)}}{\langle n \rangle^2} \]  

(7)

And noise strength \((\sigma^2/\mu)\):

\[ \langle F \rangle = \frac{(1+b)\langle n \rangle - \langle n \rangle^2 + b \bar{r} \bar{n}_{(1)}}{\delta} \]  

(8)

We solve the master equation for a number of different promoter architectures, where we define \(\hat{K}\) and \(\hat{R}\) for each system to describe the specific promoter states, the transitions between them and the transcriptional activity of each state.

Case ZRT1:

We describe gene expression and regulation of ZRT1 using a two state kinetic scheme that represents switching between an active (ON) and inactive (OFF) promoter configuration. We assume that on switching (with rate \(K_{on}\)) and off switching (with rate \(K_{off}\)) are a function of binding and unbinding respectively of the Zap1 transcriptional activator at the ZRT1 promoter. The Zap1 bound (ON) state is transcriptionally active (with rate \(r_1\)) and we allow the unbound (OFF) state to have some (leaky) transcriptional activity (with rate \(r_2\)). \(\hat{K}\) and \(\hat{r}\) thus become:

\[ \hat{K} = \begin{pmatrix} -K_{off} & K_{on} \\ K_{off} & -K_{on} \end{pmatrix} \]  

(9)

\[ \hat{r} = \begin{pmatrix} r_1 & r_2 \end{pmatrix} \]  

(10)
The promoter off rate ($K_{off}$) is a function of Zap1 binding affinity and therefore assumed to be constant. We describe the promoter on rate ($K_{on}$) with a Hill-equation (see Eq.11) with $K_{min}$ and $K_{max}$ as the minimum and maximum possible rates respectively, $[Zn]$ as the zinc concentration (induction level), $[Zn]_{mid}$ as the zinc concentration that gives half maximal induction and $H$ as the Hill-coefficient, i.e. the sensitivity of $K_{on}$ to changing zinc.

$$K_{on} = K_{min} + \frac{(K_{max} - K_{min})}{1 + ([Zn]/[Zn]_{mid})^H}$$

(11)

Case ZRT2:

ZRT2 is both activated and repressed by Zap1. We model Zap1 binding ($K_{on}$), unbinding at the activating binding site ($K_{off}^{ac}$) and unbinding at the repressive binding site ($K_{off}^{rep}$). We describe $K_{on}$ with a Hill-equation as a function of $[Zinc]$ (see Eq.11). Transcription can occur from each state (i.e. expression is leaky), however we assume that the state where the activator, and not the repressor, is bound has the highest transcriptional activity (with rate $r1$). $\hat{K}$ and $\hat{\rho}$ therefore become:

$$\hat{K} = \begin{pmatrix}
-(K_{off}^{ac} + K_{on}) & K_{on} & 0 & K_{off}^{rep}
\end{pmatrix}$$

$$K_{off}^{ac} = \begin{pmatrix}
-K_{off}^{ac}
\end{pmatrix}$$

$$\hat{\rho} = \begin{pmatrix}
r1 & r2 & r3 & r4
\end{pmatrix}$$

(12)

(13)

Case ADH1:

ADH1 is activated by Rap1 and repressed by Zap1. We model the switching between the active (Rap1 bound) and repressed (Zap1 bound) states with the two-state kinetic scheme that we used to model ZRT1 activation by Zap1. Repression of ADH1 by Zap1 occurs through (one of) two hypothesized mechanisms: nucleosome occlusion and transcription factor dislodgement. We model both mechanisms by a subtle difference in the dynamics of repression.

Case ADH1, nucleosome occlusion:

Zap1 mediated intergenic transcription may repress ADH1 by causing nucleosome deposition in the otherwise nucleosome free core promoter region, thus preventing
the activator (Rap1) or PolII from binding. We model this mechanism by changing $Kon$ as a function of induction, as occlusion (accessibility) effectively changes the on-switching rate of the promoter. More specifically we model $Kon$ as a sigmoid that is a function of [Zinc] (see Eq.14), where increasing zinc increases $Kon$ (as Zap1 decreases) while $Koff$ is constant.

$$Kon = K_{\text{min}} + \frac{(K_{\text{max}} - K_{\text{min}})}{1 + (\frac{[\text{Zinc}]}{[\text{Zinc}]_{\text{mid}}})^n}$$

Case ADH1, transcription factor dislodgement:

In the hypothesized TF dislodgement mechanism repression occurs as the interfering transcript (caused by upstream Zap1 binding) dislodges the already bound activator (Rap1) or the PolII holoenzyme. This would effectively change the rate at which the promoter switches from on into the off state, hence we model this by changing $Koff$ as a (sigmoidal) function of [Zinc] (see Eq.15), while keeping $Kon$ constant.

$$Koff = K_{\text{min}} + \frac{(K_{\text{max}} - K_{\text{min}})}{1 + (\frac{[\text{Zinc}]}{[\text{Zinc}]_{\text{mid}}})^n}$$

4.5.5 Model fitting and robustness analysis

We fit the kinetic scheme's analytical solutions of mean and noise of protein abundance to the measured mean and noise of fluorescence intensity (See supplementary information for a detailed description of the fitting procedure and parameter constraint). The goodness of fit is measured by the root mean squared error (distance, $\Delta$) of both mean and noise.

To investigate the hypothesized effect of promoter mutations we simultaneously fit the model to wild type and mutant promoters while only one parameter is allowed to change between the fits.

We distinguish between two hypothesized ADH1 regulatory mechanisms by fitting two models to the measured data. While ADH1 nucleosome occlusion gives a better fit than TF dislodgement, both models give have a good fit to the data. To investigate if nucleosome occlusion is a significantly better fit to the data, for each fit found by optimization we perform 2-fold perturbations on each parameter. By looking at the distribution of fits after perturbation we get an idea of which model is more robust and as a result is more likely to be the correct model. We find that the NO model is significantly more robust than the TD model.
4.5.6 Sensitivity analysis of the kinetic model

To measure the sensitivity of the kinetic model to variations in each parameter, we performed a rigorous sensitivity analysis procedure described by Marino et al. 60 that uses the Latin Hypercube Sampling based Partial Rank Correlation Coefficient (LH5-PRCC). First, we uniformly sampled 10,000 instances of the model (without fitting), each with a unique parameter setting sampled from the entire allowed parameter space using Latin Hypercube sampling, and evaluated each of these models by measuring the distance to the experimental data. Next, we calculate the Partial Rank Correlation Coefficient of the parameter value to the model score (goodness of fit) to measure the sensitivity of that parameter. We find that the NO model is significantly less sensitive to parameter variation than the TD model (See Figure 4.14 and Figure 4.15 for sensitivity analyses of the ZRT1 and ADH1/3 models respectively).

4.5.7 Simulating coupled and decoupled activation and repression

To investigate the effect on gene expression noise of activation and repression by the same TF (coupled) versus activation and repression by two different TFs (decoupled), we extended the ZRT2 kinetic model to incorporate fluctuations in the concentration of TF. We use a kinetic scheme in which on-switching rates for activator and repressor can be changed independently (Konact and Konrepr, see Eq.16). These rates are determined by the distributions of activator TF and repressor TF, respectively. We therefore assume that the on-switching rates have Gamma distributions with a constant shape parameter (burst size) and varying scale parameter (burst frequency) as the activator and repressor are induced. The means of the on-switching rates were chosen to be in the range of our model fits (10^{-3} to 10^{1}), which are in accordance with previously determined promoter switching rates. 28,40,49 Next, we calculate the shape parameter of the distribution of Kon using the ratio between the mean of the measured protein distribution and the chosen mean of the on-switching rates (ratio of ~10^{0}), which we apply to the measured noise strength (~10^{0}). This gives a shape parameter value of around 10^{-1}. Because the product of shape and scale is equal to the mean, we can compute the values of the scale parameter (10^{2} to 10^{3}). We note that the qualitative result of predicted noise reduction (Figure 4.6B) is robust to 10-fold changes (up and down) of both shape and scale parameter of the distributions of Konact and Konrepr. Finally, to simulate coupled and decoupled activation and repression we sampled the on-switching rates of the activator and repressor from a bivariate gamma distribution with a normalized covariance of zero (decoupled) or one (coupled). Each sample represents a single cell with some amount of activator and repressor, and therefore some Konact and Konrepr. We then computed the mean expression for each ‘cell’ using the analytical solution of the ZRT2 model and calculated the predicted noise that results from fluctuations of activator and repressor as the squared coefficient of variation (sensitivity to TF fluctuations, \eta^{2+\tau}).
Promoter sequence determines the relationship between expression level and noise

\[
\hat{K} = \begin{pmatrix}
-(K_{off}^{rel} + K_{on}^{rel}) & K_{on}^{rel} & 0 & K_{off}^{rel} \\
K_{off}^{rel} & -K_{on}^{rel} - K_{on}^{rel} & K_{off}^{rel} & 0 \\
0 & K_{on}^{rel} & -(K_{on}^{rel} + K_{off}^{rel}) & K_{off}^{rel} \\
K_{off}^{rel} & 0 & K_{on}^{rel} & -(K_{off}^{rel} + K_{off}^{rel}) \\
\end{pmatrix}
\]  
(16)

4.6 Financial Disclosure
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4.8 Author Contributions
The authors have made the following declarations about their contributions: Conceived and designed the experiments: LBC DD ES. Performed the experiments: LBC DD. Analyzed the data: LBC DD. Conceived the models: DD LBC. Wrote the paper: LBC DD ES PS JK.
4.9 References

Promoter sequence determines the relationship between expression level and noise.

4.10 Supplemental information

4.10.1 Flow cytometry with a dual-reporter dual-gene system can accurately measure promoter-specific changes in intrinsic noise

It is important to note that quantification of changes in burst size and burst frequency through changes in noise assumes an intrinsic measurement of expression in which variability in expression between cells is a result of stochasticity at the promoter and not at the general transcriptional/translational machinery. Any extrinsic influences will distort the noise-burst frequency and noise strength-burst size relationships. In order to correct for ‘extrinsic noise’ (expression capacity) we used a dual-gene system with the promoter of interest driving YFP and a constitutively expressed mCherry, and use the ratio between YFP and mCherry as the measured expression level. Because mCherry expression does not change with zinc concentration (Figure 4.8), this normalization can be used to remove significant amounts of extrinsic variability consistently throughout induction. To further eliminate extrinsic variation we perform stringent gating on forward scatter, side scatter, and mCherry expression, which results in the removal of ~70-90% of the cell population. Finally, we note that we quantify changes in noise, not absolute noise, and therefore we only need to accurately measure changes in intrinsic noise, and not intrinsic noise itself. For these reasons we therefore expect that the reported YFP/mCherry measurements accurately reflect a combination of pathway specific and promoter specific noise. Furthermore, we believe that pathway specific noise represents a small fraction of the reported noise, and that this does not affect our results. The strongest evidence is that the noise for all promoters does not change uniformly with zinc or with measured ZAP1 promoter driven YFP. For example, noise of ADH1 and ADH3 is high at low zinc concentrations, while noise of ZRT2 and ZRT1 is low at low zinc concentrations. Furthermore, our ability to measure differences in noise between different promoter and ATG context mutants (which, presumably, do not affect pathway-specific noise), strongly suggests that intrinsic noise is the dominant source of noise in our measurements.

4.10.2 Flow cytometry with an Elowitz style dual-reporter measures intrinsic noise similar to our dual-gene dual-reporter system

To validate our claim that the dual-gene dual-reporter system measures intrinsic noise, we constructed an Elowitz style dual-reporter for the ZRT2 promoter. Figure 4.4d (inset) shows that intrinsic noise as a function of induction gives the characteristic curve that we observed using our dual-gene system.

4.10.3 Sensitivity analysis

To investigate the robustness and sensitivity of the parameters of our model we perform a rigorous sensitivity analysis procedure described by . First, we sample 10,000 instances of the model, each with a unique parameter setting. This sampling is done using a Latin Hypercube, to ensure uniform sampling in the multidimensional parameter space of our model. Next we do a rank transformation
on the sampled instances using the distance of the model instances to the measured data (for both mean expression and noise) and quantify the correlation that each parameter has with the goodness of fit measure. Figure 4.14 shows the scatter plots and correlation coefficient for each parameter of the ZRT1, ADH1 NO/TD and ZRT2 models.

We note that the NO model is significantly less sensitive than the TD model. The most sensitive parameter in the model is the scaling parameter. This parameter converts measured fluorescence to number of proteins and therefore we would expect this parameter to influence model outcome hugely.

### 4.10.4 Robustness analysis

Barkai et al. describe a method of model validation that is based on the robustness of a model to parameter perturbations. The idea is that a free parameter model will often have a parameter setting that fits the data, regardless of it being the right model. However, biological systems are noisy and parameter values are not fixed but fluctuate around some mean. These fluctuations do not prevent the biology from working. Therefore a model of a biological system should be robust to parameter perturbations. A model that is not robust is likely not the right model.

We proposed two different models for ADH1 repression. We found that although the NO model gave a better fit, both models have good fits to the measured data. To investigate which of the models is more robust we performed a perturbation analysis. For each of 100 best fits, and for each parameter, we sampled 10,000 perturbations in the range of -2 to 2 fold change. We did this for both alternative models. Figure 4.3E shows the cumulative distribution of the goodness of fit (distance of model to data) for both models. We find that the NO model is significantly more robust than the TD model and therefore more likely to be the correct model for ADH1 repression.

### 4.10.5 Notation and choice of parameter values

While we do not know the precise values of many of the parameters in our model, biologically realistic bounds can be estimated for most parameters. We chose to set the upper and lower bounds of each free parameter as loose as reasonable, and we obtained good fits to data for a wide range of parameters. This robustness to parameter variation shows that the promoter-switching model accurately replicates the experimental data despite both uncertainties in the values of individual biochemical values and in experimental error.

Here follows a description of all parameters used in the model and their respective value constraints:

(All rate parameters are in minute$^{-1}$)

**Protein degradation** ($\delta$). YFP is highly stable. We therefore assume that protein degradation comes only from dilution. While the population doubling time does
increase with as the zinc concentration drops below 150 μM, per-cell rates of protein production also decrease with decreasing growth rate. For reasons of simplicity we chose to fix δ. This approximation does not affect our conclusions. We set the degradation rate (δ) to ln(2)/90 = 0.0077. Where 90 is the average measured doubling time (in minutes) in our experiments.

**Burst size (b).** Burst size is the average number of YFP molecules produced from each mRNA molecule. This parameter combines both translation and mRNA degradation assuming geometrically distributed protein abundance. Lu et al. found that ~80% of yeast proteins have between 100-10,000 proteins per mRNA. We therefore set the bounds for expression of the yeast codon-optimized YFP to be 100 ~ 10,000 proteins/mRNA.

**Transcription rate (r1, r2, r3, r4).** The transcription rate is the rate of production of stable mRNAs while the promoter is in each respective state. Experimentally measured transcription rates combine both on and off promoter states. Therefore, the total rate of transcription for a gene is the sum, for all states, of the fraction of time spent in that state times the transcription rate in that state. The upper bound for expression rate is between 4 transcripts/minute and 10 transcripts/minute. We note that these rates represent the combination of on and off promoter states. We set the transcription rate bounds to be 0-1 for off states, and 2-8 for on states.

**Promoter switching rates (Kon, Koff).** To estimate the minimum rate with which a promoter can switch between off and on we used expression data from the repressed GALI promoter. We assume that this promoter is off most of the time, but occasionally switches on. Cai et al. measured a burst frequency of 0.2 events per cell-cycle for the GALI promoter on a plasmid with a copy number of 10-40. We therefore set the minimum switching rate (Kmin, see Eq.11,14,15) to be 10^-4 (0.2 transcripts/cell-cycle / 90 minutes/cell-cycle / 20 plasmid copies/cell). High Kon values for a TF means that the TF is essentially always bound, while high Koff values mean that the TF is never bound. We know that the off-switching rate for a promoter can be relatively rapid, as transcription of POL1 occurs as a series of uncorrelated events, each resulting in the production of a single mRNA molecule. This implies that the promoter off-switching rate can be high enough so that only a single transcription event occurs each time the promoter switches on. We therefore set the maximal switching rate (Kmax) to be 10.

**Promoter switching as a function of [zinc].** We describe promoter switching with a hill equation as a function of [zinc]. This function has four parameters: Kmin and Kmax (described above), and [Zn]mid and H, which is the [zinc] of half maximal K value (threshold) and Hill-coefficient (sensitivity) respectively. We allow [Zn]mid to take on any value that is within the input [zinc] range – between 1 and 3000 uM zinc. H can be any positive value, where zero is a linear response and any non-zero positive value a sigmoidal response.
Scaling of YFP to proteins/cells (S). To convert measured fluorescence into molecules of YFP we determined how the measured YFP/mCherry ratio for each promoter at 3mM zinc compares to measured protein molecules / cell [Wang:2012eu]. We find a normalized fluorescence to protein scaling of: YFP/mCherry * 0.0146 = Protein (molecules/cell). We allow the scaling to be a free parameter, within a range of 10 fold up and down from the determined scaling value.

4.10.6 Parameter values of best fits
ZRT1 (ATG):

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kmin</td>
<td>10^-5.5014</td>
</tr>
<tr>
<td>Kmax</td>
<td>10^-0.9406</td>
</tr>
<tr>
<td>ZNmid</td>
<td>10^-3.8179</td>
</tr>
<tr>
<td>H</td>
<td>10^-0.5778</td>
</tr>
<tr>
<td>Koff</td>
<td>10^-0.7332</td>
</tr>
<tr>
<td>r1</td>
<td>10^-0.0867</td>
</tr>
<tr>
<td>r2</td>
<td>10^-0.3211</td>
</tr>
<tr>
<td>b1 (each ATG variant has its own b)</td>
<td>550</td>
</tr>
<tr>
<td>b2</td>
<td>843</td>
</tr>
<tr>
<td>b3</td>
<td>1100</td>
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<td>b5</td>
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<td>b6</td>
<td>1312</td>
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ADH1 NO:

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<tbody>
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<tr>
<td>Kmax</td>
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<tr>
<td>ZNmid</td>
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<tr>
<td>H</td>
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<tr>
<td>Koff</td>
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<tr>
<td>r1</td>
<td>10^-0.0331</td>
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<tr>
<td>r2</td>
<td>10^-2.0000</td>
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<tr>
<td>b</td>
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ADH1 TD:

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<tbody>
<tr>
<td>Kmin</td>
<td>10^-2.8635</td>
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</table>
Promoter sequence determines the relationship between expression level and noise

Kmax | $10^{0.5724}$
---|---
ZNmid | $10^{1.9606}$
H | $10^{3.2449}$
Kon | $10^{1.8496}$
r1 | $10^0$
r2 | $10^2$
b | $10^{2.4002}$

ZRT2:

Kmin | $10^{-6.0000}$
---|---
Kmax | $10^{5.3546}$
ZNmid | $10^{2.0913}$
H | $10^{0.1965}$
5 Kon_rep (ratio Kon_act to Kon_rep) | $10^{1.2548}$
Koff_act | $10^{0.4506}$
5 Koff_rep (ratio Koff_act to Koff_rep) | $10^{-0.1878}$
r1 | $10^{0.3281}$
r2 | $10^{5.0000}$
r3 | $10^0$
r4 | $10^{0.2273}$
b | $10^{3.1694}$

4.10.7 Supplementary Table 1. Cloned promoter sequences lengths

<table>
<thead>
<tr>
<th>Promoter</th>
<th>Cloned sequence length (upstream of ATG)</th>
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<tbody>
<tr>
<td>ADH1</td>
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<tr>
<td>ADH3</td>
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<tr>
<td>ADH4</td>
<td>1000</td>
</tr>
<tr>
<td>DPP1</td>
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<tr>
<td>ENO1</td>
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<td>ZAP1</td>
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<tr>
<td>ZRC1</td>
<td>1000</td>
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</tbody>
</table>
4.11 Supplemental figures

Figure 4.8: Zap1 regulated targets change expression in response to changes in zinc concentration. Shown is measured mean expression for three different Zap1 targets (ZAP1, ZRT1, ADH4 and TKL2) showing quantitatively different basal (high zinc, low Zap1) expression levels as well as different induction curves. Also shown is expression of YFP from a truncated ENO2 promoter that lacks the two Zap1 binding sites, and is thus insensitive to changes in zinc concentration. For all YFP data, error bars show the standard deviation from at least three biological replicates. Shown in red is measured expression of TEFpr-mCherry from all of the data from all strains shown.
Figure 4:9: Predicted Zap1 occupancy of each promoter is predictive of each activated promoter’s change in expression in response to increasing Zap1. The range of expression (lowest to highest measured values) graphed against the predicted number Zap1 molecules bound to a 500bp window from -600 to -100 relative to the transcription start site for each promoter. A thermodynamic model of promoter TF occupancy [37] shows that the measured Zap1 dose-response curve for each promoter highly correlates with the predicted occupancy of Zap1 at each promoter, suggesting that the number and affinity of Zap1 binding sites plays a large role in determining each promoter-specific dose-response curve. To identify sequence features in each promoter, we used a thermodynamic model in which Zap1 binding along the promoter sequence is determined by the concentration of the TF, its measured sequence specificities, and competition with nucleosomes [37]
Figure 4.10: The correlation of noise and noise strength with mean expression for all measured Zap1 targets throughout the induction. The correlation between expression and noise (A) and expression and noise strength (B) is shown for all measured expression data for each Zap1 target promoter. For each target expression is normalized between zero and one. The mean Spearman correlation coefficient for all promoters is shown.
Figure 4.11: Gene-specific slopes are significantly different from each other. Distributions show the mean-noise slopes obtained by bootstrapping all biological replicate experimental measurements of noise ($\eta^2$) and mean expression ($\mu$) and fitting the line $\eta^2=\mu k$ 1000 times for each promoter. The distributions show that the slope ($k$) values are significantly different and that slope value estimation is robust for most promoters.
Figure 4.12: Only part of the change in expression due to ATG context variants can be explained by changes in mRNA level. Shown are the fold differences in protein and mRNA between start codon context variants of the ZRT1 promoter. In order to determine if changes of the four nucleotides upstream of the ATG lead to differences in mRNA levels we performed RT-qPCR on three ATG context variants plus the WT ZRT1 promoter. Because mCherry is expected to be constant between the different strains, YFP/mCherry ratios are used as measurements for both fluorescence and mRNA. In addition, because both measurements are in arbitrary units, we cannot compare numeric values directly. However, both measurements are linear, and therefore ratios relative to a common control (the CTTT strain) can be compared. We find a 2.1 fold change in protein levels and a 1.3 fold change in mRNA levels. In addition we observe no correlation between mRNA and protein. These results are consistent with previous data [Yun, Laz, Clements & Sherman MM 1996] showing that the start codon context can change protein expression without affecting mRNA levels.
Figure 4.13: A model in which zinc concentration changes promoter $Kon$, and ATG context variants change $b$, best explains the experimental data. There are many possible regulatory mechanisms by which zinc concentration and ATG context may change expression of ZRT1. In order to determine which regulatory mechanism best fits our data we fit the model represented by kinetic scheme in Fig 2a to our data 12 times. In each time, we mandated that a different pair of regulatory mechanisms be used to fit the induction of the ATG context variants. We find that a model in which the induction increases $Kon$, and ATG context variants change $b$ (first column) obtains the best fit to data. We note that similar regulatory mechanisms in which ATG context variants change burst size (columns 2 and 3) obtain fits that are almost as good. In contrast, a model in which zinc changes promoter off switching rate ($K_{off}$) never obtains as good a fit to the data, and is only capable of obtaining a reasonable fit to the data when ATG context variation changes the rate of transcription.
Figure 4.14: Sensitivity analysis of the ZRT1 model. To determine how sensitive the ZRT1 model is, we used LHS-PRCC (see materials and methods). We find that the fit of the model to data is highly only to sensitive only to $S$, a scaling factor we use to convert measured YFP/mCherry per cell signal to number of YFP protein molecules per cell. (A) Density scatter plots from LHS sampling of the parameter space show how the fit to data (y-axis) changes as a function of each parameter (x-axis). Correlations of the data in (A) are shown together for comparison in (B).
Figure 4.15: Sensitivity analysis of both proposed ADH1 models shows that the nucleosome occlusion (NO) model is less sensitive to parameter variation than the TF dislodgment (TD) model. To determine how sensitive each of the ADH1 models are we performed LHS-PRCC sensitivity analysis. (A) Density scatter plots from LHS sampling of the parameter space show how the fit to data (y-axis) changes as a function of each parameter (x-axis). Correlations of the data in (A) are shown together for comparison in (B). The NO model is far less sensitive to variation in biological parameters.
Figure 4.16: Gating of the ZRT2pr dual reporter causes a 10-fold reduction in extrinsic noise. For each cell, mCherry is plotted against YFP for one induction point from the ZRT2pr dual reporter. Extrinsic noise was reduced by gating using either a very wide (black) or very narrow (red) gate on forward and side scatter.