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A rule-based kinetic model of RNA polymerase II C-terminal domain phosphorylation

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The complexity of many RNA processing pathways is such that a conventional systems modelling approach is inadequate to represent all the molecular species involved. We demonstrate that rule-based modelling permits a detailed model of a complex RNA signalling pathway to be defined. Phosphorylation of the RNA polymerase II (RNAPII) C-terminal domain (CTD; a flexible tail-like extension of the largest subunit) couples pre-messenger RNA capping, splicing and 3’ end maturation to transcriptional elongation and termination, and plays a central role in integrating these processes. The phosphorylation states of the serine residues of many heptapeptide repeats of the CTD alter along the coding region of genes as a function of distance from the promoter. From a mechanistic perspective, both the changes in phosphorylation and the location at which they take place on the genes are a function of the time spent by RNAPII in elongation as this interval provides the opportunity for the kinases and phosphatases to interact with the CTD. On this basis, we synthesize the available data to create a kinetic model of the action of the known kinases and phosphatases to resolve the phosphorylation pathways and their kinetics.

1. Introduction

Ordinary differential equation and stochastic modelling techniques are applicable to RNA processing and signalling pathways. However, a significant obstacle must be overcome: the explosion of entities and reactions that follows when RNA species, their precursors, complexes and states are represented. Rule-based modelling has previously been shown to address combinatorial complexity in protein interactions [1,2]; here, we explore the potential of this new methodology for modelling RNA metabolic pathways. Rule-based models in the Kappa language that we adopt [3] are simulated stochastically, and thus the approach accounts for low molecule numbers and the discrete states that molecules can adopt. We discuss transcription by RNA polymerase II (RNAPII) as an example of a complex system that can be modelled in detail using a rule-based approach.

We present a novel rule-based model of transcription that includes the phosphorylation states of multiple heptapeptide repeats in the representation of the RNAPII enzyme. The model represents the kinases and phosphatases that act on these repeats during initiation, elongation, 3’ end maturation and RNAPII recycling. We demonstrate that this model can help explain both genome-wide patterns of RNAPII phosphorylation on yeast genes, and changes in phosphorylation that take place when an intron-containing yeast reporter gene is induced.

All protein-coding genes and most small non-coding RNAs are transcribed by RNAPII [4]. The C-terminal domain (CTD) of the largest subunit of RNAPII contains the heptad repeat, YnS2P3T4S5P6S7, and functions in coupling transcription to mRNA processing and chromatin modifications [5,6]. In yeast, the CTD consists of 26 repeats of this heptad (52 in humans), each of which can be phosphorylated at the serines (S) in positions 2, 5 and 7, as well as at the tyrosine...
Phosphorylation of serines 2, 5 and 7 (Ser2, Ser5 and Ser7) on the CTD of RNAPII. (Y; position 1) and threonine (T; position 4). In addition, the proline (P) at position 6 (at least) undergoes isomerization between cis- and trans-configurations, yielding a substrate with a vast potential for signalling [7]. Synthetic CTD peptides have been shown to bind proteins with a wide range of functions, including Set2, Ssd1, Ppr40, Hrr25 and Ess1, with a specificity that varies significantly with the pattern of serines 2 and 5 phosphorylation on the heptad [8]. CTD phosphorylation facilitates recruitment of capping factors at the 5′ end of genes, 3′ end processing factors and certain splicing factors in vivo [7,9].

In this paper, we synthesize the in vivo, in vitro and biochemical evidence on the action, substrate and context specificity of the known CTD kinases and phosphatases to construct a kinetic model of the RNAPII CTD cycle, focusing on the phosphorylation of serines 2, 5 and 7. Formalizing the reactions and kinetics of this key RNA signalling pathway has the benefit of making all assumptions explicit and easy to scrutinize. The Kappa rule-based approach to modelling that we adopt [3] makes the assumptions particularly easy to communicate, and simplifies the process of extending the model to include additional factors and modifications as they are discovered.

Chromatin immunoprecipitation (ChIP) analysis is the prevalent technique for mapping the extent of RNAPII phosphorylation with respect to genes in vivo. Modelling can assist the interpretation of ChIP data by accounting for the substrate specificity of the antibodies used [10], and by distinguishing the changes in phosphorylation due to signalling from those due to RNAPII accumulation should the polymerase pause on the DNA. The development of the formal model was motivated by the desire to interpret genome-wide ChIP data [11], and kinetic data linking CTD signalling to a splicing-related pause observed in yeast [12]. Data from each of these experiments are presented to illustrate the use of the model.

2. The C-terminal domain kinases and phosphatases

The process of messenger RNA transcription, the phases of the CTD cycle and the various states that an individual heptapeptide repeat can adopt in each phase are illustrated in figure 1. In addition to summarizing the rule-based model, figure 1b serves as a reference for the following survey of the actions of the kinases Kin28, Ctk1, Bur1 and Srb10, and the phosphatases Rtr1, Fcp1 and Ssu72 on an individual heptapeptide are indicated by a change of state of one of Ser2, Ser5, Ser7 to P from U, or vice versa. The specific actions of these proteins at the promoter, during elongation, at the 3′ UTR and on the free RNAPII (recycling) must be distinguished. Higher reaction rates are indicated by broader arrows. Two reactions supported by biochemical evidence but not in vivo data are indicated by dashed arrows.

Figure 1. Phosphorylation of serines 2, 5 and 7 (Ser2, Ser5 and Ser7) on the CTD of RNAPII. (a) Ser5 and Ser7 are phosphorylated at the promoter by TFIIH/Kin28. Ser2 phosphorylation increases towards the 3′ end of the gene and is a requirement for 3′ end maturation. Serine phosphorylation has been linked to cotranscriptional splicing (the excision of an intron, in red, is illustrated). (b) The actions of the kinases Kin28, Ctk1, Bur1 and Srb10, and the phosphatases Rtr1, Fcp1 and Ssu72 on an individual heptapeptide are indicated by a change of state of one of Ser2, Ser5, Ser7 to P from U, or vice versa. The specific actions of these proteins at the promoter, during elongation, at the 3′ UTR and on the free RNAPII (recycling) must be distinguished. Higher reaction rates are indicated by broader arrows. Two reactions supported by biochemical evidence but not by in vivo data are indicated by dashed arrows.
distinct site that may mediate its effect on elongation [16]. The
dephosphorylation of Ser5 by Fcp1 after the termination of
transcription, in vitro, can be explained by the lower specificity
of Fcp1 for a ternary complex of DNA, RNAPII, TFIH in com-
parison with that for free RNAPII [17]. Consequently, Fcp1 is
modelled as acting on Ser2→P during elongation and on both
Ser2→P and Ser5→P during recycling.

The Ser2 kinase Bur1 is recruited to CTD repeats of
elongating RNAPII phosphorylated on Ser5. Bur1 augments
the major Ser2 kinase (Ctk1) and is capable of phosphorylating
CTD repeats at Ser2, when Ctk1 is inactivated [18]. Thus,
during elongation, Bur1 acts only on repeats phosphorylated
on Ser5, whereas Ctk1 potentially acts on three of the four
possible CTD states (figure 1b).

Rtr1 is a Ser5 phosphatase that localizes to DNA coding
regions [19]. Rtr1 regulates the transition in the phosphoryl-
ation of the CTD that takes place between the promoter,
where serines 5 and 7 are phosphorylated, and around
1000 nt from the transcription start site (TSS), by which point
Ser2 phosphorylation has increased and Ser5 phosphorylation
has diminished [19]. Rtr1 mutants show a large increase in Ser5
phosphorylation, indicating a loss of phosphatase activity, and
an increase in Ser2 phosphorylation in the coding region rela-
tive to the wild-type. If Ser2 phosphorylation primarily
occurs through repeats that are unphosphorylated at both ser-
ines 2 and 5 (i.e. through the state that results from Rtr1
phosphatase action downstream of the promoter) then Ser2
phosphorylation would be expected to reduce considerably,
rather than increase in a Rtr1 mutant. This finding, together
with the lack of biochemical evidence to support the generation
of Ser2 phosphorylation from doubly unphosphorylated
repeats, indicates that Rtr1 may compete kinetically with the
Ctk1 and Bur1 CTD kinases to regulate the Ser5 to Ser2
transition by removing their preferred substrate.

A recent report has failed to identify an active site on Rtr1
[20]. Experiments to demonstrate CTD phosphatase activity
were unsuccessful which suggests that Rtr1 may have a
non-catalytic role in CTD dephosphorylation [20]. Thus we
consider a complex involving Rtr1 to mediate the Ser5→P to
Ser5→U reaction, and refer to this complex as Rtr1 for simpli-
city. In summary, during elongation Rtr1 acts on both CTD
states where Ser5 is phosphorylated (figure 1b).

Ssu72 is a component of the cleavage/polyadenylation
factor complex that localizes predominantly to the 3′ end of
genes [21], and a CTD phosphatase capable of dephosphory-
lating Ser5 on singly and doubly phosphorylated repeats in vitro [22]. Ssu72 may dephosphorylate the CTD at the
3′ end of genes to recycle the RNAPII into an initiation-
competent form [22]. It is also proposed to be a transcription
elongation factor, mediated by its activity as a CTD phospha-
tase and its physical interaction with TFIIB, TFIID, TFIH and
RNAPII [23].

A recent study by Bataille et al. [11] confirms Kin28 to be a
serine 7 (Ser7) kinase [24] and Ssu72 to be a Ser7 phospha-
tase. Antibodies specific for Ser2 (H5 and 3E10), for Ser5
(3E8 and H14) or for Ser7 (4E12) were used to compose ‘metagene’ profiles of CTD phosphorylation across the yeast
genome. The patterns of Ser5 dephosphorylation and Ser2
phosphorylation are the same in long and short genes: the
changes in phosphorylation are a function of distance from the
transcription start site (or equivalently, of time spent in
elongation) rather than as a function of the proportion of
the gene transcribed. The level of Ser2 phosphorylation is
less at the end of short genes than at the end of long genes
owing to the reduced opportunity for kinases to act. Serines
5 and 7 are phosphorylated with the same kinetics near the
promoter. Serine 5 phosphorylation reduces over the sub-
sequent 750 nt, while Ser2 phosphorylation accumulates with slower kinetics to reach a plateau around 1000 nt
from the TSS [11]. The data suggest that the polyA site is
the trigger for the dephosphorylation of serines 5 and 7
at the 3′ end [11].

3. Methods

A model of the events in RNAPII elongation necessarily includes
the positions that RNAPII may occupy on the DNA (for example,
to match target ChiP sites), and must account for the possible
patterns of phosphorylation that each heptapeptide repeat can
adopt. If N positions of RNAPII on the DNA are included
in the model, and assuming only two repeats of serines 2 and 5
are represented (giving 2^2 × 2^5 = 16 combinations of
phosphorylation states), the number of species of RNAPII to
be modelled is 16 × N, and the number of possible transitions
is 16 × 4 × (N – 1) (assuming each of the 16 states can change
in four possible ways). In a conventional model, rather than represen-
ting a single species with multiple states, we must represent
multiple species, resulting in unacceptable model complexity.

Rule-based modelling in Kappa [3,25,26] provides a solution
to this problem as rules, representing binding/unbinding reac-
tions, need only match a partial description of the state of an
agent, and only modify a subset of the bonds between agents.

Entities are referred to as agents in Kappa, and written
RNAPII() DNA(). Agents have named sites through which
they interact; for example, p can represent the promoter
in DNA: DNA(p); and agents form complexes by creating bonds
between sites. To state that RNAPII is bound to DNA at the
promoter we can write RNAPII(a!1), DNA(p!1), where the bond
1 is shared by sites a and p (expressed as a!1 and p!1 within
the respective agents).

Sites can have states, for example, RNAPII phosphorylated
at Ser5 but not Ser2 would be written RNAPII(Ser2~U,Ser5→P),
rules can depend on the phosphorylation of RNAPII at one site,
and can include or ignore the state of other sites and the position
of the RNAPII on the DNA as required. The binding of Rtr1
to RNAPII at the Ser5 site, and the subsequent dephosphorylation
of this site and release of Rtr1 can be expressed by two rules of
the form precondition -> postcondition @ rate as follows:

Rtr1(a), RNAPII(a!_,e,Ser5→P) ->
Rtr1(a!1), RNAPII(a!_,e,Ser5→P!1) @0.1
Rtr1(a!1), RNAPII(Ser5~P!1) ->
Rtr1(a), RNAPII(Ser5~U) @1

The first rule specifies the substrate specificity (Rtr1 binds
phosphorylated Ser5) and limits the applicability of the rule to
the coding region where RNAPII is bound to some site on the
DNA() (by the inclusion of RNAPII(a!_) excluding the 3′
UTR (by the inclusion of RNAPII(e) as e is always bound
when RNAPII is at the 3′ UTR). The substrate specificity of the
other kinases and phosphatases may place conditions on Ser2,
Ser5 and Ser7 as necessary. (The complete set of 56 rules for
phosphorylation is provided in the electronic supplementary
material, file phosphorylation.ka.)

The proposed model represents 80 positions on the DNA that
can be occupied by RNAPII. These are encoded as 80 binding sites
on the DNA agent. Each site has an associated rule that specifies
when RNAPII moves to the subsequent site. The phosphorylation
rules apply to RNAPII independently of the site it occupies on the
DNA, hence combinatorial explosion is avoided. In contrast, a
4. Results

A detailed Kappa model of 219 rules describing the entire transcription pathway has been constructed (see figure 1, §6 and electronic supplementary material, file model.tar.gz). Defining the transcription pathway allows rules specifying the interaction of the kinases and phosphatases with sites on the CTD of RNAPII to take the context of the CTD into account as it progresses through the transcription cycle. As discussed earlier, these proteins may act on the CTD in specific ways at the promoter, during elongation, at the 3' UTR and on free RNAPII, and hence the model must distinguish these contexts. The states that an individual heptad may adopt, and the transitions between them, are indicated in figure 1 for each of the four contexts.

We now consider the phosphorylation patterns in two different kinds of yeast data: metagene profiles obtained from genome-wide data [11], and kinetic data obtained from the induction of a reporter gene [12]. As the reporter gene contains a single intron (for the study of splicing), we focus on single-intron genes in the genome-wide analysis.

4.1. Metagene profiles

Genome-wide profiling of highly expressed genes shows Ser5~P to reduce rapidly towards a steady state as RNAPII leaves the promoter, and Ser2~P to increase [11]. We find that this pattern also occurs in yeast genes with a single intron where the intron is long (300–600 nucleotides; figure 2). This subset of the genome is highly expressed on average. The distributions of exon, intron and gene lengths in

![Figure 2. Ser2, Ser5 and Ser7 phosphorylation in the coding regions of single-intron genes. (a) Model predictions of the ratios of Ser2~P, Ser5~P and Ser7~P to RNAPII. (b–d) Scatter plots of the ratios of Ser2~P, Ser5~P and Ser7~P to RNAPII genome-wide for genes with introns between 300 and 600 nucleotides in length derived from the data in [11]. (See electronic supplementary material, figure S1 for intron and exon length distributions.) Data sampled from the promoter region (100 nucleotides upstream from the transcription start site (TSS)) are plotted in green, exon 1 (blue), the intron (red) and exon 2 (grey). In (b–d), the black lines indicate the model simulations of (a) thresholded and scaled to best approximate the measured phosphorylation.](rsif.royalsocietypublishing.org)
single-intron yeast genes are plotted in the electronic supplementary material, figure S1, and the CTD phosphorylations of all highly expressed genes are presented as a scatter plot in the electronic supplementary material, figure S2, for comparison with figure 2b–d (data from [11]).

The Kappa model of the CTD cycle is capable of reproducing the observed pattern of Ser2, Ser5 and Ser7 phosphorylation under different assumptions about the ability of Ctk1 to act as a Ser5 kinase during elongation (a controversial issue in RNAPII biology). These reactions have been observed in vitro, but in vivo evidence is lacking. To explore the inclusion, or otherwise, of the possible Ctk1 Ser5 kinase activity in the model, we examine the fit of four versions of the model to the genome-wide data. We consider models that lack any Ctk1 Ser5 kinase activity (see the electronic supplementary material, figure S3), include Ctk1 Ser5 kinase activity from the Ser2~U, Ser5~U, Ser7~P substrate (see the electronic supplementary material, figure S4), include Ctk1 Ser5 kinase activity from the Ser2~P, Ser5~U, Ser7~P substrate (see the electronic supplementary material, figure S5), and finally include Ctk1 Ser7 kinase activity from both Ser2~U, Ser5~U, Ser7~P and Ser2~P, Ser5~U, Ser7~P substrates (see the electronic supplementary material, figure S6).

To widen the basis of model comparison, we also add three assumptions: that Rtr1 binds faster than, at the same rate or slower than the rate of which Ctk1 and Bur1 bind when acting as Ser2 kinases. For Rtr1 to mediate the Ser5~P to Ser2~P transition as proposed by Mosley [19], it is to be expected that the Rtr1 binding rate would be faster than that of the competing Ser2 kinases, and hence that the fit of the model to the data should be better for faster Rtr1 binding.

Qualitatively, the loss of Ser5~P and gain of Ser2~P along the gene is maintained under the alternative modelling assumptions. However, the kinetics of these changes differ considerably when the model predictions are mapped to the genome-wide data. The possible Ser5~P kinase reaction from substrate Ser2~P, Ser5~U, Ser7~P to Ser2~P, Ser5~P, Ser7~P does not improve the fit of the model to the data, either by itself or in conjunction with that from Ser2~U, Ser5~U, Ser7~P, and is not included in the model. In contrast, the addition of the reaction from Ser2~U, Ser5~U, Ser7~P to Ser2~P, Ser5~P, Ser7~P quantitatively improves the fit of the model to the data and maximizes the dynamic range of predicted values that correspond to observed values. Consequently, this Ctk1 Ser5 kinase reaction is included in the model henceforth.

The predictions of the model (figure 2a) are indicated by the solid black lines in the scatterplots of the genome-wide data in figure 2b–d. Ser7~P is predicted to be constant as no Ser7 kinase or phosphatase has been proposed to act during elongation, and hence there are no rules for the modification of this residue. Figure 2d shows that a number of intron-containing genes have elevated Ser7~P at the TSS and on exon2, which may indicate a regulatory role [30]. A general tendency for Ser7~P to increase along the gene can be seen in the electronic supplementary material, figure S2 (potentially attributable to Bur1 [31]).

In the Kappa model, changes in phosphorylation are not dependent on the length of the gene, but on the time RNAPII spends in elongation which provides the opportunity for the kinases and phosphatases to act. Hence the model provides mechanisms to explain genome-wide observations, including the proposed regulatory role of Rtr1 [19].

4.2. Sensitivity analysis

The model specifies that the rate at which Bur1 and Ctk1 bind to sites on RNAPII is half that of Rtr1 binding, and consequently Rtr1 tends to bind first and reduce the extent of Ser5~P. Nonetheless, some RNAPII heptads are directly phosphorylated on Ser2 by Bur1 and Ctk1, and Ser5~P can be restored by Ctk1 allowing these kinases to act. When these binding rates are reduced, few heptads are phosphorylated on Ser2 and, as this is a requirement for 3’ end maturation, RNAPII accumulates at the 3’ end. In contrast, when the binding rates are increased, Ser2~P and Ser5~P reach their steady-state values within 150 nt of the promoter (that is, more rapidly than observed).

The effects of varying the two parameters that govern the binding and release rates of the kinases and phosphatases that act during elongation were explored systematically by sensitivity analysis. Figure 3 presents heatmaps showing the difference of simulated RNAPII, Ser2~P and Ser5~P with respect to simulations based on the parameters used in the baseline model (figure 2). The binding rate $p_0$ (see §6) was varied over two orders of magnitude (0.01–1) and the unbinding rate $p_3$ over four orders of magnitude (0.1–1000). The binding rates for all kinases were kept at a constant $p_0$ acts as a ‘meta-parameter’.
Similarly, all unbinding reactions occur at $p_3$. All other rates were kept constant, most importantly, those governing the progression of RNAPII along the gene as this defines the window of opportunity for CTD modifications. This computational experiment determines the robustness of the predictions to parameter values.

The heatmap in figure 3a shows that the predicted profile of RNAPII is insensitive to the phosphorylation parameters except with values for $p_0$ of 0.01 or less: should there be no Ser2 phosphorylation at the 3′ end of the gene as the result of the low binding rate, the model requires RNAPII to pause as 3′ end maturation cannot proceed without Ser2~P and this results in an accumulation of RNAPII at the 3′ end. The heatmaps for Ser2~P and Ser5~P show a greater sensitivity for these predictions on values of $p_0$ greater and less than those of the baseline model. The value of $p_3$ does not have an impact on the predictions while $p_3$ is 10 times the value of $p_0$ or greater. Lower values of $p_3$ combined with greater values of $p_0$ give rise to predictions comparable with those of the baseline model as the duration of the binding/unbinding sequence is comparable. Thus, the potential trade-off between binding rates illustrates the importance of direct measurement of binding constants (e.g. as in [32]) as their values cannot be inferred with confidence from model fitting.

4.3. Kinetic profiles
Having established that the typical profiles of intronless and intron-containing genes are similar at steady state, and that the Kappa model reproduces this profile, we apply the model to data from the induction of a single gene. Data from individual genes often provide insights into regulation and opportunity for more detailed investigations than genome-wide datasets, which typically reflect steady-state conditions.

The ChIP data on a splicing-related pause in the Ribo1 yeast gene provide an opportunity to explore the relationship between RNAPII density and serine phosphorylation [12]. Briefly, Ribo1 is a chimeric yeast gene that contains the single intron from the ACT1 gene and the 3′ end processing signal from PGK1. The reporter gene is integrated in the genome, transcribed under the control of a doxycycline-responsive promoter in a doxycycline-inducible strain of Saccharomyces cerevisiae. Cells in culture respond to doxycycline in synchrony, and provide a mechanism whereby Ser5~P and the density of RNAPII are each normalized to their respective values on induction, and hence are not comparable to each other on an absolute scale. (b) Model simulation of Ribo1 with a pause introduced 600 nucleotides downstream of the TSS. (a) Real and (b) simulated pauses in RNAPII lead to an accumulation of RNAPII that reverses the typical reduction in the absolute level of Ser5~P and raises the level of Ser2~P.

5. Conclusions
Messenger RNA transcription is a complex process with many regulatory interconnections acting through RNAPII subunits. The proposed model of the CTD cycle accounts for both the substrate specificity of the CTD kinases and phosphatases, and the contexts that influence their recruitment. The model was created by surveying and reconciling the evidence in the literature, and this leads to the novel observation that Rtr1 regulates the Ser5~P to Ser2~P transition by removing the substrate for the Ser2 kinases on many (but not all) heptads. We demonstrate that the model reproduces the prototypical pattern of phosphorylation observed from the promoter, through to the 3′ UTR, based solely on the binding kinetics of the kinases and phosphatases with the CTD substrate. Modelling suggests that Ctk1 may have a Ser5 kinase activity (as has been demonstrated in vitro) as this improves the fit of the model to the data, and provides a mechanism whereby Ser5~P can be reduced considerably while retaining the possibility of restoring this state as a substrate for the known Ser2 kinases.

Undoubtedly there are other, yet to be discovered, interactions between these proteins and RNAPII, and with each other. The addition of new rules, or the refinement of existing rules, will allow such interactions to be added to the rule-based model in a straightforward fashion. For example,
were it to be shown that Bur1 recognizes the bivalent mark Ser5~P + Ser7~P as hypothesized in [24], the rules for Bur1 binding could be strengthened to represent this finding.

Rule-based modelling addresses combinatorial expansion in systems modelling, and enables the simulation and analysis of reactions whose formal analysis would otherwise be intractable [2,27,28]. The rule-based approach is being extended to multi-level modelling [29,33], where model entities can be nested, and downward and upward causation between different levels is possible, and to the representation of spatial relations in models [34]. Thus, the approach holds great potential at theoretical and practical levels.

6. Material and methods

A detailed Kappa model of 219 rules describing the entire transcription pathway has been constructed (see the electronic supplementary material, file model.tar.gz). This model represents PIC assembly, followed by pre-mRNA capping, elongation, 3' end maturation and polyadenylation, and release of the mature mRNA [4,6], and is based on a validated stochastic model of a yeast reporter [35]. The complex processing represented in the model yields realistic behaviour in terms of time required for RNAPII to transcribe the simulated gene, and the net synthesis rate of one mature RNA every 4 s previously observed in a yeast reportor [36]. The transcription initiation rules (see the electronic supplementary material, file transcription.ka) define how Activator and Mediator bind to DNA, followed by RNAPII and TFIIH. The phosphorylation of serines 5 and 7 of RNAPII, and capping of the mature transcript and RNAPII are defined (see the electronic supplementary material, file maturation.ka). Pcf11, synthesis of the polyA tail, binding of Rtt103 and release of polymerase as those behind are prevented from progressing.

Initiation of elongation (see the signature.ka) define how Activator or Mediator bind to DNA, followed by RNAPII and TFIIH. The phosphorylation of serines 5 and 7 of RNAPII, and capping of the mature transcript and RNAPII are defined (see the electronic supplementary material, file maturation.ka). Pcf11, synthesis of the polyA tail, binding of Rtt103 and release of polymerase as those behind are prevented from progressing. Rules for the maturation of the RNA through the binding of Pcr11, synthesis of the polyA tail, binding of Rtt103 and release of the mature transcript and RNAPII are defined (see the electronic supplementary material, file maturation.ka). Pcr11 binding requires RNAPII Ser2 to be phosphorylated. Maturation occurs over 20 sites on DNA (pA1→pA20) that RNAPII occupies in sequence until release. The rules for phosphorylation of the CTD are defined in the electronic supplementary material, file phosphorylation.ka. These specify the actions of Bur1, Ctk1, Fcp1, Rtr1 and Ssu72 as described in the text. The binding rates for these proteins are p0, p0/2 or p0/10 (denoted by phosph0, phosph1 and phosph2, respectively, in the electronic supplementary material, file phosphorylation.ka). The rate for release is p3 (denoted by phosph3 in the electronic supplementary material, file phosphorylation.ka). The binding of Ctk1 to RNAPII sites ser2a and ser2b (representing Ser2 on heptad repeats a and b) is defined in rules binds1 and binds2 below. The combination of RNAPII sites e, a creates a condition that is only met while RNAPII is transcribing the coding region of the gene, namely, e is unbound and a is bound to something (the model allows RNAPII sites a and b to bind to DNA). The subsequent unbinding reactions are release1 and release2. Serine 5 is phosphorylated on release. Two heptapeptide repeats are modelled as this number is sufficient for generating steady-state estimates of phosphorylation from three discrete levels (0, 1 or 2 repeats phosphorylated) obtained from 500 stochastic simulations with good reproducibility and acceptable standard deviation.

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