

# A rule-based model of Base Excision Repair.

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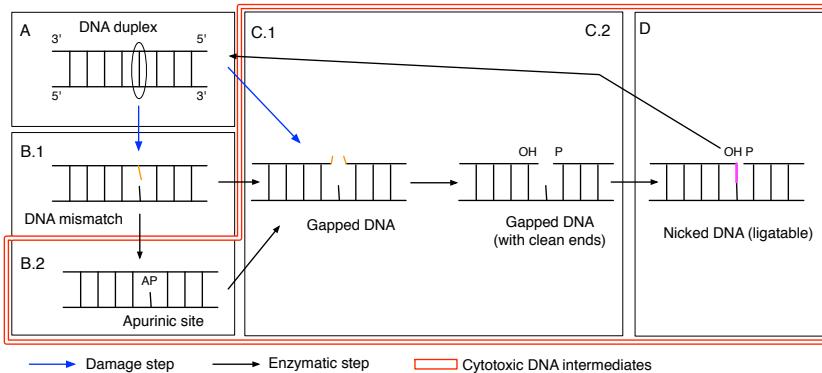
**Abstract.** There are ongoing debates in the DNA repair community on whether the coordination of DNA repair is achieved by means of direct protein-protein interactions or whether substrate specificity is sufficient to explain how DNA intermediates are channeled from one repair enzyme to the other. In order to address these questions we designed a model of the Base Excision Repair pathway in Kappa, a rule based formalism for modeling protein-protein and protein-DNA interactions. We use this model to shed light on the key role of the scaffolding protein XRCC1 in coordinating the repair process.

## 1 Introduction

A modern trend of Systems Biology sees high-throughput experiments being set up, resulting in an inflation of the publication volume in Biology and medicine<sup>3</sup>. As a consequence it has become impossible for a biologist, specialist of a certain system, to remain up-to-date with all relevant information pertaining to her topic of interest. To counter for this problem, biologists make an intensive use of review papers which are regularly published on a given system<sup>4</sup>.

As an alternative to classical reviews, which are static objects with a natural obsolescence, we propose to use rule-based modeling [1, 2] to designing formal updatable reviews that are at the same time executable [3, 4].

More specifically, this paper presents the first executable model of the *Base Excision Repair* (BER) pathway that includes protein-DNA interactions. The outline of the paper is as follows: in Section 2 we briefly present the BER system (reviewed for instance in Ref. [5, 6]), we discuss our tools and methods in Section 3 and we present some results in Section 4.



**Fig. 1.** Abstract Base Excision Repair pathway.

## 2 Base Excision Repair

Figure 1 gives a possible *unfolding* of the *abstract* Base Excision Repair (BER) pathway: Various types of damage (A) may modify a nucleotide (oxydation, deamination) and induce a mismatch in the DNA (B.1) or a single strand break (C.1). Enzymes from the family of DNA Glycosylase may recognize mismatches and excise the modified base, creating an Apurinic (AP) site (B.2). Enzymes with AP endonuclease capacity may open DNA at the lesion locus, generating a single strand break. End cleaning enzymes may prepare the 3' and 5' moieties for the polymerase step (C.2). Eventually DNA ligases can seal the DNA backbone (D) to retrieve a well-formed DNA duplex.

This scenario corresponds to only one possible *unfolding* of BER and the story could diverge at various points: for instance a direct single strand break may induce the loss of more than one nucleotide. Also when the end cleaning enzymes fail to prepare a proper substrate, some polymerases may synthesize more than one new nucleotide and trigger an alternative *long patch repair* pathway.

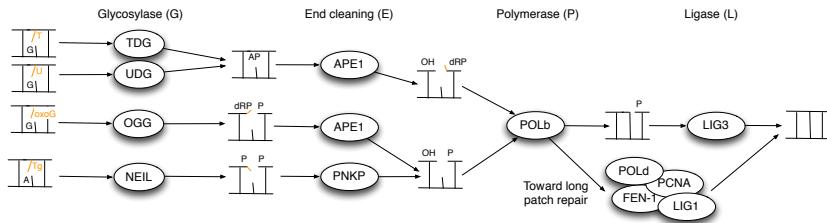
Furthermore this map is *abstract* as several enzymes may engage in the various catalytic steps that are described. For instance the transition from (B.1) to (B.2) or directly (C.1) is realized by different glycosylases, the identity of which depends on the type of nucleotide modification that has occurred. Ten glycosylases have been found so far in higher eukaryotic cells, we modeled the activity of four of them and used UDG (for uracil excision in U/G mismatches)

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<sup>3</sup> In 2000 about 500,000 papers were published in Biology and Medicine. In 2012 this number had escalated to 1,000,000 (source Pubmed.org).

<sup>4</sup> There are 520 review papers mentioning Base Excision Repair in the title or abstract (source Pubmed.org)

as default enzyme in our simulations. We give a more concrete description of the BER enzymes in Figure 2.



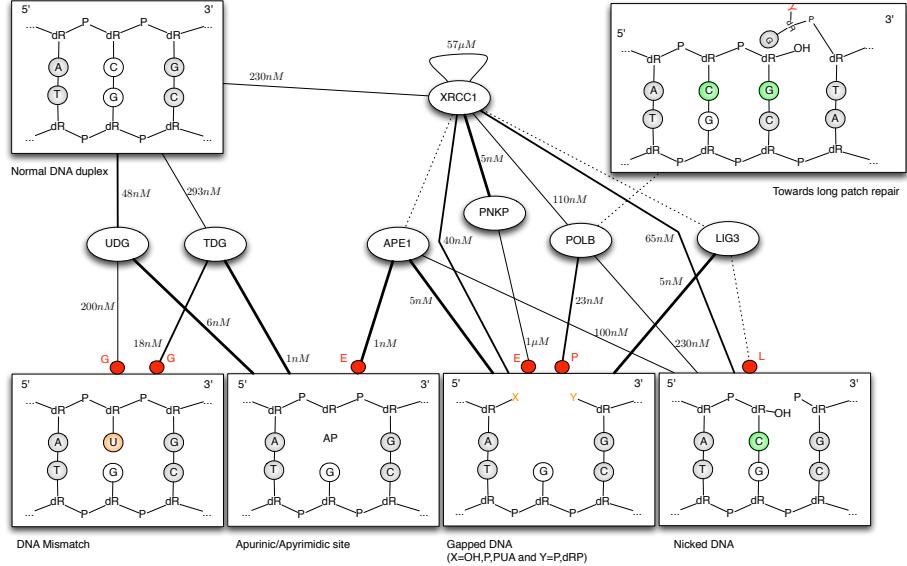
**Fig. 2.** A more concrete view of BER.

Together, Figure 1 and Figure 2 give an almost complete view of BER and ODE based models have been proposed to formalize this part [7, 8]. However they only reveal the catalytic steps that transform DNA, and do not take into account important proteins that have no direct enzymatic activity but are important to coordinate the repair process. More importantly, BER enzymes do not behave as typical enzymes that often have little affinity for their products. We will see that most enzymes of Fig. 2 have a non negligible affinity for various DNA intermediates, and this feature is probably critical for channeling DNA products to the next enzyme in the pathway, through protein-protein or protein-DNA interactions [9].

This last point is the key to our modeling project, since (1) it is difficult to model as it entails a combinatorial explosion in the number of variables of the model, and (2) these complex interactions can give us insight into the coordination of the repair pathway i.e passing the baton between the different enzymes of Fig. 2.

Coordination is not so much an issue of efficiency, since high enzymatic turnover would probably yield a faster global repair rate. Figure 1 shows that the intermediate substrates (B.2), (C.1), (C.2) and (D) of the repair pathway are cytotoxic. In a nutshell, AP sites (a missing base), gapped and nicked DNA induce genomic instability and BER has probably evolved so as to prevent these substrates from being accessible to enzymes that may trigger apoptosis if such damage is detected (such as Topoisomerases).

The main protein that is believed to act as a coordinator of BER is the X-Ray Cross Complementing protein 1 (XRCC1). Although it has no known catalytic activity, this protein can bind to all BER enzymes that are downstream of the glycosylase. It is noteworthy that proteins interacting with XRCC1 are also those operating on the cytotoxic substrates. It is therefore assumed that XRCC1 acts as a scaffolding protein that coordinates BER, as well as a patch over the lesion to protect it from the environment.



**Fig. 3.** The contact map of the BER model. Lines ending with a red circle signify catalytic activity. The red letters map to steps in Fig. 2.

We give Figure 3, the protein-protein and protein-DNA contact map that we inferred from the literature. The strength of the interaction is depicted here through various line widths and the dissociation constant ( $K_d$ ) is shown. Dotted lines represent known interactions the  $K_d$  of which could not be found. This map makes apparent that several proteins compete for the same family of substrates. For instance APE1 and  $\text{POL}\beta$  tend to bind to gapped DNA. Since DNA substrates are complex polymers one cannot assume that binding to a particular DNA substrate is exclusive of any other binding. Notably, it is assumed that XRCC1 can stay connected to gapped DNA throughout the whole repair process.

### 3 Methods

**Data.** We have assembled qualitative (mechanisms of action) and quantitative (concentration, dissociation constant, catalytic rates) data from 59 papers pertaining to BER or to its participants<sup>5</sup>. For lack of space we do not include the complete references in the present paper but they are included in the model repository as an annotated bibtex file.

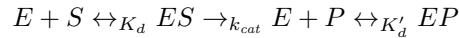
<sup>5</sup> We thank Dr. S. Mitra (Houston Methodist Hospital), Dr. D. M. Wilson III (National Institute on Ageing), Dr. S. H. Wilson (NIEHS, NIH) and Dr. K. Caldecott (Univ. Sussex), for direct discussions which directed us to relevant publications.

Quantitative data are particularly difficult to find. For testing the model under plausible conditions, we extracted BER protein copy numbers from Ref.[10] which evaluates protein concentration for HeLa cell extracts. Note that we expect repair accuracy to be robust with respect to variation of protein numbers, as the chromatin state might create local concentration effects on DNA [11].

Catalytic rates for enzymatic activities are easier to find although product inhibition (enzyme with a non negligible binding affinity for its product), which is typical of BER, complicates the interpretation of the rates which are often given in terms of steady state kinetics. More precisely, as can be seen in Fig. 3, most BER enzymes exhibit a scheme of the form:



with a reasonably low  $K'_d$ . Experimental catalytic rates  $k_{cat}$  are measures of the production speed of  $P$ , which, in the above case, is slowed down by product inhibition. Some experiments [12–14] give a measure of  $k_{chem}$  for the above scheme, but most paper will only give  $k_{cat}$  (which underestimates the hidden  $k_{chem}$ ). Whenever  $k_{chem}$  is not available we assumed the scheme:



which simply lets the enzyme rebind to its product according to the given  $K'_d$  when available.

Yet, dissociation constants for protein-protein and protein-DNA interactions are also complicated to find. Whenever facing unknown data, we used the rate of a similar interaction. For instance we assumed that all glycosylases have the same facilitated diffusion on DNA, using data published for hOGG1 [15].

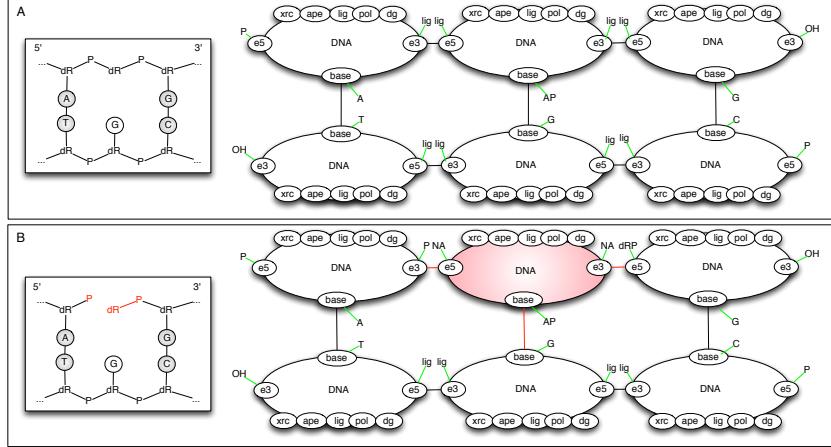
Importantly, KASIM requires concrete on and off rates for complex formation. When only steady state dissociation constants are known, we used a default  $k_{on}$  (randomized in simulations) to deduce  $k_{off}$  ( $K_d = k_{off}/k_{on}$ ). Importantly, complex formation occurring in a uni-molecular fashion are assumed to be fast ( $k_{uni} = 10^4 s^{-1}$ ). Whenever the kinetic data was unknown for a given reaction, we used a default kinetic rate  $k$  (taken from realistic values for the type of reaction), and randomized it uniformly in the interval  $[\frac{k}{10}, 10 * k]$ . The list of complete kinetic rates is provided in Supp. data<sup>6</sup> A.2.

**Rule-based modeling.** The input language of KASIM simulator is Kappa [2], a (rule-based) graph rewriting language, the syntax of which is recalled in Supp. Data A.1.

Figure 4 illustrates how DNA polymers are encoded in our model: (A) an apurinic -AP- site and (B) a one nucleotide gapped DNA. The ports on top of DNA nodes allows one to connect various BER enzymes. Internal states are mapped to the corresponding port via a green edge. There are a few key modeling features to notice. Our DNA nodes denote either physical DNA bases, or an

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<sup>6</sup> <https://github.com/ramdiv/ber-model/blob/master/ber.pdf>

**Fig. 4.** Two oligonucleotides in Kappa.

empty slot on DNA. Hence a DNA node can either be part of the (physical) DNA backbone, as in the encoding of (A), or be a place holder for enzymes that recognize holes on DNA, as in the red part of the encoding of substrate (B). In the latter substrate, one may read from the Kappa encoding that the middle node is in fact a gap on DNA because it is no longer ligated to the 3' and 5' neighbors (internal state of the e3 and e5 ports set to NA). Notice that the e3 port of upper left DNA node of part (B) is set to P, indicating that the 3' end of the gap bears a phosphate group (that can be for instance recognized by APE1).

**Simulation.** Simulations of the model were conducted on a dedicated HP server (1.60GHz/4-cores) with 128 GB of RAM. Iterations of simulations under various parameters and randomization of kinetic rates are piloted by a python script (included in the model repository) which requires python 2.7 and simplejson. KASIM 3.5 is necessary to run simulations and is available on github<sup>7</sup>.

Unless specified otherwise, simulation results are obtained as the average of 16 simulations ran on a DNA substrate of 100,000 bp randomly generated according to the distribution: (0.6 : GC, 0.4 : AT). In addition to the DNA substrate, initial number of BER enzymes are 2200 UDG; 30,000 APE1; 3,000 POL $\beta$ ; 400 LIG3 and 1200 XRCC1 (ratios are taken from Ref. [10] and normalized so that the lowest number of potentially modeled enzyme (TDG) is greater than 100). Simulations are run without any damage on DNA for 2 seconds (biological time unit) after which we induced 2% of cytosine deamination, generating U/G mismatches on DNA. Simulations are conducted until complete repair is observed, on average after  $t \sim 6$  minutes (biological time). Efficiency of simulations is discussed in Supp. Data A.3.

<sup>7</sup> <https://github.com/jkrivine/KaSim>

**Causality analysis.** Causality analysis of Section 4 were performed by enabling KASIM’s causal tracking of the ligation rule, on simulations on a 25K bp DNA substrate. From a single simulation, KASIM computed 189 causally ordered traces (causal flows) leading to the ligation steps occurring between t=20s and t=80s (ligation activity is constant after 10s, data not shown). We then performed weak compression [16] that quotiented the number of causal flows to 122 (36% compression) incompressible scenarios<sup>8</sup>.

## 4 Results

**A Kappa model of Base excision Repair including protein-DNA interactions.** We have assembled the first executable model of BER that incorporates protein-protein and protein-DNA interactions as well as enzymatic activity on DNA substrates. The actual model contains the interaction rules for 4 glycosylases (UDG, TDG, NEIL and OGG1); the AP-endonuclease (APE1) and the end cleaning enzyme PNKP; the polymerase (POL $\beta$ ) and the ligase (LIG3). The interactions with scaffold protein XRCC1 is also included. Various DNA substrates for initial conditions can be generated using a python script.

The complete model as well as python and json configuration files are accessible as a github repository<sup>9</sup> and can be tested under the requirements specified in the Methods section. The repository also contains the complete listing of rules with a short description, separated by file<sup>10</sup>. The Kappa syntax, used to define the rules is described in Supp. data.

The rules of the model essentially implement the catalytic activities reported in Fig. 2 as well as the interactions depicted in Fig. 3 using the encoding of DNA shown in Fig. 4.

We used the module `sanity.ka` to detect invariant violation during the elaboration of the model. We included this file in the model repository because it can be used to test further invariants. The idea is to write rules of the form  $I \rightarrow I + Err()$  where  $I$  is an invariant violation (for instance an invalid DNA polymer) and  $Err()$  is an “error” protein. We can then use the causality analysis features of KASIM to have an explanation on how  $Err()$  (and hence the invariant) was created.

*DNA Glycosylase.* For the simulations presented in the present paper, we focused on the UDG glycosylase the behavior of which is similar to TDG, the other mono-functional glycosylase of the pathway (although rates differ greatly, TDG having a very slow chemical step, followed by a strong product binding).

The rules pertaining to glycosylases interactions are given in the `DG.ka` and `sliding.ka` files of the model repository. We describe below the main ones, and we give their graphical description in Fig. 5.

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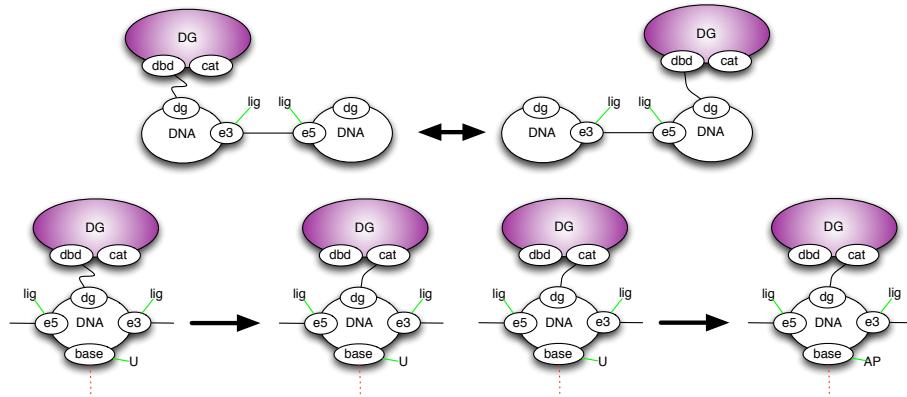
<sup>8</sup> Incompressible flows are partial ordering of simulation events with the property that all the events are (transitively) a cause of the final event (the observable) and no trace containing a strict subset of these events may still contain the observable.

<sup>9</sup> <https://github.com/ramdiv/ber-model>

<sup>10</sup> <https://github.com/ramdiv/ber-model/blob/master/list.md>

**Table 1.** Kappa files of the model. The notation (+x) indicates additional rules not used in simulations.

File name	rules #	binding and catalytic activity
DG.ka	13 (+7)	Glycosylase activities for UDG, TDG, NEIL and OGG1
APE1.ka	11	AP, gaped and nicked DNA; pho'diesterase; endonuclease
POLb.ka	17 (+4)	gaped and nicked DNA; dRP lyase; polymerase
PNKP.ka	3	gaped DNA; phosphatase
XRCC1.ka	29 (+2)	XRCC1 (in xrcc_dimer.ka), APE1, POLb, PNKP, LIG3 and DNA
LIG3.ka	8	gaped and nicked DNA ; ligase
sliding.ka	2 (+1)	facilitated diffusion on DNA (approx. in alter_sliding.ka)
damage.ka	3	deamination and direct single strand break
sanity.ka	(+9)	sanity check



**Fig. 5.** Main DNA Glycosylase rules.

Glycosylases are assumed to use *facilitated diffusion* on DNA (i.e. a random walk on DNA) to find mismatches at a rate that exceeds what can be achieved by mere random binding after diffusion in the nucleus (see for instance [15]).

Facilitated diffusion can be simply modeled by a rule that enables the glycosylase to "jump" to the next base 3' or 5' to its current position:

```
'slide 3' DG(dbdb!1, cat), DNA(dg!1,e3!2), DNA(dg , e5!2) -> \
    DG(dbdb!1, cat), DNA(dg , e3!2), DNA(dg!1,e5!2) @ 'DG_DNA_slide'
'slide 5' DG(dbdb!1, cat), DNA(dg , e3!2), DNA(dg!1,e5!2) -> \
    DG(dbdb!1, cat), DNA(dg!1,e3!2), DNA(dg , e5!2) @ 'DG_DNA_slide'
```

Note that sliding is no longer possible when the *cat* port (representing the catalytic pocket of the DG) is bound (to a mismatch), as a consequence of the following rule:

```
'UDG anchors DNA mismatch' \
    DNA(e3~lig?, base~U?, dg!1, e5~lig?), DG(dbdb!1, cat, type~U) -> \
```

```
DNA(e3~lig?, base~U?, dg!1, e5~lig?), DG(dbdb, cat!1, type~U) \
@ 'DG_DNA_anchors'
```

Once anchored on the mismatch, the DG flip the faulty base into its catalytic pocket for excision:

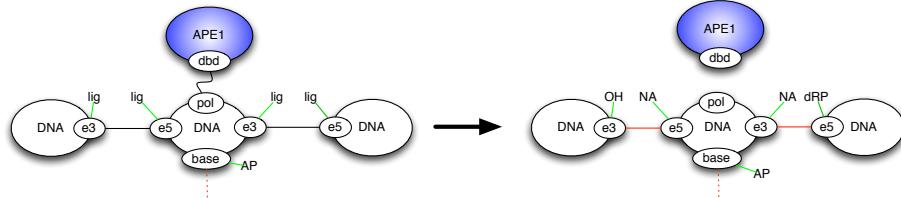
```
'UDG mismatch excision' \
DG(cat!1, type~U), DNA(e3~lig!_, dg!1, base~U?, e5~lig!_) -> \
DG(cat!1, type~U), DNA(e3~lig!_, dg!1, base~AP?, e5~lig!_) \
@ 'UDG_excision'
```

An important point of the above rule is that the DNA node is still ligated to the 3' and 5' neighboring base pairs after the nucleotide excision. This is a key difference with bi-functional glycosylases such as OGG that perform both excision and endonuclease in the same step (not included in simulations):

```
'OGG mismatch excision' \
DG(dbdb!1, cat, type~OGG), DNA(e5~lig!0), \
DNA(e3~lig!0,dg!1,base~oxoG?,e5~lig!2),DNA(e3~lig!2) -> \
DG(dbdb, cat!1, type~OGG), DNA(e5~PUA!0), \
DNA(e3~NA!0, dg!1,base~AP?, e5~NA!2 ),DNA(e3~P!2) \
@ 'OGG_excision'
```

Notice also that in both cases the DG remains bound to its product.

*APE1 endonuclease.* We present here the main rule pertaining to APE1 activity and give its graphical representation in Fig. 6.

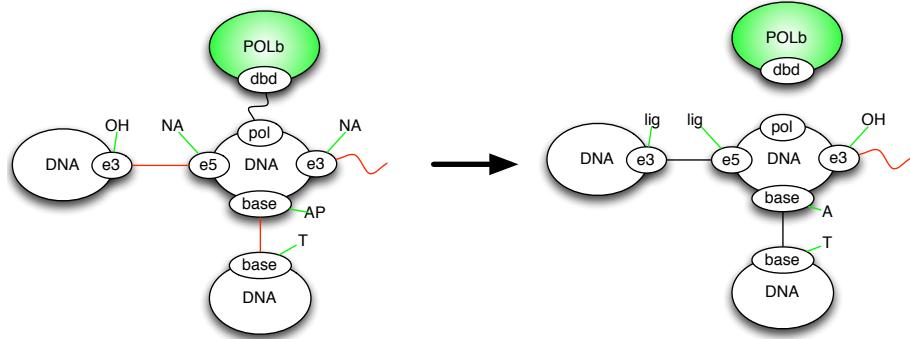


**Fig. 6.** APE1's endonuclease.

Whenever APE1 is bound to DNA and encounters an AP site, it may incise DNA 5' of the damage. The resulting gaped site has a 3' OH and a 5'dRP residues:

```
'APE1 5-endonuclease' \
APE1(dbdb!1), DNA(e3~lig!0), \
DNA(e5~lig!0, base~AP?, ape!1, e3~lig!2), DNA(e5~lig!2) -> \
APE1(dbdb), DNA(e3~OH !0), \
DNA(e5~NA!0, base~AP?, ape, e3~NA!2), DNA(e5~dRP!2) \
@ 'APE1_incision'
```

*POL $\beta$  gap filling.* The main rules of POL $\beta$  concern its gap filling activity. There are actually four variants of the rule presented below (see Fig. 7 for the graphical representation), one for each different nucleotide insertion.

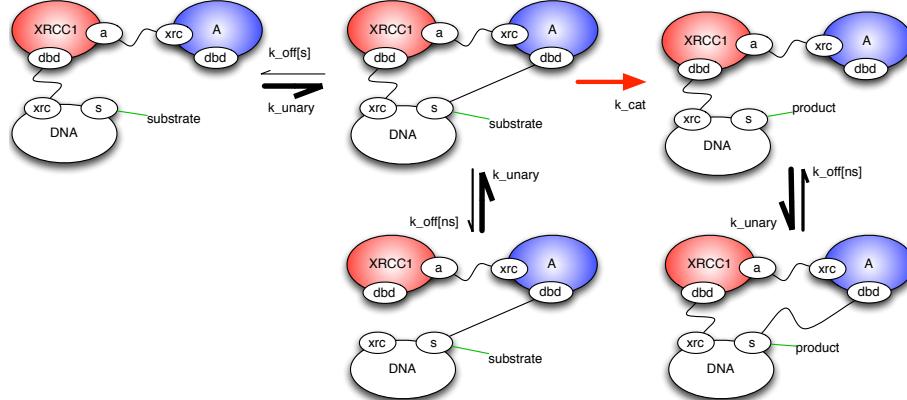


**Fig. 7.** Polymerase step: insertion of nucleotide with an adenine base.

```
'POLb polymerase A on gap' \
POLb(dbd!1), DNA(e3~OH !0), \
DNA(e5~NA!0, pol!1, base~AP!2, e3~NA!_), DNA(base~T!2) -> \
POLb(dbd ), DNA(e3~lig!0), \
DNA(e5~lig!0, pol , base~A !2, e3~OH!_), DNA(base~T!2) \
@ 'POLb_polymerase'
```

*On uni-molecular binding rules.* A fundamental assumption of the model is that uni-molecular binding events are fast. The underlying hypothesis is that steric constraints favor complex formation. This enables XRCC1 to reinforce the product inhibition following the scheme presented in Fig. 8 where  $k_{unary}$  is the uni-molecular binding rate. With a relatively weak affinity with enzyme A, and an equally moderate affinity with DNA (both have a strong  $k_{off}[ns]$  - for non specific), XRCC1 is able to stabilize efficiently A on both its substrate and product, although A has little affinity for its product ( $k_{off}[ns] > k_{off}[s]$ ).

**XRCC1 primarily impacts ligation efficiency.** There are a large number of possible *in silico* experiments one can try with our BER model. Since it is the first to incorporate protein-protein interactions, we naturally sought to study the role of the scaffolding protein XRCC1. As a first approach we ran a batch of simulations, under the conditions specified in the Methods section, with and without XRCC1. The simulations are denoted hereafter  $x^+$  (with XRCC1) and  $x^-$  (without). Figure 9 shows the average plots for both  $x^+$  and  $x^-$ . We first observed that both series of simulations were able to process the totality of initial damage (Fig. 9, left plot). However  $x^-$  exhibited a significant decrease in repair

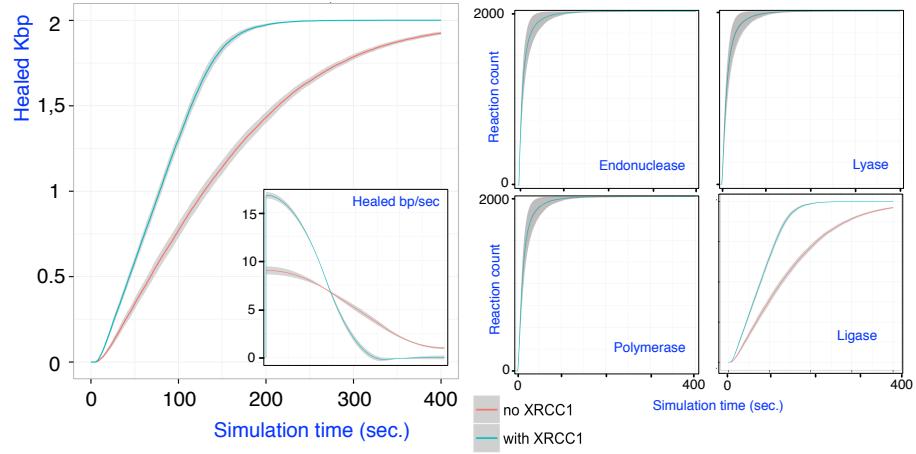


**Fig. 8.** XRCC1 stabilization ( $k_{unary} >> k_{off}[ns] > k_{off}[s]$ ).

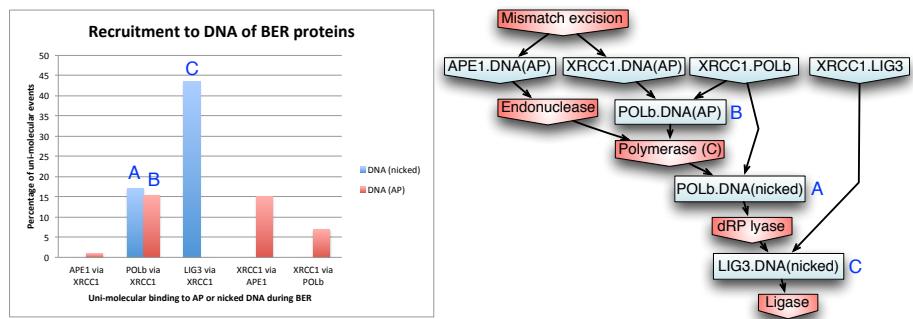
speed with respect to  $x^+$ , with 10 healed base pairs per second (maximal speed) vs. 17 healed base pairs per second (Fig. 9, left plot, small insert).

We then tried to narrow down the origin of that speed difference by decomposing the global repair into the 4 catalytic steps that follow the glycosylase reaction (Fig. 9, right). No significant difference between  $x^-$  and  $x^+$  could be observed for endonuclease (APE1), lyase and polymerase (POL $\beta$ ) reactions. Therefore the only possible difference of total repair activity lies in the ligation step. These observations are consistent with the fact that XRCC1 is dispensable for complete repair in vitro [17] and that XRCC1 deficient cells are defective in processing nicked DNA intermediates [18], although the authors propose that this is due to a hypothetical stabilising effect of XRCC1 on LIG3.

**Mechanistic insights into the transition from POL $\beta$  to LIG3.** XRCC1 is commonly referred to as a scaffolding protein for BER enzymes. The intuitive idea is that XRCC1 maintains APE1, POL $\beta$ , and LIG3 at the lesion site, throughout the whole repair process. As suggested by our simulations, the scaffolding role of XRCC1 is unevenly distributed among its potential partners. In order to investigate whether BER enzymes are actually brought to DNA by XRCC1, we used KASIM's causal tracking mode for the ligation step. To do so, we analyzed 122 (compressed) causal flows generated by a ligase event, produced under the conditions described in the Methods section. According to the sample, approximately 80% of ligation events contained an action of XRCC1 in their causal history (data not shown). We therefore sought to analyze more in detail what the exact role of XRCC1 was in the ligation pathways. The histogram of Fig. 10 indicates that nearly 45% of uni-molecular binding events occurring on DNA, that are in the causal past of a ligation event, correspond to the recruitment of LIG3 to the nicked DNA intermediate by XRCC1 (C). XRCC1 is also found recruiting POL $\beta$  to AP sites (B) and nicked DNA (A) in about 15% of the



**Fig. 9.** (Left plot) Simulation efficiency with and without XRCC1, shadows indicate standard deviation. (Right plot) Efficiency of BER catalytic steps, with and without XRCC1.

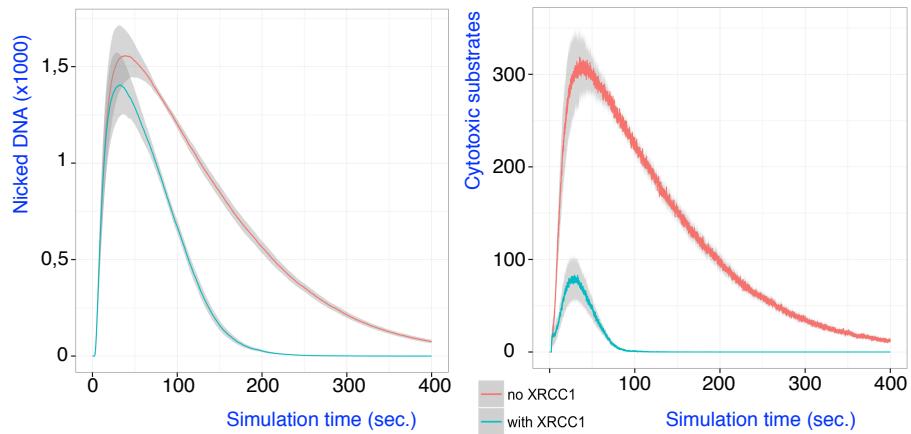


**Fig. 10.** (Left) Analysis of causal 122 flows exhibiting the intervention of XRCC1 and leading to a ligation event. (Right) A example of causal flow containing POL $\beta$  and LIG3 binding events via XRCC1.

scenarios leading to ligation. Interestingly XRCC1 is recruited to DNA by APE1 (15%) and POL $\beta$  (7%) in a significant number of scenarios. The little impact of XRCC1 on the recruitment of APE1 (less than 1% of scenarios) to the lesion sites is likely due to the relatively low turnover rate of UDG coupled with the large amount of APE1 in the system which enable a smooth transition between UDG and APE1 over the AP substrate. A characteristic causal flow obtained from a simulation is given in Fig. 10 (right): nodes correspond to rule applications and arrows represent causality between them. As a labeling convention, X.Y indicates a complex formation between proteins X and Y and rectangular nodes indicate uni-molecular reactions that occurred under the scaffolding of XRCC1. Red nodes correspond to the chemical steps of the pathway.

Overall, causality analysis confirms the key role of XRCC1 in securing the transition between the polymerase step and ligation.

**XRCC1 limits cytotoxicity BER.** Since XRCC1 plays an active role in passing the baton between POL $\beta$ 's products and LIG3's substrate, we wondered whether this coordination impacts on the cytotoxicity of BER. To do so we analyzed the amount of visible toxic DNA intermediates over time in  $x^+$  and  $x^-$ . A toxic substrate is understood here as either an AP site, a gapped DNA or a nicked DNA node that is not bound by any BER protein. Figure 11 shows the

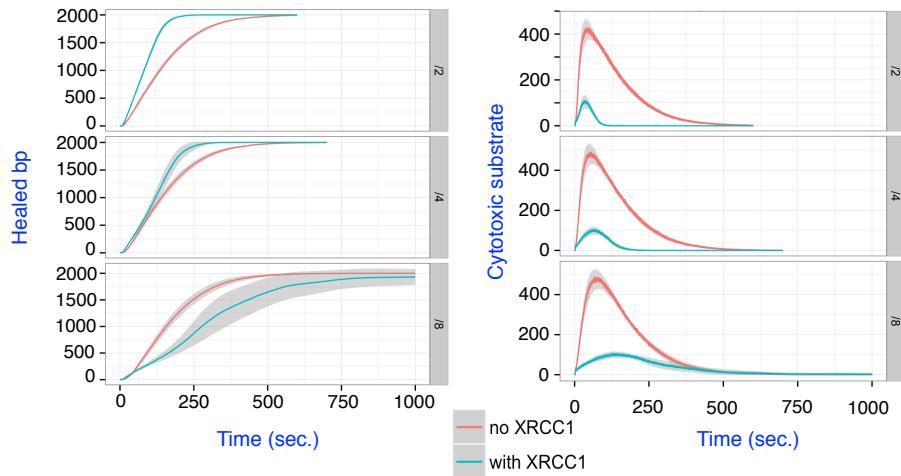


**Fig. 11.** Nicked DNA intermediates (left) and cytotoxic substrates in the presence and absence of XRCC1.

amount of total nicked DNA that is present in silico over the duration of BER (Left plot). As expected,  $x^+$  and  $x^-$  produce approximatively the same amount of nicked intermediates in the pre-steady state phase, since the ligation step is rate limiting ( $k_{cat} = 0.04 s^{-1}$  for LIG3 which is half the speed of the second slowest reaction, see Supp. Data A.2). However  $x^+$  has an apparent faster rate for

processing nicked DNA. Interestingly this results in a much higher cytotoxicity of  $x^-$  simulations (Fig. 11, right plot) which is almost entirely caused by unprotected nicked DNA (data not shown). This is consistent with the experimentally observed sensitivity of XRCC1 mutant cells to induced DNA damage [11].

**A tradeoff between accuracy and efficiency under varying amount of POL $\beta$ .** The nucleus is a very crowded medium and the local chromatin state can induce local concentration effects [11]. We thus investigated further the role of XRCC1 under decreasing amount of available POL $\beta$  (Figure 12). These ex-



**Fig. 12.** Repair efficiency and cytotoxicity of simulations with increasing dilution of POL $\beta$  (/2, /4 and /8 with respect to default amount).

periments showed that when the system is moderately deprived of POL $\beta$  (up to 1/4 dilution of the default amount), XRCC1 contributes to maintaining a fast repair rate by holding LIG3 at lesion sites, waiting for the product of POL $\beta$ 's reactions. Surprisingly, at higher dilution of POL $\beta$ , the price of this coordination becomes rate limiting for the overall repair speed. This is likely due to LIG3 being sequestered too long on AP sites in the absence of POL $\beta$  when ligatable substrates are elsewhere available. Importantly, under such extremal conditions XRCC1 still actively limits the amount of cytotoxic substrates (mainly in the form of nicked DNA) available to the environment.

This observation could imply that partial mutant cells (XRCC1 $^-$ ,POL $\beta^-$ ) would have a global faster repair activity than simple (XRCC1 $^+$ ,POL $\beta^-$ ) mutants, although with a very likely higher sensitivity to damage.

## 5 Discussion

**A Kappa model of BER.** We have collated a set of mechanisms of action pertaining to BER, as a set of Kappa rules. It results in an executable model of DNA repair that can be used to test various hypothesis on DNA repair mechanisms. As an instance of such applications, we have investigated the impact of the scaffolding protein XRCC1 on repair activity. Consistent with experimental observations, our model shows that complete repair can be achieved in the absence of XRCC1. Furthermore the model successfully predicts the impact of XRCC1 on BER, the absence of which resulted in the accumulation of unprotected nicked DNA intermediates and an impaired repair speed in simulations. Beyond available experiments, our model indicates that XRCC1 might be recruited by APE1 to the damage site. It would afterward proceed with the recruitment of POL $\beta$  and, to a higher degree, LIG3. Eventually we showed that XRCC1 contributes to the robustness of BER with respect to large variation of POL $\beta$ 's concentration, preserving the repair efficiency up to a certain dilution level (/4), and maintaining a low amount of cytotoxic substrate over time.

**Towards a comprehensive model of BER.** More studies on the dynamics of the present model can be performed, beyond the scope of this paper. Also more biological facts need to be incorporated. Among them, the addition of PARP1, that plays an important role in an alternative way to recruit BER enzymes to the damaged site, seems to be a priority. We would also like to model the alternative *long patch repair* which occurs when BER is unable to produce a ligatable substrate. It will be particularly interesting to see how XRCC1 can regulate the switch between long patch and short patch BER, as experimental studies indicate.

**Perspectives.** Our stance is to take both qualitative and quantitative data seriously and collate them into a comprehensive model. We believe this model can be used to raise challenges to the biologist community about missing information and also highlight key points where the DNA repair community agrees or disagrees. We also believe that a comprehensive model can be used to make predictions on possible experiments and help the biologists to explore the wet lab perturbation space in a rational manner.

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## A Supplementary Data

### A.1 The Kappa Language

We adapt here the presentation of Kappa, given in KaSim's manual<sup>11</sup>.

**General remarks** The *Kappa File* (KF) is the formal representation of a model. We use KF to denote the union of the files that are given as input to KASIM (argument **-i**). Each line of the KF is interpreted by KASIM as a *declaration*. If the line is ended by the escape character '\' the continuation of the declaration is parsed onto the next line. Declarations can be: agent *signatures*, *rules*, *variables*, *initial conditions*, *perturbations* and *parameter configurations*. The KF's structure is quite flexible and can be divided in any number of sub-files in which the order of declarations does not matter (to the exception of variable declarations). Comments can be used by inserting the marker # that tells KASIM to ignore the rest of the line.

**Agent signature** In Kappa there are two entities that can be used for representing biological elements: *agents* and *tokens* (we don't consider token here). Agents are used to represent complex molecules that may bind to other molecules on specific sites.

In order to use agents in a model, one needs to declare them first. *Agent signatures* constitute a form of typing information about the agents that are used in the model. It contains information about the name and number of interaction sites the agent has, and about their possible internal states. A signature is declared in the KF by the following line:

```
%agent: signature-expression
```

according to the grammar given Table 2 where terminal symbol are denoted in (blue) typed font. Symbol **Id** can be any string generated by regular expression  $[a - z A - Z][a - z A - Z 0 - 9 _ - +]^*$ . Terminal symbol  $\varepsilon$  stands for the empty symbol.

**Table 2.** Agent signature expression

$signature\_expression ::= \textcolor{blue}{\text{Id}}(\text{sig})$ $\text{sig} ::= \textcolor{blue}{\text{Id}} \text{internal\_state\_list}, \text{sig} \mid \varepsilon$ $\text{internal\_state\_list} ::= \textcolor{blue}{\sim} \text{Id} \text{internal\_state\_list} \mid \varepsilon$
--

For instance the line:

```
%agent: A(x,y~u~p,z~0~1~2) # Signature of agent A
```

---

<sup>11</sup> <http://www.pps.univ-paris-diderot.fr/~jkrvine>

will declare an agent  $A$  with 3 (*interaction*) *sites*  $x, y$  and  $z$  with the site  $y$  possessing two *internal states*  $u$  and  $p$  (for instance for the unphosphorylated and phosphorylated forms of  $y$ ) and the site  $z$  having possibly 3 states respectively 0, 1 and 2. Note that internal states values are treated as untyped symbols by KA\$IM, so choosing a character or an integer as internal state is purely matter of convention.

**Rules** Once agents are declared, one may add to the KF the rules that describe their dynamics through time. A *pure rule* looks like:

'my rule'  $\kappa\text{-expression} \rightarrow \kappa\text{-expression} @ rate$

where 'my rule' can be any name that will refer to the subsequent rule that can be decomposed into a *left hand side* (LHS) and a *right hand side* (RHS)  $\kappa$  expressions together with a *kinetic rate expression*. One may also declare a *bi-directional rule* using the convention:

'bi-rule'  $\kappa\text{-expression} \leftrightarrow \kappa\text{-expression} @ rate^+, rate^-$

Note that the above declaration corresponds to writing, in addition of 'my-rule', a backward rule named 'my\_rule\_op' which swaps left hand side and right hand side, and with rate  $rate^-$ .

Kappa and rate expressions are generated by the grammar given in Table 3.

**Table 3.** Kappa expressions

```

 $\kappa\text{-expression} ::= agent\text{-expression} , \kappa\text{-expression} \mid \varepsilon$ 
agent\text{-expression} ::= Id(interface)
interface ::=  $\varepsilon \mid \text{Id}$  internal\_state link\_state
internal\_state ::=  $\varepsilon \mid \text{Id}$ 
link\_state ::=  $\varepsilon \mid !n \mid !_- \mid ?$ 

token\_name ::= Id

rate\_expression ::= algebraic\_expression
                  \mid algebraic\_expression binary\_op algebraic\_expression
                  \mid unary\_op (algebraic\_expression)

```

**Table 4.** Algebraic expressions

```

algebraic\_expression ::=  $x \in \mathbb{R} \mid \text{variable}$ 
                      \mid algebraic\_expression binary\_op algebraic\_expression
                      \mid unary\_op (algebraic\_expression)

```

**Simple rules** With the signature of  $A$  defined in the previous section, the line

```
'A dimerization' A(x),A(y~p) → A(x!1),A(y~p!1) @ γ
```

denotes a dimerization rule between two instances of agent  $A$  provided the second is phosphorylated (say that is here the meaning of  $p$ ) on site  $y$ . Note that the bond between both  $A$ s is denoted by the identifier  $!1$  which uses an arbitrary integer ( $!0$  would denote the same bond). In Kappa, a bond may connect exactly 2 sites so any occurrence of a bond identifier  $!n$  has to be paired with exactly one other sibling in the expression. Note also the fact that site  $z$  of  $A$  is not mentioned in the expression which means that it has no influence on the triggering of this rule. This is the *don't care don't write convention* (DCDW) that plays a key role in resisting combinatorial explosion when writing models.

**Adding and deleting agents** Sticking with  $A$ 's signature, the rule

```
'budding A' A(z) → A(z!1),A(x!1) @ γ
```

indicates that an agent  $A$  free on site  $z$ , no matter what its internal state is, may beget a new copy of  $A$  bound to it *via* site  $x$ . Note that in the RHS, agent  $A'$ 's interface is not completely described. Following the DCDW convention, KASIM will then assume that the sites that are not mentioned are created in the *default state*, *i.e* they appear free of any bond and their internal state (if any) is the first of the list shown in the signature (here state  $u$  for  $y$  and  $0$  for  $z$ ).

Importantly, KASIM respects the *longest prefix convention* to determine which agent in the RHS stems from an agent in the LHS. In a word, from a rule of the form  $a_1, \dots, a_n \rightarrow b_1, \dots, b_k$ , with  $a_i$ s and  $b_j$ s being agents, one computes the biggest indices  $i \leq n$  such that the agents  $a_1, \dots, a_i$  are pairwise consistent with  $b_1, \dots, b_i$ , *i.e* the  $a_j$ s and  $b_j$ s have the same name and the same number of sites. In which case we say that the for all  $j \leq i$ ,  $a_j$  is *preserved* by the transition and for all  $j > i$ ,  $a_j$  is *deleted* by the transition and  $b_j$  is *created* by the transition. This convention allows us to write a deletion rule as:

```
'deleting A' A(x!1),A(z!1) → A(x) @ γ
```

which will remove the  $A$  agent in the mixture that will match the second occurrence of  $A$  in this rule.

**Side effects** It may happen that the application of a rule has some *side effects* on agents that are not mentioned explicitly in the rule. Consider for instance the previous rule:

```
'deleting A'A(x!1),A(z!1) → A(x) @ γ
```

The  $A$  in the graph that is matched to the second occurrence of  $A$  in the LHS will be deleted by the rule. As a consequence all its sites will disappear together with the bonds that were pointing to them. For instance, when applied to the graph

$$G = A(x!1, y~p, z~2), A(x!2, y~u, z~0!1), C(t!2)$$

the above rule will result in a new graph  $G' = A(x!1, y~p, z~2), C(t)$  where the site  $t$  of  $C$  is now free as side effect.

*Wildcard* symbols for link state ? (for bound or not), !\_ (for bound to someone), may also induce side effects when they are not preserved in the RHS of a rule, as in

'Disconnect A'  $A(x!_) \rightarrow A(x) @ \gamma$

or

'Force bind A'  $A(x?) \rightarrow A(x!1), C(t!1) @ \gamma$

**Rates** As said earlier, Kappa rules are equipped with *kinetic rate(s)*. A rate is a real number, or an algebraic expression evaluated as such, called the *individual-based or stochastic rate constant*, it is the rate at which the corresponding rule is applied per instance of the rule. Its dimension is the inverse of a time [ $T^{-1}$ ].

The stochastic rate is related to the *concentration-based rate constant*  $k$  of the rule of interest by the following relation:

$$k = \gamma(\mathcal{A} V)^{(a-1)} \quad (1)$$

where  $V$  is the volume where the model is considered,  $\mathcal{A} = 6.022 \cdot 10^{23}$  is Avogadro's number,  $a \geq 0$  is the arity of the rule (*i.e* 2 for a bimolecular rule).

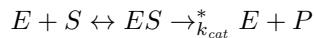
In a modeling context, the constant  $k$  is typically expressed using *molars*  $M := \text{moles } l^{-1}$  (or variants thereof such as  $\mu M$ ,  $nM$ ), and seconds or minutes. If we choose molars and seconds,  $k$ 's unit is  $M^{1-a}s^{-1}$ , as follows from the relation above.

Concentration-based rates are usually favored for measurements and/or deterministic models, so it is useful to know how to convert them into individual-based ones used by KASIM.

## A.2 The Kinetic rates of the BER model

**Complex formation rates.** The contact map illustrated Fig. 3 is derived from the papers the references of which are listed in Table 5. Italic fonts denote qualitative studies. Question marks denote postulated interactions without explicit references.

**Catalytic rates.** As pointed out in Section 3, the catalytic rate of an enzyme,  $k_{cat}$ , is usually given in terms of steady state kinetics, *i.e* following the scheme:



But as we pointed out, in the presence of non negligible product inhibition, enzymatic activity is better accounted for using the scheme:



Table 6 gives the catalytic rates and the reference paper(s) that were used in our model. Both  $k_{cat}$  and  $k_{chem}$  are given when available.

**Table 5.** Protein-DNA and protein-XRCC1 interactions. (†) Private conversation with Dr. S. H. Wilson (NIH).

Protein	DNA duplex Mismatch	AP site	Gaped DNA	Nicked DNA	XRCC1
XRCC1	[1]	?	[2]	[1]	[1]
APE1			[3], [4], [5]	[5]	(†)
UDG	[7]	[7]	[7]		[6]
TDG	[8]	[8]	[8]		
PNKP				[9]	[10]
POL $\beta$				[11]	(†)
LIG3				[13]	?
					[14]

**Table 6.** Catalytic rates used in the model. The notation [15] (from Ref X) indicates that the number comes from reference X of paper [15].

Protein	$k_{chem}$ ( $s^{-1}$ )	$k_{cat}$ ( $s^{-1}$ )	Reference
APE1 (3' PUA cleaning)		0.05	[15] (from Ref. 60)
APE1 (Endonuclease)	1000	3	[15], [16]
PNKP		0.14	[17]
LIG3 (Ligase)		0.04	[15] (from Refs. 56 and 63)
POL $\beta$ (3' dRP cleaning)		0.075	[15] (from Ref. 62)
POL $\beta$ (gap filling)	10	0.45	[11], [15] (from Refs. 29 and 61)
TDG	0.03		[8]
UDG		15	[18]

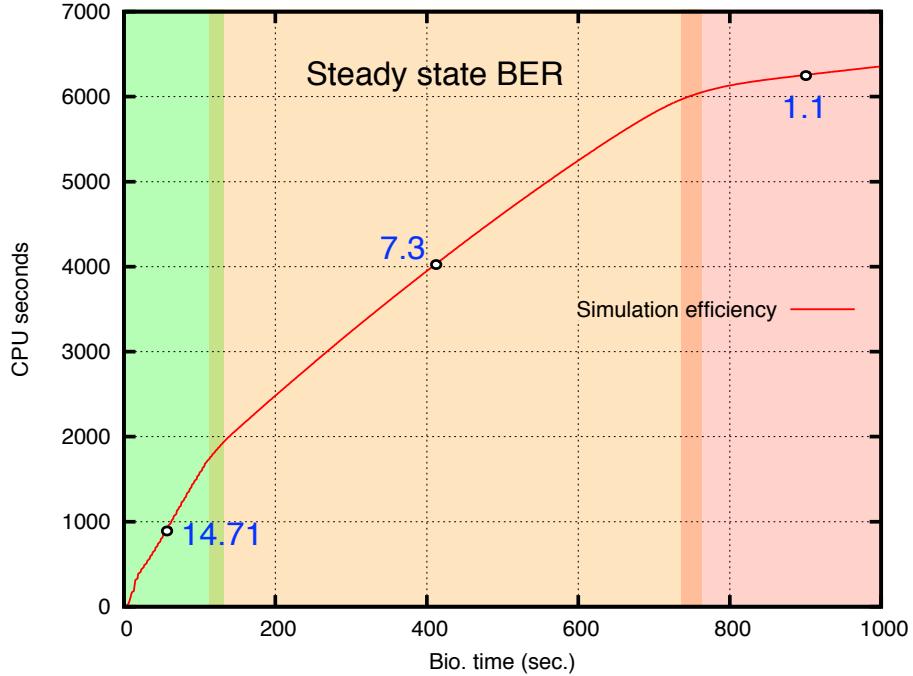
**Default rates.** When no quantitative data is known, we used “realistic” default rates that are randomized at each simulation from the intervals presented in the table below:

process	interval	rate
general bi-molecular binding	$[10^7 - 10^9]$	$M^{-1}s^{-1}$
general uni-molecular binding	$[10 - 10^4]$	$s^{-1}$
general unbinding	$[10^{-3} - 10^{-1}]$	$s^{-1}$

### A.3 Simulation efficiency

The efficiency of an *in silico* experiment with respect to a wet lab experiment is usually measured in terms of time and money consumption. It is interesting to check, for a given model, how long it takes (in CPU seconds) to simulate one (biological world) second of the real system. Fig. 13 shows the evolution of the efficiency of one simulation running with the parameters specified in the Methods section.

A good measure of the efficiency of a simulation at time  $t$  can be given by  $eff(t) \stackrel{def}{=} \frac{dCPU_{time}(t)}{dt}$ . As can be seen in Fig. 13,  $eff(t)$  has three distinguished phases during which it becomes quasi-linear. The three phases correspond to the pre-steady state ( $eff(t) \sim 15$  CPU seconds for 1 bio second) and steady



**Fig. 13.** A global picture of the CPU cost of a BER simulation. The derivative at distinguished points are given (pre-steady state, steady state and post BER).

state of BER ( $eff(t) \sim 7$  CPU seconds for 1 bio second) and the phase at which no more repair is conducted ( $eff(t) \sim 1$  CPU seconds for 1 bio second).

Importantly *in silico* BER efficiency varies quite a lot as different simulations are run with randomized dissociation constants, though they still exhibit the same distinct phases (data not shown).

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