DRAFT: NCT

RA

2022-02-13

1 Introduction

TODO(1): intro

We are particularly interested in the nuclear-to-cytoplasmic contrast (henceforth, N:C contrast) of certain molecular species at steady state: Ran · GTP, Imp β , CAS, and NLS.

Abbreviations. FG-nups = FG-nucleoporins; NCT = nucleocytoplasmic transport; NPC = nuclear pore complex; NE = nuclear envelope; IBB = importin beta binding; ODE = ordinary differential equations; SPR = surface plasmon resonance;

2 NCT models

2.1 GSR'03 model of NCT

Ran gradient. The Ran gradient, i.e. the nuclear accumulation of $Ran \cdot GTP$, is the base layer of nucleocytoplasmic transport. We implement it as the "minimal Ran gradient system" from [GSR03]. The equations are recapitulated in §5.1 and the constants are collected in Table 2. Following [GSR03], the "dynamic capacity" Ex is an optional maximal steady-state (positive) flux of nuclear $Ran \cdot GTP$ to cytoplasmic $Ran \cdot GDP$, which we determine using the additional equation (25). The fluxes are in units of concentration/time ($\mu M/s$). The ones across the nuclear boundary have positive sign when exiting the nucleus and are normalized to the nuclear volume. Thus, the *amount* exiting the nucleus per unit of time is flux $\times V_{nuc}$.

Simulating the ODE across the scenarios of [GSR03] we obtain results that are sufficiently close to the original, see Table 3. Importantly, an order of 1000-fold nuclear enrichment of Ran · GTP is sustained in steady-state. Moreover, the dynamic capacity clocks in at around $0.6\,\mu\text{M/s}$ in most cases, meaning the Ran gradient is established within seconds. Therefore, we will replace the whole Ran gradient layer by a virtual pump

cytoplasmic
$$Ran \cdot GDP \longrightarrow nuclear Ran \cdot GTP$$
 with kinetic rate $0.1 s^{-1}$. (1)

This rate is chosen conservatively (a concentration of $1 \,\mu\text{M}$ of cytoplasmic Ran · GDP generates a flux of $0.1 \,\mu\text{M/s}$) but will be sufficient for our purposes.

Code #1.

Coupling to Imp β -mediated transport. A coupling of the Ran gradient to importing cargo transport was proposed in [GSR03, Fig. 6A]. We now formulate a version of it. The following equations comprise the handling of cargo by Imp β in the cytoplasm,

$$\label{eq:loss_equation} \frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Imp}\beta\cdot\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} = -\mathsf{R}_{\mathsf{cyt}} + \mathsf{F}_{\mathsf{Imp}\beta\cdot\mathsf{Ran}\cdot\mathsf{GTP}} \frac{\mathit{V}_{\mathrm{nuc}}}{\mathit{V}_{\mathrm{cyt}}} - \mathsf{GAP}_{\mathsf{Imp}\beta} + \mathsf{Knockoff}_{\mathsf{cyt}} \qquad (2a)$$

$$\frac{d}{dt}[Imp\beta]_{cyt} = +R_{cyt} + C_{cyt} + F_{Imp\beta} \frac{V_{nuc}}{V_{cyt}} + GAP_{Imp\beta}$$
(2b)

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Imp}\beta\cdot\mathsf{Cargo}]_{\mathrm{cyt}} = -\mathsf{C}_{\mathsf{cyt}} + \mathsf{F}_{\mathsf{Imp}\beta\cdot\mathsf{Cargo}} \tfrac{V_{\mathrm{nuc}}}{V_{\mathrm{cyt}}} - \mathsf{Knockoff}_{\mathsf{cyt}} \tag{2c}$$

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Cargo}]_{\mathrm{cyt}} = +\mathsf{C}_{\mathsf{cyt}} + \mathsf{F}_{\mathsf{Cargo}} \frac{V_{\mathrm{nuc}}}{V_{\mathrm{cyt}}} + \mathsf{Knockoff}_{\mathsf{cyt}} \tag{2d}$$

with the fluxes

$$\mathsf{R}_{\mathsf{cyt}} := -k_{\mathsf{on}}^{\mathsf{R}}[\mathsf{Imp}\beta][\mathsf{Ran} \cdot \mathsf{GTP}]_{\mathsf{cyt}} + k_{\mathsf{off}}^{\mathsf{R}}[\mathsf{Imp}\beta \cdot \mathsf{Ran} \cdot \mathsf{GTP}]_{\mathsf{cyt}} \tag{3a}$$

$$\mathsf{C}_{\mathsf{cvt}} := -k_{\mathsf{on}}^{\mathsf{C}}[\mathsf{Imp}\beta][\mathsf{Cargo}]_{\mathsf{cvt}} + k_{\mathsf{off}}^{\mathsf{C}}[\mathsf{Imp}\beta \cdot \mathsf{Cargo}]_{\mathsf{cvt}}. \tag{3b}$$

The forward flux of the reaction

$$Imp\beta \cdot Cargo + Ran \cdot GTP \longrightarrow Imp\beta \cdot Ran \cdot GTP + Cargo$$
 (4)

is called Knockoff. It is modeled as a one-way reaction with forward rate k_{knockoff} . The GSR equations are modified accordingly:

$$\frac{d}{dt}[\mathsf{Ran} \cdot \mathsf{GDP}]_{cyt} = (19a) + \mathsf{GAP}_{\mathsf{Imp}\beta} \tag{19a'}$$

$$\frac{d}{dt}[\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} = (19\mathrm{b}) + \mathsf{R}_{\mathsf{cyt}} - \mathsf{Knockoff}_{\mathsf{cyt}} \tag{19\mathrm{b'}}$$

Analogous nuclear equations (without GAP) are implemented but are omitted here. Analogously to (23a)/(23b) we have the additional nuclear-to-cytoplasmic diffusion fluxes

$$F_{Imp\beta \cdot Ran \cdot GTP}$$
, $F_{Imp\beta}$, $F_{Imp\beta \cdot Cargo}$, F_{Cargo} (5)

with the permeability constants given in Table 1.

SPR experiments of [Cat+01] indicated that the IBB domain of importin- α binds importin- β and undergoes a conformational change,

$$A + B \rightleftharpoons AB \rightleftharpoons A^*B. \tag{6}$$

We therefore assume the analogous reaction

$$\mathsf{Cargo} + \mathsf{Imp}\beta \xleftarrow[k_{a1}]{\mathsf{k}_{a1}} \mathsf{Cargo} \cdot \mathsf{Imp}\beta \xleftarrow[k_{a2}]{\mathsf{k}_{a2}} \mathsf{Cargo}^* \cdot \mathsf{Imp}\beta. \tag{7}$$

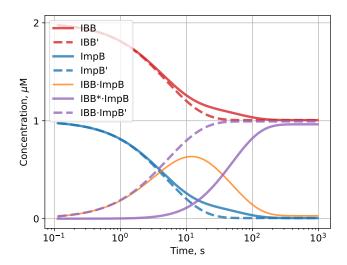


Figure 1: Stand-alone simulation of (6) starting with $2 \mu M$ IBB and $1 \mu M$ Imp β with the constants (8). The dashed counterpart is the effective system of the form $A + B \rightleftharpoons AB$, cf. §2.1.

(3a)	$k_{\text{on}}^{\text{R}} = 0.096 \mu\text{M}^{-1}\text{s}^{-1}, k_{\text{off}}^{\text{R}} = 4.8 \times 10^{-6}\text{s}^{-1}$	[GSR03, Supp. Table A], [RM05, Table II]
(3b)	$k_{\text{on}}^{\text{C}} = 0.11 \mu\text{M}^{-1}\text{s}^{-1}, k_{\text{off}}^{\text{C}} = 7.2 \times 10^{-4}\text{s}^{-1}$	[Cat+01, Table I], [RM05, Table II]
(4)	$k_{\text{knockoff}} = 2 \times 10^{-2} \mu\text{M}^{-1}\text{s}^{-1}$	[RM05, Table II]
(5)	$D_{\text{Imp}\beta \cdot \text{Ran} \cdot \text{GTP}} = 0.07 \text{s}^{-1}, D_{\text{Imp}\beta} = 0.4 \text{s}^{-1}$ $D_{\text{Imp}\beta \cdot \text{Cargo}} = 0.25 \text{s}^{-1}, D_{\text{Cargo}} = 5 \times 10^{-4} \text{s}^{-1}$	[RM05, Table III]

Table 1: Constants for the $Imp\beta$ -mediated transport from §2.1.

Examples of the kinetic constants are available in [Cat+01, Table I], e.g.,

$$k_{a1} = 0.11 \,\mu\text{M}^{-1}\,\text{s}^{-1}, \quad k_{d1} = 0.024\,\text{s}^{-1}, \quad k_{a2} = 0.024\,\text{s}^{-1}, \quad k_{d2} = 7.4 \times 10^{-4}\,\text{s}^{-1}, \quad (8)$$

for an IBB domain binding to $Imp\beta$. The intermediate state in (6) is transient on a moderately relevant time-scale, see Fig. 1 (code #2). Therefore, in the present model we lump the complexed states together and take $k_{\text{on}}^{\text{C}} := k_{a1}$ and $k_{\text{off}}^{\text{C}} := k_{d1} \frac{k_{d2}}{k_{a2} + k_{d2}}$ as the effective kinetic constants for (3b), cf. Table 1.

With the constants from Table 1, the steady-state of the model (reached after some 10^4 s) is reported in Fig. 2. Nuclear accumulation of free cargo is 37-fold. Sensitivity analysis shows that, in relative terms, the final nuclear concentration of free cargo depends most strongly on k_{knockoff} . Doubling k_{knockoff} almost doubles the nuclear concentration. Code #3.

This model predicts a slight accumulation of $Img\beta$ in the nucleus, with $Imp\beta \cdot Ran \cdot GTP$ contributing most of the excess. We improve on it in §2.3.

2.2 GTP hydrolysis and role of RanBP1

According to [LM97, Fig. 4A], Impβ blocks hydrolysis of Ran·GTP by RanGAP but RanBP1 rescues it for most part. Similarly, [BG97] showed that RanBP1 transiently detaches Ran

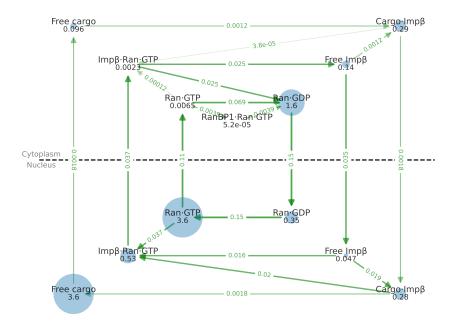


Figure 2: Steady-state of the transport system from §2.1 with conditions of Table 1. The free cargo shows 37-fold accumulation in the nucleus; total nuclear to total cytoplasmic cargo is 10-fold. Units are μM for species and $\mu M \, s^{-1}$ for fluxes. Initial conditions: $[{\sf Ran \cdot GDP}]_{\rm cyt} = 5 \, \mu M$, $[{\sf Imp}\beta]_{\rm cyt} = 1 \, \mu M$, $[{\sf Cargo}]_{\rm cyt} = 3 \, \mu M$, all else zero.

from the complex $\mathsf{Kap} \cdot \mathsf{Ran} \cdot \mathsf{GTP}$ (where Kap can be importin β , transportin or CAS), where-upon hydrolysis by $\mathsf{Ran}\mathsf{GAP}$ disassembles the complex; and that efficient disassembly of $\mathsf{Imp}\beta \cdot \mathsf{Ran} \cdot \mathsf{GTP}$ required $\mathsf{Ran}\mathsf{BP1}$ and $\mathsf{Imp}\alpha$ [BG97, §3.2, cf. Fig. 4], [FBR97]. Importantly, Kaps and RanBP1 bind Ran at distinct sites [BG97, p.253].

Further, [See+03, Fig. 13] characterizes the kinetics of the formation of the complex between $Ran \cdot GTP$, RanBP1 and RanGAP and the hydrolysis. In particular, the release rate of the γ -phosphate, on the order or $10 \, \mathrm{s}^{-1}$ in [See+03, Fig. 13], is barely influenced by RanBP1, which instead stimulates the association of Ran with RanGAP. A computational model of hydrolysis with these parameters qualitatively reproduces the experimental data from [LM97, Fig. 4A]. We omit the details that can be found in Code #4.

For simplicity, we will take the constant

GTP hydrolysis rate of
$$0.1 \,\mathrm{s}^{-1}$$
 (9)

for all cytoplasmic-side species containing $Ran \cdot GTP$, and no GTP hydrolysis elsewhere. This should be compared with the effective Ran gradient rate (1).

TODO(2): cf [KKL21] citing [Kle+95a] or [Kle+95b]

2.3 NPC as compartment

Introduction. It has been observed [KKL21] that Impβ accumulates inside the NPCs as they bind to the FG-nups, suggesting a regulatory role, and possibly shuttling the cargo across the pore repeatedly. To account for this we propose a model with cytoplasm, nucleus and the NPCs as three compartments. The following dual observation is essential (cf. [Hof20]):

- 1. cytoplasmic and nuclear species initially react with NPC components in proportion to the number of NPCs, and
- 2. the observed fluorescence signal from Kaps accumulating inside the NPCs correlates with the total volume or the capacity of the NPC channel (rather than their number).

The model includes the following main components:

- Generic NLS cargo. TODO(3): on NLS
- $Imp\alpha TODO(4)$: on ImpA
- Impβ TODO(5): on ImpB
- CAS TODO(6): on CAS
- The NPCs are described as vacant NPC channel space, the cytoplasm-facing opening NPC(c) and the nucleus-facing opening NPC(n). To transition the nuclear pore, a species has to bind to the opening, transition into the channel, bind to the other opening, and unbind on the other side. This allows us to model the capacity of the NPC and the dwelling time (but we make no distinction between different transiting species). There is no directionality, i.e. a species currently residing in the channel is equally likely to bind to either opening next.
- Ran · GTP in the nucleus and Ran · GDP in the cytoplasm. The consumption of Ran · GTP that have transitioned to the cytoplasmic side by hydrolysis is compensated by an effective pump as in (1). The hydrolysis itself is described by one effective kinetic rate as in (9).

An overview of the model is shown in Fig. 3. The code is found in Code #5. The computational results for this model are summarized in Fig. 4. For details see the URL

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numpde.github.io/nct1/code/20211018-Appli/checkpoint/20220209-143110/ (10)
```

Main reactions. Here we comment on the main reactions of the model. For the complete set we refer to Fig. 3 as well as the URL (10).

The nuclear Ran · GTP is converted directly to cytoplasmic Ran · GDP as in Eqn. (1).

The $Imp\beta$ can shuttle on its own through the NPC or in complex with $Imp\alpha$. We assume that the complex does not form on the nuclear side (due to nuclear $Ran \cdot GEF$, which is not modeled explicitly).

The cytoplasmic NLS cargo associates with free cytoplasmic $Imp\alpha \cdot Imp\beta$ before binding to the cytoplasmic side of the NPC, or with those already attached there. Once the complex is shuttled to the nuclear side, the "knockoff" reaction releases the cargo (the suffix (n) is omitted):

$$Ran \cdot GTP + NLS \cdot Imp\alpha \cdot Imp\beta \cdot NPC \longrightarrow Ran \cdot GTP \cdot Imp\beta \cdot NPC + Imp\alpha + NLS.$$
 (11)

Thereupon, the complex $Ran \cdot GTP \cdot Imp\beta$ can transition from the nuclear to the cytoplasmic side to be hydrolized as in Eqn. (9).

Like $Imp\beta$, CAS can shuttle through the NPC. On the nuclear side, it can first bind to $Ran \cdot GTP$ then form the $Imp\alpha \cdot CAS \cdot Ran \cdot GTP$ complex. This complex can shuttle through the NPC but on the cytoplasmic side, the hydrolysis reaction (9) disassembles it.

Baseline parameters. Here we comment on the choice of selected model parameters, such as concentrations and kinetic rates. For the complete set see the URL (10).

We estimate the total NPC channel capacity as 2000 NPCs per nuclear envelope (BioNumbers #111130) times 300 Kaps per NPC TODO(7): refs for those numbers. Note that

$$1 \text{ pL} \times 1 \text{ }\mu\text{M} \approx 300 \times 2000 \text{ units},$$
 (12)

which implies a concentration of 1 µM in a computational volume of 1 pL. The computation itself is performed in amounts (rather than concentration), so to convert to apparent concentration of Kaps at the NE we estimate TODO(8): automate insertion of this volume

For the initial concentration of $Imp\beta$ we take $5\,\mu\rm M$ in nucleus and cytoplasm based on [?] TODO(9): ref.

[NPW19, Fig. 4a] – probably from [Wüh+14]

[YM06]

For the initial concentration of $Imp\alpha$ we considered taking $4\,\mu M$ throughout the cell, slightly below that of $Imp\beta$, based on the immunoblots of [ZAH13, Fig. 7] and the mass spectrometry measurements for KPNAs from [Wüh+14, Table S5]. However, this seemed incompatible with other parameters in that the steady state showed unexpected results, e.g. the NLS remained tied to $Imp\alpha$ and nearly equipartitioned between nuclear and cytoplasmic sides. We settled on the $Imp\alpha$ concentration of $0.4\,\mu M$ for the baseline model.

[KKL21] [K1r+15]

TODO(10): complete section

Variants. We have defined a handful of scenarios to illustrate how parameter choice affects the steady-states. The results are summarized in Fig. 4. All parameter changes are with respected to the baseline scenario, and are reported at the URL (10).

- Decrease $Imp\beta$ tenfold. TODO(11): Why
- Increase the number of NPC tenfold. TODO(12): Why
- Increase $Imp\alpha$ tenfold.
- Decrease $Imp\alpha$ tenfold.
- Turn off Ran·GTP regeneration, starting from the baseline scenario. We obtain a breakdown of N:C contrast for all species, as expected.

3 Conclusions

TODO(13): conclude

4 Old stuff dump – ignore

The crux is now that the nuclear envelope, having small volume, has a high concentration of NPCs. At the nuclear envelope we posit the reactions

$$Imp\beta_i + NPC_{vacant} \rightleftharpoons Imp\beta \cdot NPC$$
 (14a)

$$\mathsf{Cargo} \cdot \mathsf{Imp} \beta_i + \mathsf{NPC}_{\mathsf{vacant}} \Longrightarrow \mathsf{Cargo} \cdot \mathsf{Imp} \beta \cdot \mathsf{NPC} \tag{14b}$$

TODO(14): ref with $k_{\text{on}} = 10^{-3} \, \mu \text{M}^{-1} \, \text{s}^{-1}$ and $k_{\text{off}} = 10^{-4} \, \text{s}^{-1}$, as well as

$$\mathsf{Cargo}_i + \mathsf{Imp}\beta \cdot \mathsf{NPC} \Longrightarrow \mathsf{Cargo} \cdot \mathsf{Imp}\beta \cdot \mathsf{NPC} \tag{15}$$

with $k_{\rm on}^{\rm C}=0.11\,\mu{\rm M}^{-1}\,{\rm s}^{-1}$ and $k_{\rm off}^{\rm C}=7.2\times10^{-4}\,{\rm s}^{-1}$, where i can be "cytoplasmic" or "nuclear". This envelope compartment is in diffusive exchange with cytoplasm ($i={\rm cyt}$) and nucleus ($i={\rm nuc}$) with the permeability constant $D=1\,{\rm s}^{-1}$. In both, we also allow

$$\mathsf{Cargo} + \mathsf{Imp}\beta \Longleftrightarrow \mathsf{Cargo} \cdot \mathsf{Imp}\beta \tag{16}$$

with the same $k_{\text{on}}^{\text{C}}/k_{\text{off}}^{\text{C}}$. For simplicity, we assume [RanGTP] = $3\,\mu\text{M}$ and [RanGDP] = $2\,\mu\text{M}$ are maintained at fixed concentrations and are only relevant at the envelope, where we have

$$cargo \ knockoff: \ \mathsf{RanGTP}_{\mathsf{nuc}} + \mathsf{Cargo} \cdot \mathsf{Imp}\beta \cdot \mathsf{NPC} \longrightarrow \mathsf{Cargo} + \mathsf{RanGTP} \cdot \mathsf{Imp}\beta \cdot \mathsf{NPC} \ \ (17)$$

$$GTP\ hydrolysis: \qquad \qquad \mathsf{RanGTP} \cdot \mathsf{Imp}\beta \cdot \mathsf{NPC} \longrightarrow \mathsf{RanGDP}_\mathsf{cyt} + \mathsf{P} + \mathsf{Imp}\beta \cdot \mathsf{NPC}. \eqno(18)$$

For hydrolysis we assume the reaction rate $v_{\rm GAP}/(1+K_{\rm GAP}/[{\sf RanGTP}\cdot{\sf Imp}\beta\cdot{\sf NPC}])$, similarly to (24a). We take $v_{\rm GAP}=0.07\,\mu{\rm M\,s^{-1}}$ and $K_{\rm GAP}=0.1\,\mu{\rm M}$. This reaction rate about $100\times$

smaller than in (24a) but in view of TODO(15): ref, this seems more realistic and has little effect on the course of the simulation.

Starting from $[\mathsf{Cargo}]_{\mathrm{cyt}} = 1\,\mu\mathrm{M}$ and $[\mathsf{Imp}\beta]_{\mathrm{cyt}} = [\mathsf{Imp}\beta]_{\mathrm{nuc}} = 0.5\,\mu\mathrm{M}$, this model predicts a 6-fold accumulation of total cargo in the nucleus in steady-state. Meanwhile, the concentration of $\mathsf{Imp}\beta$ at the envelope is approximately $10^3\,\mu\mathrm{M}$.

Code #6.

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5 Appendix

5.1 Minimal Ran gradient system

Here we recapitulate the minimal Ran gradient system from [GSR03, Fig. 2], cf. §2.1. The following account for the cytoplasmic species. Here, $[\dots]$ abbreviates the (cytoplasmic) concentration of the complex RanBP1 · Ran · GTP. Ex is an additional potentially useful flux of nuclear Ran · GTP to cytoplasmic Ran · GDP, set by default to zero.

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Ran}\cdot\mathsf{GDP}]_{\mathrm{cyt}} = \mathsf{F}_{\mathsf{Ran}\cdot\mathsf{GDP}} \frac{V_{\mathrm{nuc}}}{V_{\mathrm{cyt}}} + \mathsf{GAP} + \mathsf{GAP}_{\mathsf{RanBP1}} + \mathsf{Ex} \frac{V_{\mathrm{nuc}}}{V_{\mathrm{cyt}}} \tag{19a}$$

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} = \mathsf{F}_{\mathsf{Ran}\cdot\mathsf{GTP}} \frac{V_{\mathrm{nuc}}}{V_{\mathrm{cyt}}} - \mathsf{GAP} - k_{\mathrm{on}}^{\mathrm{rbp}}[\mathsf{RanBP1}][\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} + k_{\mathrm{off}}^{\mathrm{rbp}}[\ldots] \tag{19b}$$

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{RanBP1}\cdot\mathsf{Ran}\cdot\mathsf{GTP}] = -\mathsf{GAP}_{\mathsf{RanBP1}} \\ + k_{\mathrm{on}}^{\mathrm{rbp}}[\mathsf{RanBP1}][\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} - k_{\mathrm{off}}^{\mathrm{rbp}}[\ldots]$$
 (19c)

The following account for the nuclear species. As in [GSR03], E denotes free RCC1.

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Ran} \cdot \mathsf{GDP}]_{\mathrm{nuc}} = -\mathsf{F}_{\mathsf{Ran} \cdot \mathsf{GDP}} + r_{8}[\mathsf{IntC}] - r_{1}[\mathsf{E}][\mathsf{Ran} \cdot \mathsf{GDP}]_{\mathrm{nuc}} \tag{20a}$$

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{Ran} \cdot \mathsf{GTP}]_{\mathrm{nuc}} = -\mathsf{F}_{\mathsf{Ran} \cdot \mathsf{GTP}} + r_4[\mathsf{IntA}] - r_5[\mathsf{E}][\mathsf{Ran} \cdot \mathsf{GTP}]_{\mathrm{nuc}} - \mathsf{Ex}$$
 (20b)

The nucleotide-exchange reaction $Ran \cdot GDP + GTP \Longrightarrow Ran \cdot GTP + GDP$ is catalyzed by RCC1. It is modeled as in [Kle+95b, Fig. 6] / [GSR03, Fig. 1] with three intermediates. Note that it depends on the availability of GDP and GTP.

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{IntA}] = -(r_4 + r_6)[\mathsf{IntA}] + r_5[\mathsf{E}][\mathsf{Ran} \cdot \mathsf{GTP}]_{\mathrm{nuc}} + r_3[\mathsf{GTP}][\mathsf{IntB}] \tag{21a}$$

$$\frac{d}{dt}[IntB] = r_6[IntA] + r_2[IntC] - (r_3[GTP] + r_7[GDP])[IntB]$$
 (21b)

$$\frac{\mathrm{d}}{\mathrm{d}t}[\mathsf{IntC}] = -(r_2 + r_8)[\mathsf{IntC}] + r_1[\mathsf{E}][\mathsf{Ran} \cdot \mathsf{GDP}]_{\mathrm{nuc}} + r_7[\mathsf{GDP}][\mathsf{IntB}] \tag{21c}$$

Constraints on the total concentration:

Free RCC1:
$$[E] = RCC1_{total} - ([IntA] + [IntB] + [IntC])$$
 (22a)

Free RanBP1:
$$[RanBP1] = RanBP1_{total} - [RanBP1 \cdot Ran \cdot GTP]$$
 (22b)

Gradient-driven fluxes from the nucleus to the cytoplasm:

$$\mathsf{F}_{\mathsf{Ran}.\mathsf{GTP}} = D_{\mathsf{Ran}\cdot\mathsf{GTP}} \left([\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{nuc}} - [\mathsf{Ran}\cdot\mathsf{GTP}]_{\mathrm{cyt}} \right) \tag{23a}$$

$$\mathsf{F}_{\mathsf{Ran.GDP}} = D_{\mathsf{Ran} \cdot \mathsf{GDP}} \left([\mathsf{Ran} \cdot \mathsf{GDP}]_{\mathrm{nuc}} - [\mathsf{Ran} \cdot \mathsf{GDP}]_{\mathrm{cyt}} \right) \tag{23b}$$

RanGAP hydrolyzes the γ -phosphate of Ran · GTP. This is more efficient when Ran · GTP is bound to RanBP1 [Bis+95], reducing the IC50 seven-fold [GSR03, Table I, p. 1091].

$$GAP = k_{GAP}[RanGAP]/(1 + K_{GAP}/[Ran \cdot GTP]_{cyt})$$
(24a)

$$\mathsf{GAP}_{\mathsf{RanBP1}} = k'_{\mathsf{GAP}}[\mathsf{RanGAP}]/(1 + K'_{\mathsf{GAP}}/[\mathsf{RanBP1} \cdot \mathsf{Ran} \cdot \mathsf{GTP}]) \tag{24b}$$

To determine the dynamic capacity Ex at steady-state we introduce the additional equation:

$$\frac{\mathrm{d}}{\mathrm{d}t}\mathsf{Ex} = k_{\mathsf{Ex}} \left[\mathsf{Ran} \cdot \mathsf{GTP} \right]_{\mathsf{nuc}}, \quad k_{\mathsf{Ex}} := 10 \, \mathsf{s}^{-2}, \quad \text{initial} \quad \mathsf{Ex} := 0 \, \mu \mathrm{M} \, \mathsf{s}^{-1}. \tag{25}$$

(19a)	$V_{ m nuc} = 1.2 m pl, V_{ m cyt} = 1.8 m pl$	[GSR03, Table II]	
${}$ (19a)	initial condition $[Ran \cdot GDP]_{cyt} = 5 \mu M$	[GSR03, Table II]	
(19b)- $(19c)$	$k_{\text{on}}^{\text{rbp}} = 0.3 \mu\text{M}^{-1}\text{s}^{-1}, k_{\text{off}}^{\text{rbp}} = 4 \times 10^{-4}\text{s}^{-1}$	[GSR03, Supp. Table A]	
	$r_1 = 74 \mu\text{M}^{-1}\text{s}^{-1}, r_8 = 55\text{s}^{-1}$		
(20a)–(21c)	$r_7 = 11 \mu\text{M}^{-1}\text{s}^{-1}, r_2 = 21\text{s}^{-1}$	[GSR03, Supp. Table A]	
(20a)=(21c)	$r_3 = 0.6 \mu\text{M}^{-1}\text{s}^{-1}, r_6 = 19\text{s}^{-1}$	[Kle+95b, Fig. 6]	
	$r_5 = 100 \mu\text{M}^{-1}\text{s}^{-1}, r_4 = 55\text{s}^{-1}$		
(21a)-(21c)	$[GTP] = 500 \mu M, [GDP] = 1.6 \mu M$	[GSR03, Table II]	
(22a)	$RCC1_total = 0.7\mu\mathrm{M}$	[GSR03, Supp. Table B]	
(22b)	$RanBP1_{total} = 2\mu\mathrm{M}$	[GSR03, Fig. 4]	
(23a)	$D_{Ran\cdotGTP} = 0.03\mathrm{s}^{-1}$	[GSR03, Table II]	
(23b)	$D_{Ran\cdotGDP} = 0.12\mathrm{s}^{-1}$		
(24a)	$k_{\text{GAP}} = 10.6 \mathrm{s}^{-1}, K_{\text{GAP}} = 0.7 \mathrm{\mu M}$	[GSR03, Supp. Table A]	
(24b)	$k'_{GAP} = 10.8 \mathrm{s}^{-1}, K'_{GAP} = 0.1 \mu\mathrm{M}$	[GSR03, Table I]	
(24a)- $(24b)$	$cytoplasmic [RanGAP] = 0.7 \mu\mathrm{M}$	[GSR03, Table II / ST B]	

Table 2: Constants for the "standard simulation condition" of §2.1 at 25 °C. Except for (19a), all species are initialized to zero at t=0.

Condition	Affected	Nuclear	Cytoplasmic	Dynamic
Condition	parameters	RanGTP, µM	RanGTP, nM	capacity, $\mu M/s$
"Standard"	See Table 2	4.26 (4.3)	7.75 (7.7)	0.59 (0.60)
Omission of RanBP1	$RanBP1_{total} := 0$	4.27 (4.3)	8.13 (8.1)	0.59 (0.60)
200% RCC1	RCC1 _{total}	3.95(4.0)	7.17 (7.1)	0.59 (0.60)
50% RCC1	RCC1 _{total}	4.31 (4.3)	7.82 (7.7)	0.58 (0.60)
10% RCC1	RCC1 _{total}	3.59(3.6)	6.50 (6.4)	0.46 (0.48)
1% RCC1	RCC1 _{total}	1.40 (1.4)	2.52(2.5)	0.075 (0.08)
GTP:GDP = 500:0	$[GDP] := 0\mu\mathrm{M}$	4.80 (4.8)	8.72 (8.6)	0.59 (0.60)
GTP:GDP = 500:50	$[GDP] := \frac{1}{10}[GTP]$	0.98 (0.8)	1.76(1.5)	0.57 (0.58)
GTP:GDP = 500:500	[GDP] := [GTP]	0.12 (0.12)	0.22(0.21)	$0.34 \ (0.34)$
Saturating NTF2	$D_{\text{Ran} \cdot \text{GDP}} := 0.48 \text{s}^{-1}$	5.12 (5.1)	9.32 (9.2)	2.18(2.2)
No NTF2	$D_{Ran\cdotGDP} := D_{Ran\cdotGTP}$	2.55(2.5)	4.60(4.5)	0.15 (0.16)
200% RanGAP	[RanGAP]	4.27(4.3)	3.95(3.9)	0.59 (0.60)
50% RanGAP	[RanGAP]	4.26 (4.3)	14.9 (14)	0.59 (0.60)
50% permeability	$D_{Ran\cdotGTP}$	4.91 (4.9)	4.44 (4.4)	0.59 (-)
200% permeability	$D_{Ran\cdotGTP}$	3.41 (3.4)	12.4 (12.3)	0.59 (-)
400% permeability	$D_{Ran\cdotGTP}$	2.46(2.5)	18.0 (17.8)	0.59 (-)

Table 3: Steady-state concentrations for the simulation scenarios from [GSR03, Table II/III], with their results shown in brackets. Value for $D_{\mathsf{Ran}\,\cdot\,\mathsf{GDP}}$ is from [GSR03, Fig. 3].

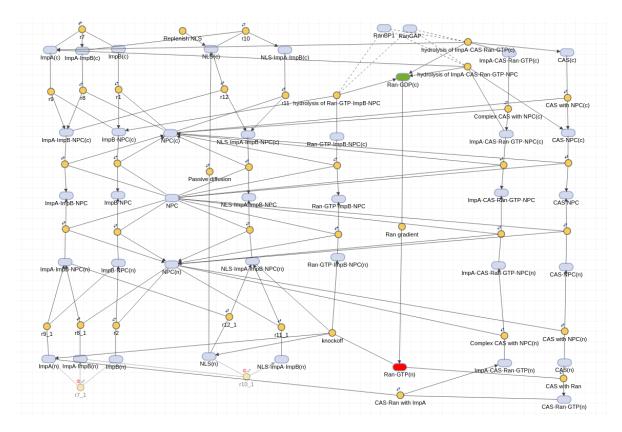


Figure 3: SimBiology diagram for the model "NPC as compartment" from §2.3.

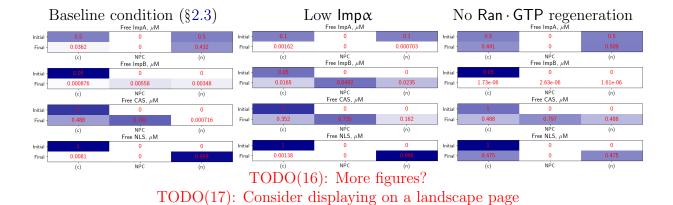


Figure 4: Initial states and steady-states for the model "NPC as compartment" from §2.3. For more full-size figures, see TODO(19): Link to the full set

5.2 NPC as compartment

5.3 List of codes

	page	https://github.com/numpde/nct1/tree/
#1	p.2	main/code/20210225-GSR/v1
#2	p.3	main/code/20210407-Rearrangement
#3	p.3	main/code/20210225-GSR/v2
#4	p.4	main/code/20210403-StickyPore/c_rangap-sequence
#5	p.5	main/code/20211018-Appli
#6	p.8	main/code/20210403-StickyPore

6 TODO

TODOs:

- 1. p.1. intro
- $2. \hspace{0.1cm} \text{p.4.} \hspace{0.1cm} \text{cf [KKL21] citing [Kle+95a] or [Kle+95b]}$
- 3. p.5. on NLS
- **4.** p.**5.** on ImpA
- 5. p.5. on ImpB
- 6. p.5. on CAS
- 7. p.6. refs for those numbers
- 8. p.6. automate insertion of this volume
- 9. p.6. ref
- 10. p.6. complete section
- 11. p.7. Why
- 12. p.7. Why
- 13. p.7. conclude
- 14. p.7. ref
- 15. p.8. ref
- 16. p.13. More figures?
- 17. p.13. Consider displaying on a landscape page
- 18. p.??. Link to the full set

19. p.13. Link to the full set