**Supplementary File 1A - Stochastic Mathematical Modeling**

The stochastic model is similar to the stochastic models previously used for both RA and its target gene expression (White et al., 2007; Cai et al., 2012; Zhang et al., 2012). Below is the basic stochastic PDE model:

where and represent extracellular and intracellular RA concentrations, and and denote the space-time white noises in extracellular and intracellular RA concentrations with small positive parameters and , respectively. and denote the concentrations of binding proteins (Crabps), RA receptors, the complex of RA and receptors, and the complex of RA and binding proteins.

represents RA degradation by Cyp26 through the following form,

where

The computational domain is a rectangle of dimension 500 m x 50 m. The parameters used in the simulation are directly from our previous studies and shown in Supplementary File 1B.

**Supplementary File 1B – Modeling parameters**

|  |  |  |
| --- | --- | --- |
| Parameters | Values | Reference |
|  | 0.1 | White et al., 2007 |
|  | 0.0001, 1000 | White et al., 2007 |
|  | 1 | --- |
|  | 100 | --- |
|  | 400 | White et al., 2007 |
|  | 0.1 |  |
| n | 4 | --- |
|  | 400 | White et al., 2007; Zhang et al., 2012 |
|  | 0.01 | --- |
|  | 100 | --- |
| V(x) |  | --- |
|  | 3 | Cai et al., 2012 |
|  | 0.001 | Cai et al., 2012 |
|  | 3 | Cai et al., 2012 |
|  | 0.0013 | Cai et al., 2012 |
|  | 2 | Cai et al., 2012 |
|  | 1 | Cai et al., 2012 |
| , | 0.0001 | Cai et al., 2012 |
| , | , | Cai et al., 2012 |
| , | 0.0001 | --- |
|  | 0.006,0.08 |  |
|  |  | White et al., 2007; Zhang et al., 2012 |

Parameters are based on (White et al., 2007; Cai et al., 2012; Zhang et al., 2012).