Dimensional equations:

|  |  |  |
| --- | --- | --- |
|  |  | (1) |
|  |  | (2) |

Scaling:

Nondimensionalized equations:

|  |  |  |
| --- | --- | --- |
|  |  | (3) |
|  |  | (4) |

Eqs. (3) and (4) will result in and . The peak number of REV-ERB in a cell is ~50,000 (Narumi). Hence,

|  |  |  |
| --- | --- | --- |
|  |  | (5) |

In order for to be larger than, say, 10 nM, the following must be satisfied

|  |  |  |
| --- | --- | --- |
|  |  | (6) |

If we consider that not all REV-ERB proteins are in the nucleus, then the total number, 50,000, needs to be reduced, and needs to be even more constrained. should be a reasonable estimate. What do you think?

Taken together, we need to find , and such that and the average of matches in the corresponding SNF model.

Alternative scaling:

Nondimensionalized equations:

|  |  |  |
| --- | --- | --- |
|  |  | (3) |
|  |  | (4) |

Eqs. (3) and (4) will result in and . The peak number of REV-ERB in a cell is ~50,000 (Narumi). Hence,

|  |  |  |
| --- | --- | --- |
|  |  | (5) |

In order for to be larger than, say, 10 nM, the following must be satisfied

|  |  |  |
| --- | --- | --- |
|  |  | (6) |

If we consider that not all REV-ERB proteins are in the nucleus, then the total number, 50,000, needs to be reduced, and needs to be even more constrained. should be a reasonable estimate. What do you think?

Taken together, we need to find , and such that and the average of matches in the corresponding SNF model.

Dimensional equations for PNF:

|  |  |  |
| --- | --- | --- |
|  |  | (1) |
|  |  | (2) |

Scaling:

Nondimensionalized equations:

|  |  |  |
| --- | --- | --- |
|  |  | (3) |
|  |  | (4) |

Eqs. (3) and (4) will result in and . The peak number of ROR in a cell is ~25,000 (Narumi). Hence,

|  |  |  |
| --- | --- | --- |
|  |  | (5) |

In order for to be larger than, say, 10 nM, the following must be satisfied

|  |  |  |
| --- | --- | --- |
|  |  | (6) |

If we consider that not all ROR proteins are in the nucleus, then the total number, 25,000, needs to be reduced, and needs to be even more constrained. should be a reasonable estimate. What do you think?

Taken together, we need to find , and such that and the average of matches in the corresponding SNF model.