

CORRECTION

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Correction to: The Kendrick modelling platform: language abstractions and tools for epidemiology

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Correction to: BMC Bioinf (2019) 20:312
<https://doi.org/10.1186/s12859-019-2843-0>

Following publication of the original article [1], the author noticed that the following lines were missing from the published article. The original article has been corrected.

In the 'Results' section under heading 'Case study I: Measles', the following lines are missing in the published article:

1. line 'KendrickModel SEIR' should be inserted before the following:

```
attribute: #(status -> S E I R);
parameters: #(beta sigma gamma mu);
equations: #(
    S: t=mu*N - beta*S*I - mu*S.
    E: t=beta*S*I - sigma*E - mu*E.
    I: t=sigma*E - gamma*I - mu*I.
    R: t=gamma*I - mu*R.
).
```

2. line 'Simulation MeaslesRKSim rungeKutta' should be inserted before the following:

```
scenarios: #(MeaslesParameters MeaslesPopulation);
from: 0.0;
to: 150;
```

step: 1.

Visualization MeaslesDiagramViz diagram

```
for: 'MeaslesRKSim';
xlabel: 'Time (days)';
exportToPng.
```

3. line 'KendrickModel SIR' should be inserted before the following:

```
attribute: #(status -> S I R);
parameters: #(beta lambda gamma mu);
transitions: #(
    S -> lambda -> I.
    I -> gamma -> R.
    status -> mu -> Empty.
    Empty -> mu -> S.
).
```

4. line 'Experiment PopRateAnalysis' should be inserted before the following:

```
on: 'Measles';
output: 'MeaslesDiagramViz';
populationSize: [ 100000 , 150000 ] @ 50000;
I: [ 1 , 21 ] @ 10;
beta: [ 0.0000150 , 0.0000250 ] @ 0.0000050;
gamma: [ 0.150 , 0.250 ] @ 0.050;
run
```

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