

0.a. Goal

[illegible]

0.b. Target

[illegible]

0.c. Indicator

[illegible]

0.e. Metadata update

□□□□□□□□□□ □□□□ [□□]

1.a. Organisation

□□□□□□□□□□□□□□□□□□ (NIS) / □□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□□ [□□□]

1.b. Contact person(s)

Sovanndy /

1.c. Contact organisation unit

[illegible]

1.d. Contact person function

□□□□□□□□□□ / □□□□ [□□]

1.e. Contact phone

[] [] [] [] [] [] [] [] / [] [] [] [] [] [] [] [] [] [] [] []

1.f. Contact mail

sovanndypoch @ gmail.com / Norvanndy @ gmail.com

{

□□□□□ (%)

[illegible][illegible]

3.c. Data collection calendar

Table 3: Data collection calendar (Quater1, 2018)

3.d. Data release calendar

Table 3: Data release calendar (2018)

3.e. Data providers

Table 3: Data providers (2018)

3.f. Data compilers

Table 3: Data compilers (2018)

3.g. Institutional mandate

Table 3: Institutional mandate (2018)

4.a. Rationale

Table 4: Rationale (2018)

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4.b. Comment and limitations

The model presented here is a simplified representation of the complex biological system under study. It is based on a set of assumptions that may not fully capture the underlying biology. For example, the model assumes that the system is at equilibrium, which may not be the case in all situations. Additionally, the model does not account for stochasticity, which is a key feature of many biological systems. Despite these limitations, the model provides a useful framework for understanding the basic principles of the system and for generating testable hypotheses. The model is implemented in the R programming language using the 'deSolve' package for solving ordinary differential equations (ODEs) and the 'ggplot2' package for visualization. The model parameters were estimated from experimental data using a least-squares fitting procedure. The model was validated by comparing its predictions with experimental data, and it was found that the model accurately captures the essential features of the system. The model is available as a supplementary file to this preprint.

4.c. Method of computation

The model was implemented in the R programming language using the 'deSolve' package for solving ordinary differential equations (ODEs) and the 'ggplot2' package for visualization. The model parameters were estimated from experimental data using a least-squares fitting procedure. The model was validated by comparing its predictions with experimental data, and it was found that the model accurately captures the essential features of the system. The model is available as a supplementary file to this preprint.

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- [illegible]

[illegible]

4.i. Quality management

[illegible]

5. Data availability and disaggregation

[illegible]

7. References and Documentation

[illegible]