Comparative Analysis of Single-Population Compartment Epidemiological Models

Kovács Fruzsina Édua

Konzulens: Simon Péter · ELTE TTK

Research Seminar in Applied Mathematics | 2025/2026/II.

Overview

1. **Foundations of compartment models**
   definition, structure, the SIR model

2. **Research question & model catalogue**
   21 single-population ODE models, computational pipeline

3. **Analysis criteria**
   model structure, equilibria, R_0, stability, bifurcation, periodic orbits, final size

4. **Results & model overview**
   criterion-by-criterion findings, summary table

5. **Conclusions & future directions**

Modelling Framework

Compartment models (Hethcote, 2000, pp. 600–601)

- Population divided into epidemiological classes
  (S – susceptible, E – exposed, I – infectious, R – recovered etc.)
- Transitions between classes modelled by ODEs
- Choice of compartments depends on the disease
- The standard mathematical framework for modelling infectious disease dynamics

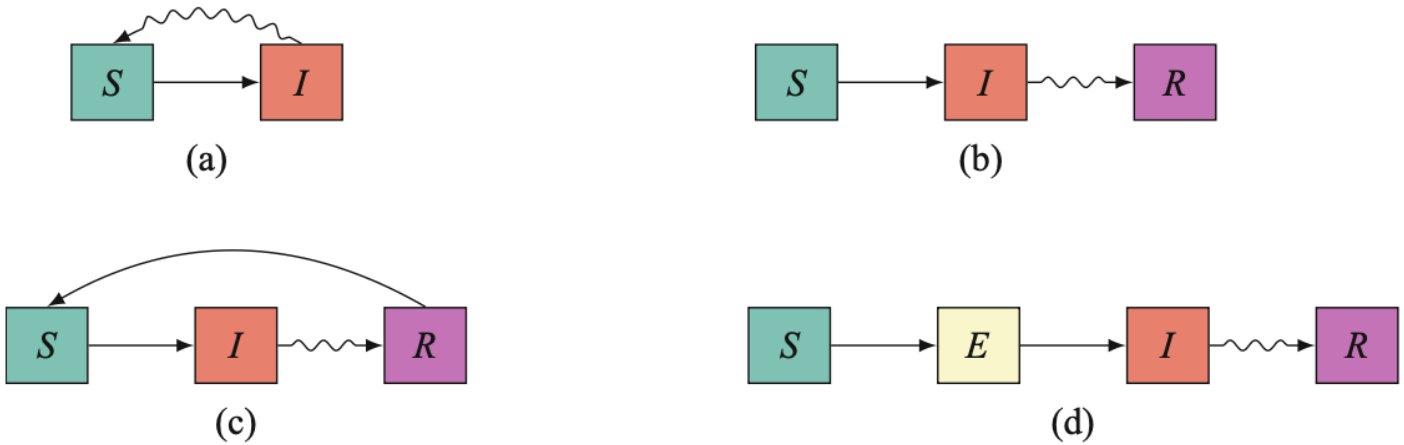
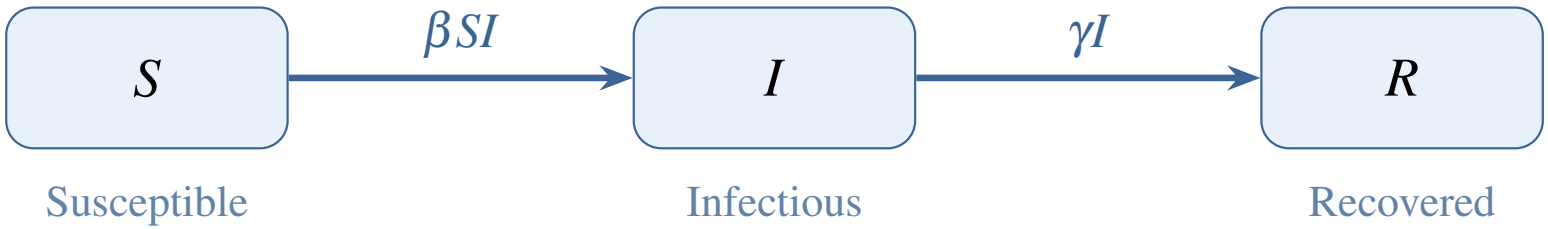


Fig. 1: Flow diagrams for (a) SIS, (b) SIR, (c) SIRS and (d) SEIR epidemic models. Boxes represent the susceptible, infectious, exposed and recovered compartments, arrows indicate transitions, wavy arrows indicate possible removal from the compartment due to death. Source: Kiss, Miller & Simon (2017), p. 6.

The SIR Model — A Starting Point



$$\dot{S} = -\beta SI, \qquad \dot{I} = \beta SI - \gamma I, \qquad \dot{R} = \gamma I$$

- β = transmission rate
- γ = recovery rate
- $N = S + I + R = \text{const}$

Basic reproduction number:

$$R_0 = \frac{N\beta}{\gamma}$$

Research Question

How are structural modelling choices reflected in the mathematical behaviour of the system?

A single structural choice can fundamentally alter the mathematical behaviour of the system — making it worth systematically investigating which structural decisions determine its properties.

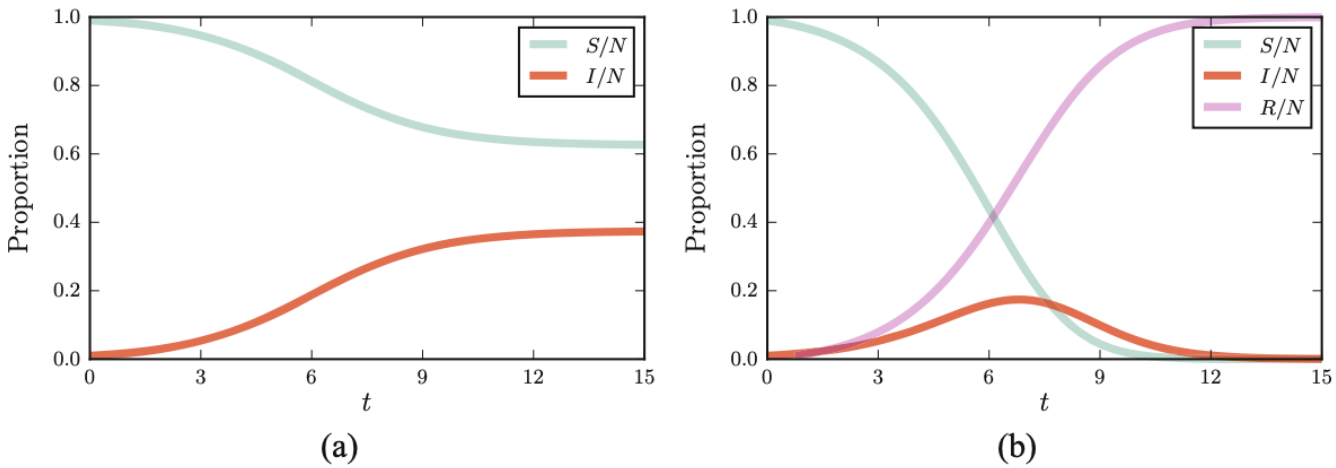


Fig. 2: SIS (endemic equilibrium) vs. SIR (epidemic wave) — same β and γ, one structural difference.

Source: Kiss, Miller & Simon (2017), Fig. 1.4, p. 7.

Research Question

How are structural modelling choices reflected in the mathematical behaviour of the system?

Structural choices:

- Compartments: $E, Q, D, M, V \ldots$
- Immunity waning ($R \to S$)
- Open or closed population
- Type of infection term

Mathematical consequences:

- Endemic equilibrium existence
- Form of R_0
- Bifurcation type at $R_0 = 1$
- Periodic orbits
- Global stability

Approach:

- Classify 21 single-population ODE models by their mathematical properties
- Analyse behaviour criterion by criterion

The Model Catalogue

- All models: single-population, deterministic, continuous-time ODEs

Group	Models	Count
Core	SI, SIS, SIR, SIRS, SEIR, SEIS	6
Demographic	SIR / SIS / SEIR dem.	3
Nonlinear	SIS / SIR saturating, SIS std. incidence	3
Vaccination	SEIRS, SIR / SIRS vacc.	3
Extended	SIRD, SEIRD, MSIR, SIS-2, SEIR-2, SIQR	6
	Total	**21**

Dimensions (reduction possible due to conservation law):

1D: SI, SIS

2D: SIR, SIRS, SEIS, SIS/SIR sat., SIS std. inc., SIR/SIS dem., vacc., SIRD

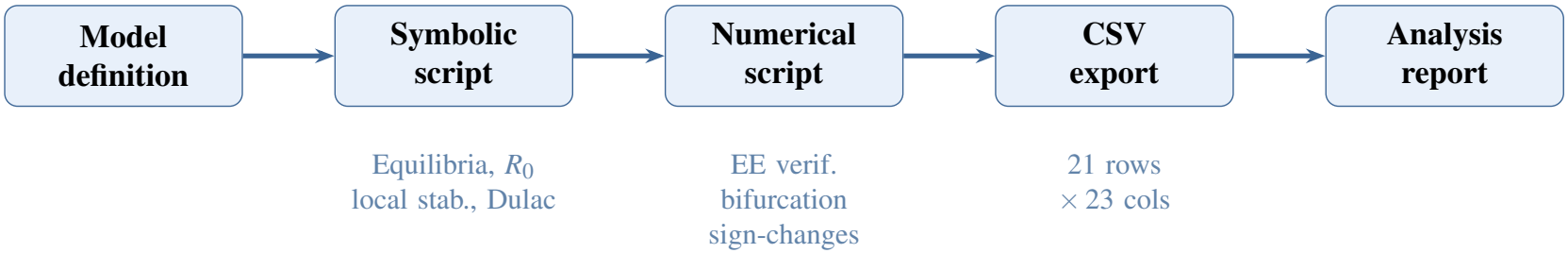
3D: SEIR, SEIRS, SIQR, SEIR dem., SIS-2, MSIR

4D: SEIRD, SEIR-2

Analysis Criteria (per Model)

1. Model structure
   dimension, population type, infection term
2. Disease-free equilibrium (DFE)
3. Endemic equilibrium (EE) existence
4. Basic reproduction number R_0
5. Local stability
6. Global stability (Lyapunov / LaSalle)
7. Bifurcation type at $R_0 = 1$
8. Periodic orbits (Bendixson–Dulac)
9. Final epidemic size S_∞

Computational Pipeline



Symbolic (MATLAB Sym. Toolbox):

- Equilibrium coordinates, R_0, eigenvalues
- Results valid for *all* parameter values
- Bendixson–Dulac criterion (2D models)

Numerical (ODE simulation):

- Verification & cases where symbolic fails
- Bifurcation type via R_0 parameter sweep
- Periodic orbit detection (sign-change count)

Why both? Symbolic computation yields general formulas (e.g. $R_0 = N\beta/\gamma$) valid for any parameter values, but fails for complex models (e.g. E-compartment NGM decomposition). Numerical simulation handles these cases and provides independent verification, but produces only concrete values for fixed parameters — not general results.

Model Structure: Number and Type of Compartments

Models are named after their compartments (e.g. SIR, SEIR, SIQR); this structure is the primary feature distinguishing them from one another.

Expected outcomes based on compartment structure:

- **Endemic equilibrium:** exists if and only if there is a feedback arc into S, otherwise the disease always dies out
- **Effect on R_0:** each extra exit from I reduces R_0 by adding to the denominator (e.g. SIQR: $R_0 = N\beta/(\gamma+\kappa)$, κ = quarantine rate). The E compartment leaves R_0 unchanged when $\mu = 0$, when $\mu > 0$: $R_0 \times \sigma/(\sigma+\mu)$.
- **Periodic orbits:** excluded in 2D via the Dulac criterion, possible in principle in 3D+ models.
- **Available tools by dimension:** in 2D the Dulac criterion and Poincaré–Bendixson theorem allow a complete qualitative analysis, in 3D the compound matrix method can exclude periodic orbits, in 4D+ global stability is generally an open question.

Model Structure: Closed vs. Open Population

$\sum_i \dot{x}_i = 0$: every individual leaving one compartment enters another $\Rightarrow N = \text{const}$ (closed). If nonzero, births or deaths change the total population size (open).

Expected outcomes based on population type:

Closed

- $N = \text{const}$
- suitable for short-term outbreaks
- conservation law allows dimension reduction
- endemic equilibrium requires feedback arc into S

SI, SIS, SIR, SIRS, SEIR, SEIS, SIS/SIR sat., SIS std. inc., SEIRS, SIR/SIRS vacc., SIRD, SEIRD, SIS-2, SEIR-2, SIQR

Open (rate μ)

- births $\mu N \to S$, deaths μx_i
- suitable for long-term endemic diseases
- demography alone enables endemic equilibrium
- even without immunity loss (e.g. SIR dem. vs. SIR)

SIR dem., SIS dem., SEIR dem., MSIR, SEIRS

Model Structure: Type of Infection Term

The form of the $S \to I$ transition determines the nonlinearity of the infection dynamics and whether R_0 depends on N.

- **Mass action:** βSI
  Contact rate proportional to both group sizes. $R_0 = N\beta/(\gamma + \cdots)$ — depends on N.
  Applicable: most core and demographic models.

- **Standard incidence:** $\beta SI/N$
  Each individual has a fixed number of contacts, independent of N. $R_0 = \beta/\gamma$ — independent of N.
  Applicable: SIS std. inc., SIS-2.

- **Saturating (Holling type II):** $\beta SI/(1+\alpha I)$
  Contact rate saturates at large I — behavioural feedback. R_0 at the DFE identical to mass-action case, but the saturating term can cause **backward bifurcation**.
  Applicable: SIS sat., SIR sat.

Key distinction: whether N enters the epidemic threshold condition.

Equilibrium Points

Disease-free equilibrium (DFE, $I^* = 0$): the disease is absent from the population.
Endemic equilibrium (EE, $I^* > 0$): the disease persists indefinitely.
The DFE exists in every model, the EE depends on the model structure.

- **DFE always exists**
  closed: $S^* = N$, open: same coordinates, different Jacobian structure, vaccination: $S^* = N(1-p)$
- **EE exists $\Longleftrightarrow$ feedback arc into S**
  either post-recovery return ($R \to S$ or $I \to S$) or demographic influx ($\mu N \to S$), without feedback, R is a one-way sink and the disease always dies out
- **EE exists for $R_0 > 1$** when feedback is present
  $R_0 < 1$: DFE stable, EE negative (irrelevant), $R_0 > 1$: EE positive and stable, DFE unstable
- **Exception — backward bifurcation** (SIS sat.)
  saturating infection term may produce a stable EE even for $R_0 < 1$, further analysis required

Basic Reproduction Number: Definition

Next-generation matrix method (van den Driessche & Watmough, 2002)

$$R_0 = \rho(FV^{-1})$$

- $F_{ij} = \left.\frac{\partial \mathscr{F}_i}{\partial x_j}\right|_{\text{DFE}}$ new infections into compartment i
- $V_{ij} = \left.\frac{\partial \mathscr{V}_i}{\partial x_j}\right|_{\text{DFE}}$ all other transfers (recovery, death, progression)
- $\rho(\cdot)$ — spectral radius (largest eigenvalue)
- evaluated at the DFE: $S^* = N$, $I^* = 0$

FV^{-1} gives the expected number of secondary infections produced in each compartment — R_0 is its dominant eigenvalue.

R_0 = average number of secondary infections caused by one infectious individual in a fully susceptible population at the start of an epidemic

Base formula
(mass action, closed, no E)

$$R_0 = \frac{N\beta}{\gamma + \text{exit terms}}$$

$R_0 = 1$ is the bifurcation threshold between disease extinction and persistence

- $R_0 < 1$: disease dies out, DFE stable
- $R_0 > 1$: disease spreads, DFE unstable
- $R_0 = 1$: bifurcation threshold

Basic Reproduction Number: Structural Patterns

- **Extra exit from I** $\Rightarrow$ shorter infectious period $\Rightarrow$ smaller R_0
  mortality δ, quarantine κ, demography μ all enter identically

- **E compartment, $\mu = 0$**
  all exposed reach I eventually $\Rightarrow$ R_0 unchanged

- **E compartment, $\mu > 0$**
  some exposed die before becoming infectious:

$$R_0 \times \frac{\sigma}{\sigma + \mu}$$

- **Standard incidence**
  $R_0 = \beta/\gamma$, independent of N

- **Script limitation**
  SEIR-type models return $R_0 = 0$ symbolically, manual NGM required

Examples

SIS	$N\beta/\gamma$
SIR dem.	$N\beta/(\gamma+\mu)$
SIRD	$N\beta/(\gamma+\delta)$
SIQR	$N\beta/(\gamma+\kappa)$
SEIR dem.	$\dfrac{N\beta\sigma}{(\sigma+\mu)(\gamma+\mu)}$
SIS std. inc.	β/γ
SEIR-2	$\dfrac{N\beta_1}{\delta_1} + \dfrac{N\beta_2}{\gamma}$
SIS-2	$\rho(2\times 2 \text{ NGM})$

Local Stability Analysis

Method: Jacobian linearisation

- examines whether small perturbations around an equilibrium grow or decay
- linearise the system: compute Jacobian J^* at the equilibrium
- stability determined by $\mathrm{Re}(\lambda_i)$ - algebraic computation
- applied to both DFE and EE for all 21 models

- **Dominant eigenvalue at the DFE:** $\lambda_{\max} = \gamma(R_0 - 1)$
  - $R_0 < 1$: $\lambda_{\max} < 0 \Rightarrow$ DFE stable
  - $R_0 > 1$: $\lambda_{\max} > 0 \Rightarrow$ DFE unstable, disease spreads
  - $R_0 = 1$: $\lambda_{\max} = 0$, non-hyperbolic $\Rightarrow$ bifurcation analysis needed
- **Nature of eigenvalues**
  - real: monotone convergence to equilibrium
  - complex: oscillatory damped convergence (occurs in SIRS, SEIR)

Global Stability Analysis

Method: Lyapunov function

- examines whether solutions from *any* initial condition converge to the equilibrium
- find $V \geq 0$ with $V(\mathbf{x}^*) = 0$ such that $\dot{V} \leq 0$ throughout the phase space
- if $\dot{V} = 0$ only at $\mathbf{x}^*$: globally asymptotically stable (LaSalle principle)
- tractability depends strongly on system dimension

- **2D models** — standard candidate $V = I$ works when $R_0 \leq 1$:

$$\dot{V} = I(\beta S - \gamma) \leq I \cdot \gamma(R_0 - 1) \leq 0$$

  holds for SIS, SIR, SIRS, SIR dem. and most 2D models

- **3D models** — case-by-case analysis

- **4D+ models** — Lyapunov candidate generally fails, global stability remains an open question

- **Exception: backward bifurcation** (SIS sat.)
  stable EE may persist for $R_0 < 1$, global stability of DFE not guaranteed

Bifurcation at $R_0 = 1$

- **Bifurcation analysis** determines how the number and stability of equilibria change as a parameter crosses a critical value — here $R_0 = 1$, the threshold between disease extinction and persistence
- at $R_0 = 1$ the Jacobian has a zero eigenvalue $\Rightarrow$ Hartman–Grobman fails, centre manifold theorem needed
- the bifurcation type answers whether the transition is smooth and reversible (transcritical) or whether bistability arises (backward bifurcation), with direct implications for disease control
- type determined via centre manifold theorem: reduces the system to the invariant manifold associated with the zero eigenvalue

Transcritical
Generic case, all 21 models

- $R_0 < 1$: DFE stable, EE negative
- $R_0 > 1$: EE stable, DFE unstable
- no bistability

Backward bifurcation
Possible: SIS saturating

- stable EE persists for $R_0 < 1$, bistability arises
- reducing R_0 below 1 may not eliminate the disease and requires manual verification

Hopf bifurcation
Not documented

- periodic orbit emerges
- cannot be ruled out in 3D+ models
- would require further analysis

Periodic Orbits

Method: Bendixson–Dulac criterion

- addresses whether the system admits solutions that trace closed paths in the phase space, i.e. oscillatory cyclic behaviour in the long run
- if there exists $B(S,I) > 0$ such that $\nabla \cdot (Bf)$ has constant sign, then no periodic orbit exists
- applicable only to 2D systems

- **Periodic orbit excluded** (Bendixson–Dulac applicable)
  with $B = 1/(SI)$:
  $$\nabla \cdot (Bf) = -\frac{\gamma}{S^2} < 0$$
  holds for SIS, SIS dem., SIS sat., SIS std. inc., and generally for every 2D model where the right-hand side is sufficiently smooth

- **Cannot be excluded in 2D** (SI)
  in the absence of a recovery term the divergence is not of constant sign, so the Dulac criterion does not apply

- **Not guaranteed in 3D+ models**
  the Poincaré–Bendixson theorem applies only in 2D, in higher-dimensional models the existence of periodic orbits must be checked numerically

Reduced Dimension & Final Epidemic Size

Reduced dimensions

Conservation law $\sum_i x_i = N$ allows reduction from d to $d-1$ dimensions.

- **1D:** SI, SIS — $I = N - S$ suffices
- **2D:** SIR, SIRS, SIS dem., etc.
- **3D:** SEIR, SEIRS, SIRD, etc.
- **Not reducible (open models):** N not constant, conservation law does not apply directly

Final epidemic size S_∞/N

Proportion of individuals never infected, meaningful only for closed models with permanent immunity after recovery.

- **Closed implicit equation** (e.g. SIR):

$$S_\infty = S_0\, e^{-R_0(1-S_\infty/N)}$$

  solvable numerically
- **Trivial:** SI — $S_\infty = 0$
- **Not defined:** open models and models with an endemic equilibrium

Both criteria depend on prior results: dimension reduction requires the conservation law (closed population), final size requires the absence of an endemic equilibrium — both are therefore structural consequences, not independent analyses.

Model Overview (1/2)

Model	Dim.	EE	R_0	Bifurcation	Periodic
SI	1	yes	∞ (degen.)	degenerate	cannot excl.
SIS	1	yes	$N\beta/\gamma$	transcritical	Dulac: none
SIR	2	no	$N\beta/\gamma$	transcritical	dim > 2
SIRS	2	yes	$N\beta/\gamma$	transcritical	dim > 2
SEIR	3	no	*manual*	transcritical	dim > 2
SEIS	2	yes	*manual*	transcritical	dim > 2
SIR dem.	2	yes	$N\beta/(\gamma+\mu)$	transcritical	dim > 2
SIS dem.	1	yes	$N\beta/(\gamma+\mu)$	transcritical	Dulac: none
SEIR dem.	3	yes	*manual*	transcritical	dim > 2
SIS sat.	1	yes	$N\beta/\gamma$	check $a(\alpha)$	Dulac: none
SIR sat.	2	no	$N\beta/\gamma$	transcritical	dim > 2

Model Overview (2/2)

Model	Dim.	EE	R_0	Bifurcation	Periodic
SIS std. inc.	1	yes	β/γ	transcritical	Dulac: none
SEIRS	3	yes	*manual*	transcritical	dim >2
SIR vacc.	2	no	missing $(1-p)$	transcritical	dim >2
SIRS vacc.	2	yes	missing $(1-p)$	transcritical	dim >2
SIRD	3	no	$N\beta/(\gamma+\delta)$	transcritical	dim >2
SEIRD	4	no	*manual*	transcritical	dim >2
MSIR	3	yes	verify μ	transcritical	dim >2
SIS-2	3	yes	$\rho(\text{NGM})$	transcritical	dim >2
SEIR-2	4	no	*manual*	transcritical	dim >2
SIQR	3	no	$N\beta/(\gamma+\kappa)$	transcritical	dim >2

Key Findings & Conclusions

Central conclusion

The analytical criteria of the 21 models are not independent — they are linked by structural relationships. A single modelling choice simultaneously affects the existence of equilibrium points, the form of R_0, the type of bifurcation, and the limits of analytical tractability.

Structural classification reveals:

- **Feedback arc into S:** simultaneously determines EE existence, R_0 threshold behaviour, and bifurcation type
- **Population type (open vs. closed):** determines whether demography alone can sustain endemic disease
- **Infection term type:** determines N-dependence of R_0 and possibility of backward bifurcation
- **System dimension:** directly limits which analytical tools apply — complete qualitative analysis is tractable in 2D, increasingly open in 3D+

Further Directions

This work: a framework

- classification of 21 models by mathematical properties
- unified criterion-based approach
- foundational observations on structure-to-dynamics relationships

Deeper analysis

- rigorous proofs of identified patterns
- implementable observations for model development
- visualisation of structural relationships
- extension of analysis criteria

Extension to complex models

- vector-borne and metapopulation models
- models with imperfect vaccines
- stochastic variants
- network models
- delay differential equations

Questions are welcome, thank you for your attention!

Comparative Analysis of Single-Population Compartment Epidemiological Models

Fruzsina Édua Kovács

ELTE Applied Mathematics MSc

Supervisor: Simon Péter