

Comparison and Integration of LOIMOS and MVT Infection Simulation Models

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Valencia, Milano, Verona, Trieste

- Comparison and integration of two infection-diffusion models:
 - Loimos - Valencia (Java-based)
 - MVT - Milano, Verona, Trieste (Python-based)
- Goal: Combine strengths while maintaining simplicity
- Focus on generalization and configurability

Main Ideas

- Province membranes
- Each province contains places for people: Schools, offices, common places (e.g. transports), etc.
- People moving around according to daily routines
- Diffusion of infections by contact

Key Integration Decisions

- Programming: Python (MVT) for simpler feature integration
- Infection States: MVT's system (Incubation - Infect - Immune)
- Symptoms: Loimos's four levels (E1-E4)
- Movement: Combined provincial system with quarantine rules
- Place Types: Houses, hospitals, ICUs, workplaces, schools, leisure centers

Infection and Recovery Model

- Two configurable infection models:
 - Viral-load based (from Loimos)
 - Fixed-day cycle (from MVT)
- Hospital system:
 - Regular hospitals (150 capacity)
 - ICUs (optional, 1 capacity)
 - Treatment duration: 7 days
- Recovery through treatment or antibody development

Generalization Features

- Configurable place capacities:
 - Schools: 300
 - Workplaces: 200
 - Leisure centers: 200
- Adjustable province connectivity
- Flexible disease parameters
- Customizable quarantine periods

The Prudence Parameter (PP)

Controls population behavior:

- $PP = 0$: No disease awareness
 - Normal movement despite symptoms
- $PP = 0.5$: Partial awareness
 - 50% reduced movement when symptomatic
- $PP = 1$: Full awareness
 - No movement when symptomatic

Parameter Tuning

Key adjustments for realistic results:

- Infection rates reduced by factor of 1.15
- Death rates significantly lowered
- Antibody generation rate tripled
- Immunity threshold set to 40 antibodies

Time complexity:

- Best performance with balanced province-to-population ratio
- "Crowded" provinces increase the time complexity

Results and Validation

- Validated against Italian COVID-19 data
- Successfully reproduced:
 - Infection peaks and valleys
 - Death rates
 - Regional variations
- Matches real-world patterns in shorter timeframes

Conclusions

- Successfully integrated best features of both models
- Improved generalization for different scenarios
- Added GUI-based configuration
- Achieved realistic epidemic simulation
- Clear understanding of scaling limitations

Open Problems and Research Directions

- Refinements: Seasons and months, home membranes for singles or groups of people, additional place membranes,...
- Parallelisation (GPUs)
- Hyper-parameters optimization
- Government measure influence: quarantine, movement restrictions, ...
- Consider different kinds of infections
- Antibiotic resistance modeling