Lecture 5
Agent Methods to Modeling Virus Pandemics - A quick reference to Complexity

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Five Lectures by
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From a Mathematics of Living Systems

to Modeling Virus Pandemics

P.1. Plan of the Lectures

Nicola Bellomo **Lecture 1. A Quest Towards a Mathematical Theory of Living Systems**

Diletta Burini **Lecture 2. Mathematical Tools of the Kinetic Theory of Active Particles**

Nicola Bellomo, Diletta Burini and Nisrine Outada **Lecture 3. Towards a Mathematical Theory of Virus Pandemics - Models with Mutations, Variants and Vaccination Programs**

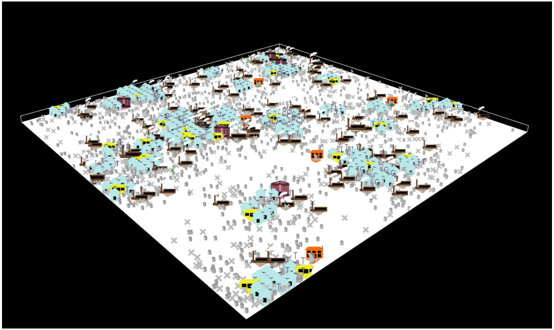
Damian Knopoff **Lecture 4. Heterogeneity and Networks**

Pietro Terna **Lecture 5. Agent Methods to Modeling Virus Pandemics - A quick reference to complexity**

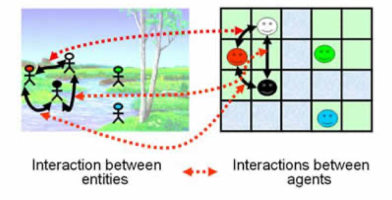
Pietro Terna **Closure, Description of the material support to the Lectures, Acknowledgments**

5.1. Agent Methods and Virus Pandemics

We introduce a model of interacting agents, following plausible behavioral rules into a world where the Covid-19 epidemic is affecting the actions of everyone. In a complexity perspective, the model is generative of dynamics emerging from the consequences of agents' actions and interactions, with high variability in outcomes and stunning realistic reproduction of the successive contagion waves in the reference region. Complexity will be also introduced as a fundamental scientific paradigm.



An image to introduce the idea of Agent Based Model (ABM).



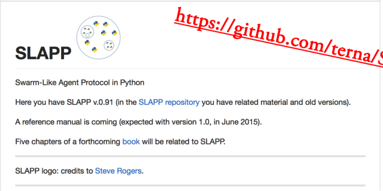
From M. Galán, L.R. Izquierdo, S.S. Izquierdo, J.I. Santos, R. del Olmo, A. López- Paredes, B. Edmonds: Errors and artefacts in agent-based modelling. *Journal of Artificial Societies and Social Simulation*, 12 (1):1, 2009. ISSN 1460-7425.

`http://jasss.soc.surrey.ac.uk/12/1/1.html`

5.3. Agent Methods and Virus Pandemics

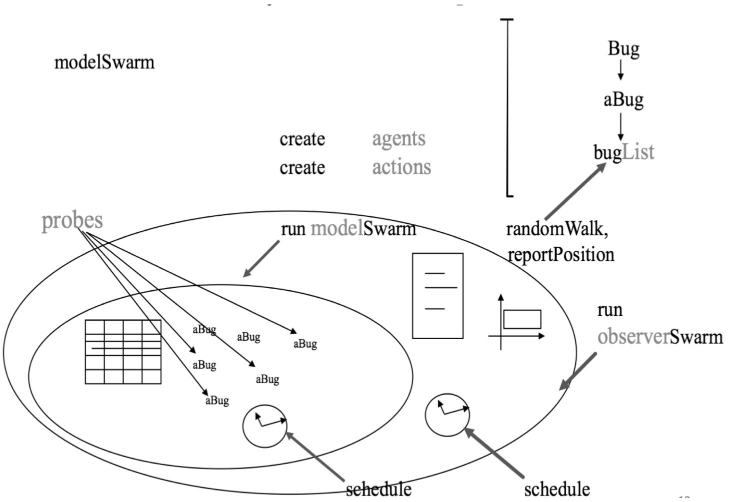
From *Santa Fe* Swarm(1995, http://www.swarm.org) to SLAPP, in Python and with a better time management

Repast4Py



https://github.com/terna/SLAPP3/

A scheme related to the *root* structure of Swarm.



5.5. Agent Methods and Virus Pandemics

An ABM on virus diffusion

G. Pescarmona, P. Terna, A. Acquadro, P. Pescarmona, G. Russo, E. Sulis, and S. Terna. An Agent-Based Model of COVID-19 Diffusion to Plan and Evaluate Intervention Policies, pp. 203–257. Birkhäuser (Springer International Publishing), Cham, 2021. ISBN 978-3-030-91646-6. doi: 10.1007/978-3-030-91646-6 9. URL https://doi.org/10.1007/978-3-030-91646-6 9.
(Preprint at `https://arxiv.org/abs/2108.08885`),

5.6. Agent Methods and Virus Pandemics

- A micro-based model of interacting agents, following plausible behavioral rules into a world where the Covid-19 epidemic is affecting the actions of everyone.
- The model works with:
  - i infected agents categorized as symptomatic or asymptomatic and
  - ii the places of contagion specified in a detailed way, thanks to agent-based modeling capabilities.
- The infection transmission is related to three factors: the infected person's characteristics and those of the susceptible one, plus those of the space in which a contact occurs.

5.8. Agent Methods and Virus Pandemics

- The micro-based structure of the model allows factual, counterfactual, and conditional simulations to investigate both the spontaneous or controlled development of the epidemic. Examples of counterfactual situations are those considering:
  - i different timing in the adoption of the non-pharmaceutical containment measures;
  - ii alternative strategies focusing exclusively on the defense of fragile people.
- The model generates complex epidemic dynamics, emerging from the consequences of agents' actions and interactions, with high variability in outcomes, but frequently with a stunning realistic reproduction of the contagion waves that occurred in the reference region.
- We take charge of the variability of the epidemic paths within the simulation, running batches of executions with 10,000 occurrences for each experiment.

5.8. Agent Methods and Virus Pandemics

- The AI and inverse generative sides of the model come from constructing a meta-agent optimizing the vaccine distribution among people groups—characterized by age, fragility, work conditions—to minimize the number of symptomatic people (deceased persons come from there).
- We can characterize the action of the planner both:
  - i introducing ex-ante rules following "plain" or "wise" strategies that we imagine as observers or
  - ii evolving those strategies via the application of a genetic algorithm.
- The genome is a matrix of vaccination quotas by people groups, with their time range of adoption.

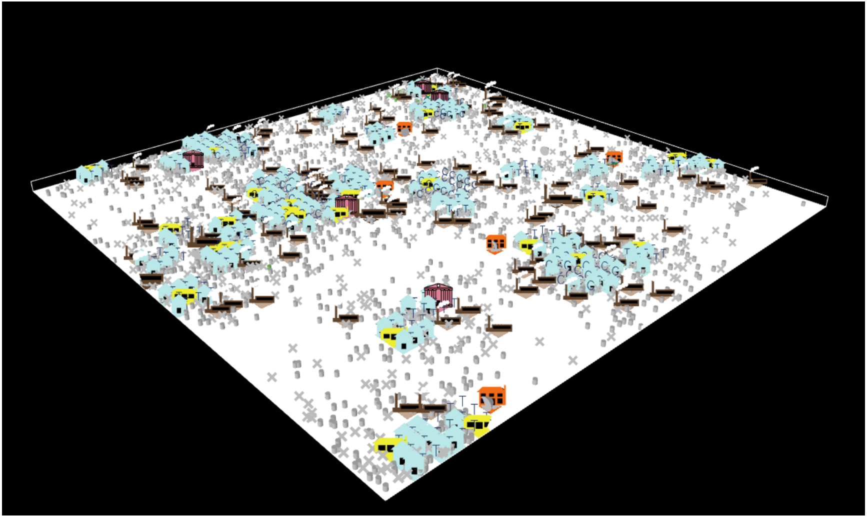
5.9. Agent Methods and Virus Pandemics

- As the agents can be Susceptible, Infected, symptomatic, asymptomatic, and Recovered, the name of the model is S.I.s.a.R., with the capital letters recalling the S.I.R. scheme.
- We use NetLogo, at `https://ccl.northwestern.edu/netlogo/`.
- S.I.s.a.R. is at `https://terna.to.it/simul/SIsaR.html` with information on model construction, and an online executable version.
- Our reference paper, from now on **"the paper"**, quoted in slide 5.5, is at `https://arxiv.org/abs/2108.08885`
- The model includes the structural data of Piedmont, an Italian region, but we can easily calibrate it for other areas. The simulation reproduces a realistic calendar (e.g., national or local government decisions) via a dedicated script interpreter.

5.10. Agent Methods and Virus Pandemics

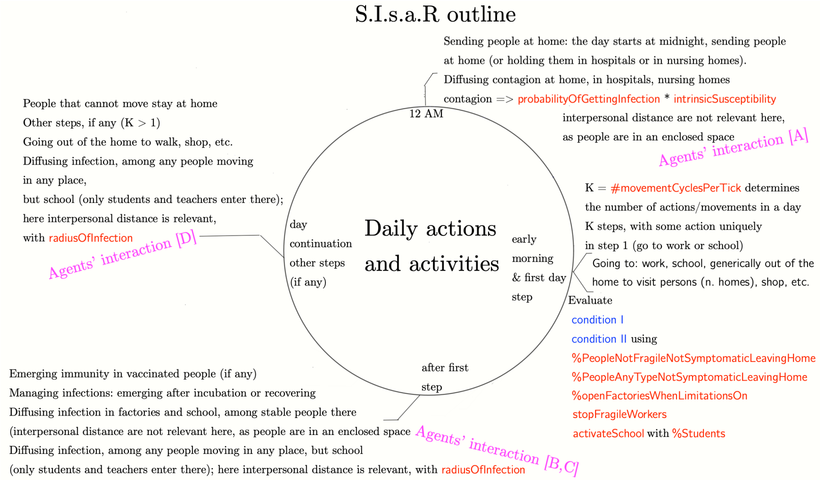
- $1 : 1000$, for a population of 4,350,000 people.

- Houses.
- Schools.
- Hospitals.
- Nursing homes,
- Factories.



The world 3D

5.12. Agent Methods and Virus Pandemics

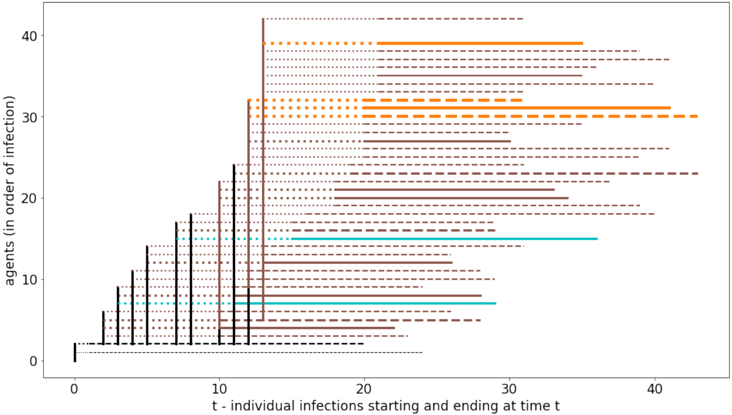


The scheme: def. and values of the parameters at
`https://terna.to.it/simul/howSIsaRworks.pdf`

Contagion representation

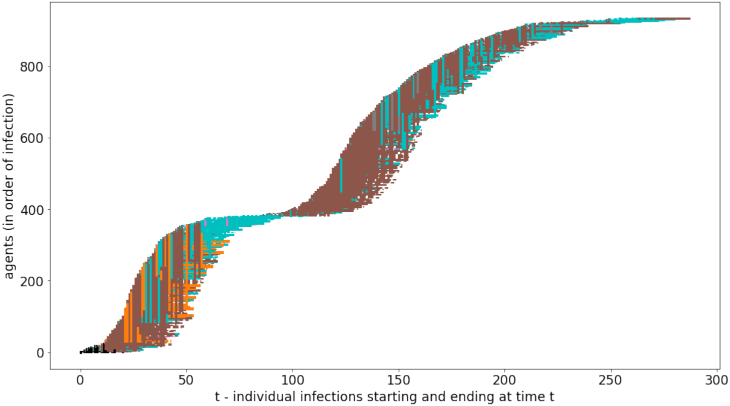
- The model allows analyzing the sequences of contagions in simulated epidemics, reporting the places where the contagions occur.
- We represent each infected agent as a horizontal segment (from the starting date to the final date of the infection) with vertical connections to other agents if they receive the disease.
  We represent the new infected agents via further segments at an upper level.
- With colors, line thickness, and styles, we display multiple information.
- This enables understanding at a glance how an epidemic episode is developing. In this way, it is easier to reason about countermeasures and, thus, to develop intervention policies.

Examples (1/2)



A case with containment measures, first 40 infections: workplaces (brown) and nursing homes (orange) strictly interweaving

Examples (2/2)

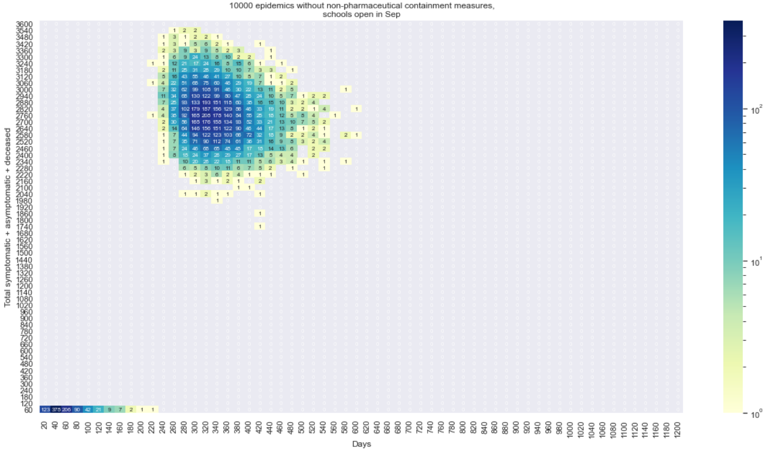


A Case with containment measures, the whole epidemics: workplaces (brown) and nursing homes (orange) and then houses (cyan), with a bridge connecting two waves

Explorations

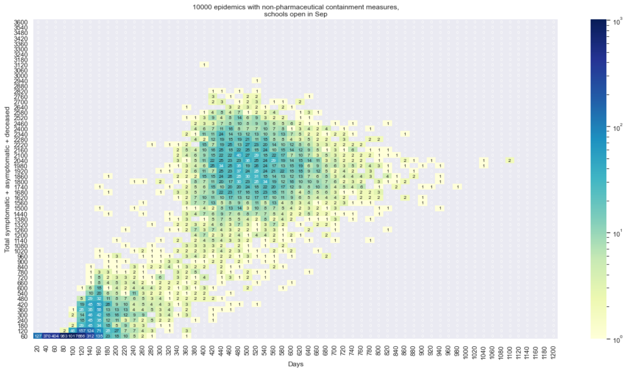
- We explore systematically the introduction of factual, counterfactual, and prospective interventions to control the spread of the contagions.
- Each simulation run—whose length corresponds to the disappearance of symptomatic or asymptomatic contagion cases—is a datum in a wide scenario of variability in time and effects.
- We need to represent compactly the results emerging from batches of simulation repetitions, to compare the consequences of the basic assumptions adopted for each specific batch.
- Each heat-map reports the duration of each simulated epidemic in the x axis and the number of the symptomatic, asymptomatic, and deceased agents in the y axis. The z axis is represented by the colors, as in the logarithmic scale on the right of each picture.
- In our batches we have 10,000 runs.

10,000 epidemics without control in Piedmont, first wave, March 2020



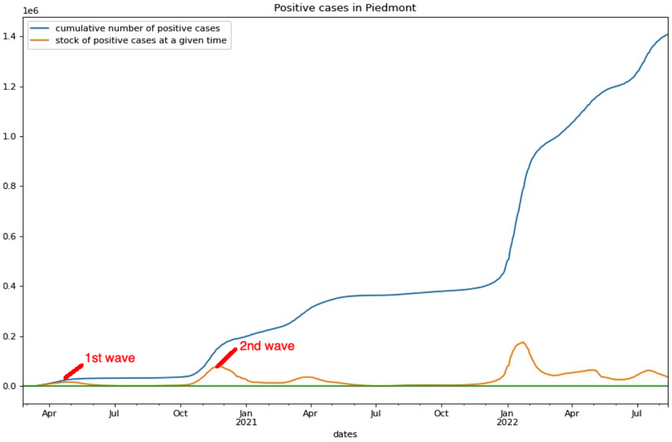
Without non-pharmaceutical containment measures

10,000 epidemic with basic control in Piedmont, first wave, March 2020



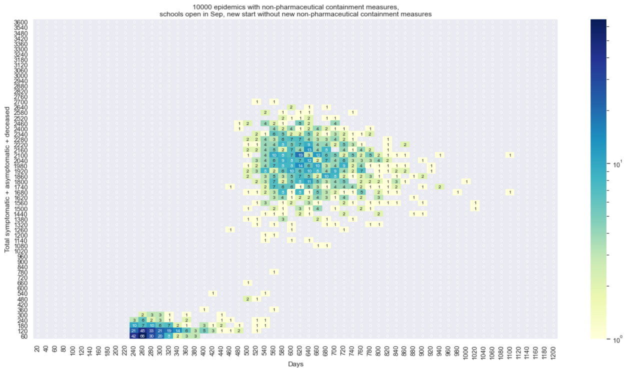
First wave with non-pharmaceutical containment measures

Contagion waves



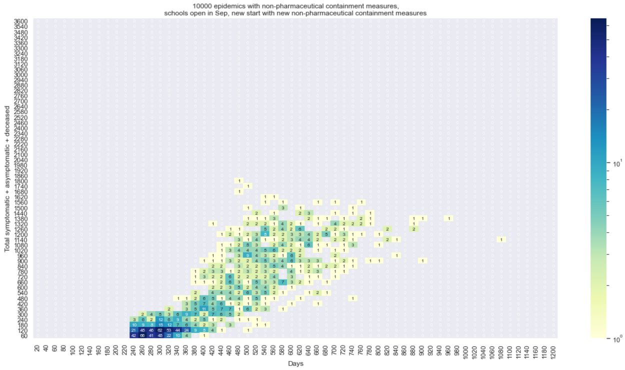
Data for Piedmont

Second wave, new infections from outside, without specific measures



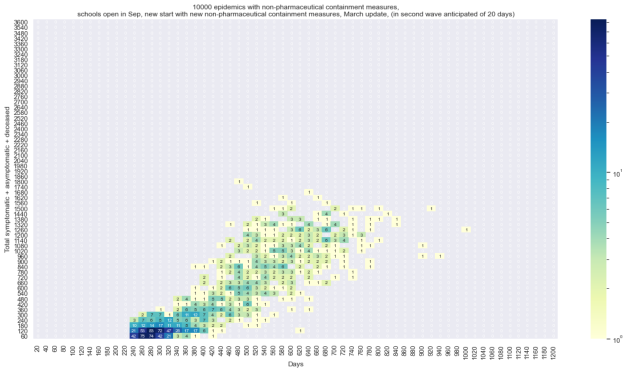
Second wave, without specific measures

Second wave, new infections from outside, with new specific non-pharmaceutical containment measures



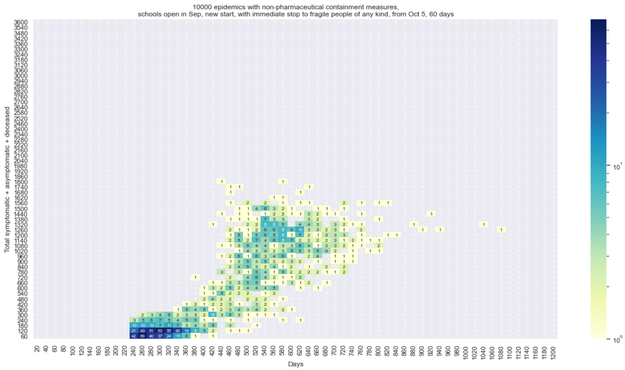
Second wave, with specific measures

Counterfactual: 3 weeks anticipation on the intervention



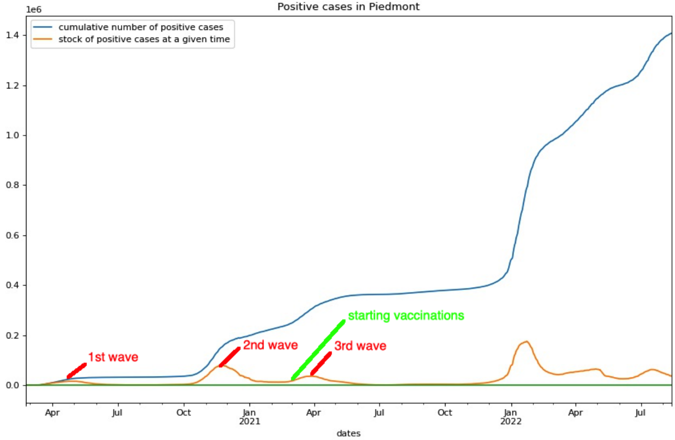
Second wave, with specific measures, 3 weeks anticipation

Counterfactual: stopping fragile people, including fragile workers



Second wave, uniquely stopping fragile people, including fragile workers

Planning a vaccination campaign using Genetic Algorithms (1/2)



Data for Piedmont

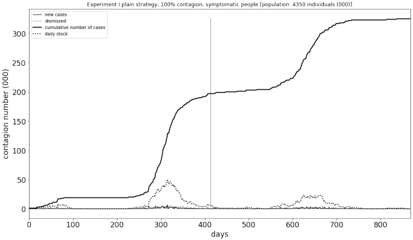
Planning a vaccination campaign using Genetic Algorithms (2/2)

- We compare the effect of choosing the vaccination quotas via GAs with two predetermined strategies, considering three hypotheses (vaccinated people: still spread the contagion; do not spread the contagion; do it in the 50% of the cases); we show here only the first case results.
- Key dates:
  - in the internal calendar of the model, day 373 is Feb. 12th, 2021, which is effectively the starting point of the vaccinations in the region;
  - the day of the effectiveness of the initial vaccinations, 40 days later, is day 413 (Mar. 22nd, 2021).

Vaccination groups

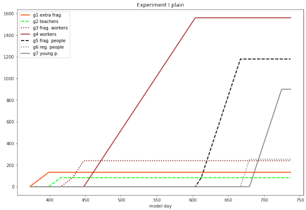
- g1 extra fragile people with three components;
  - due to intrinsic characteristics: people in nursing homes;
  - due to risk exposure:
    - nursing homes operators;
    - healthcare operators;
- g2 teachers;
- g3 workers with medical fragility;
- g4 regular workers;
- g5 fragile people without special characteristics;
- g6 regular people, not young, not worker, and not teacher;
- g7 young people excluding special activity cases (a limited number in g1).

Time dynamics without vaccinations

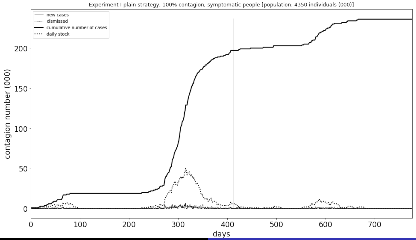


Experiment I, base symptomatic series; the vertical line is at day 413 is not relevant here

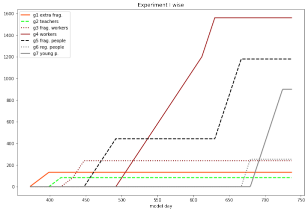
Plain vac. strategy, vac. people still spreading the infection



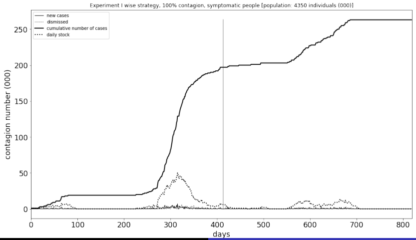
"Plain" vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)



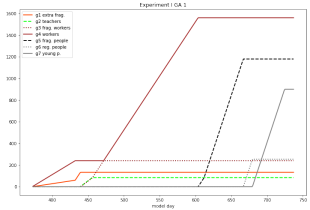
Wise vac. strategy, vac. people still spreading the infection



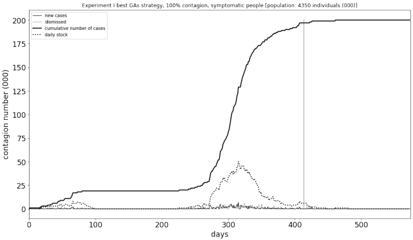
"Wise" vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)



Best GAs strategy, vac. people still spreading the infection



GAs vaccination sequence; on the y axis the number of vaccinated subjects of each group (if vaccination is complete, the line is horizontal)



5.31. Complexity in collective behaviors

- We are not living in a perfect world where anything can be explained by deterministic calculation, as in the Leibniz dream (*).
- Unfortunately (fortunately?), we have to cope with complexity.

(*) (Free translation from Latin) *In the future, when an issue is controversial, it will not be necessary to dispute between two philosophers but between two subjects able in computations. It will suffice them to keep the abacus into their hands, sit down, and say each other—in a friendly way—start making calculations.*
Gottfried Wilhelm von Leibniz, 1646–1716, in Opera philosophica, xi. De scientia universali seu calculo philosophico

https://fr.wikisource.org/wiki/Page:Leibniz_-_Opera_philosophica,_ed._Erdmann,_1840.djvu/38.

Complexity in collective behaviors

Leibniz was not aware of the existence of the "complexity" phenomenon, due to the emergence of entirely new properties at any new level of aggregation.

From where to start to understand complexity? In Aristotle, complexity seems opposed to simplicity as a matter of lifestyle. In Latin, the world *complexus* means what is woven together.

In the 40s of the last century, von Neumann was working with automata and their complexity, but: *he described his own concept of complexity as «vague, unscientific and imperfect»* (from McMullin, 2000).

***** B. McMullin. John von Neumann and the evolutionary growth of complexity: Looking backward, looking forward... In Artficial Life, volume 6, pages 347–361. MIT Press, 2000.

http://www.eeng.dcu.ie/~alife/bmcm-alj-2000/bmcm-alj-2000.pdf.

Complexity in collective behaviors

If we jump to the 60s of the last century, we have the Kolmogorov complexity, as the length of the shortest computational sequence producing a specific object as output. Beautiful, but not a reply to our search about what complexity is.

The concept was there, but missing of a clear interpretation and definition; must of all, confused with the *ascientific and antireductionist holism*, i.e., the idea that we should view many systems (physical, biological, social, our body, etc.) as wholes, not merely as collections of parts. Sure, but then what?

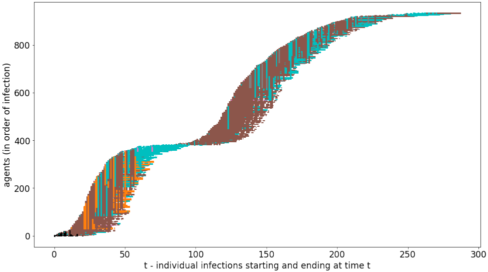
Complexity in collective behaviors

So, neither holism nor simple reductionism, but with Nobel Laureate Philip Anderson (born 1923), in 1972 we have the "More is different" clarification: *(p.393) The reductionist hypothesis may still be a topic for controversy among philosophers, but among the great majority of active scientists I think it is accepted without questions. The workings of our minds and bodies, and of all the animate or inanimate matter of which we have any detailed knowledge, are assumed to be controlled by the same set of fundamental laws (...) The main fallacy in this kind of thinking is that the reductionist hypothesis does not by any means imply a "constructionist" one (...) The constructionist hypothesis breaks down when confronted with the twin difficulties of scale and complexity. The behavior of large and complex aggregates of elementary particles, it turns out, is not to be understood in terms of a simple extrapolation of the properties of a few particles. Instead, at each level of complexity entirely new properties appear (...).*

* P. W. Anderson. More is different. Science, 177(4047):393–396, 1972.

https://www.tkm.kit.edu/downloads/TKM1_2011_more_is_different_PWA.pdf..

Back: complexity in different population layer interaction



END Lecture 5!