Disaggregation of a SIRD model for policy testing in targeted groups of the population

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ETH Workshop

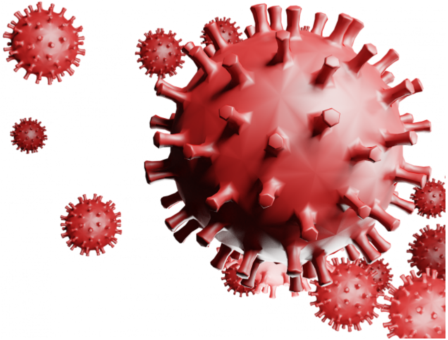
Agenda

- Introduction and Motivation
- State of the Art
- SIRD Disaggregated Model
- Results
- Conclusion

Motivation

Challenges

- Accounting for individual behaviour through an epidemic outbreak by using **large scale models**.
- Difficulty of finding **disaggregated data** to **validate** the model.
- Capturing **spread of the disease** through **daily activities**.
- Allows to **assess the impact** that a certain policy has on **different segments of the population**.
- Epidemiological datasets are becoming available.



Research gaps

Limitations

- Lack of data leads to add aggregated parameters inside the agent-based models, [TYK+20].
- Agent-based models in order to define more targeted and less disruptive interventions. Results are achieved using real-time data-driven analysis, [AMCB+20].
- Clear methodology to know which variables are meaningful inside an epidemiological model, for example income or residence place, [CPK+21].
- Make the probabilities time dependant, since an early adoption can potentially allow to contain the epidemics, [MBCV20].

Outline of this talk

1. Added value of using disaggregate models for modelling SARS-CoV-2 spreading. [1]
2. Description of the preliminary considerations and presentation of a model that accounts for virological and socio-economic variables.[2]
3. Potential of these models to study SARS-CoV-2 policy decision making.[3]

Literature:

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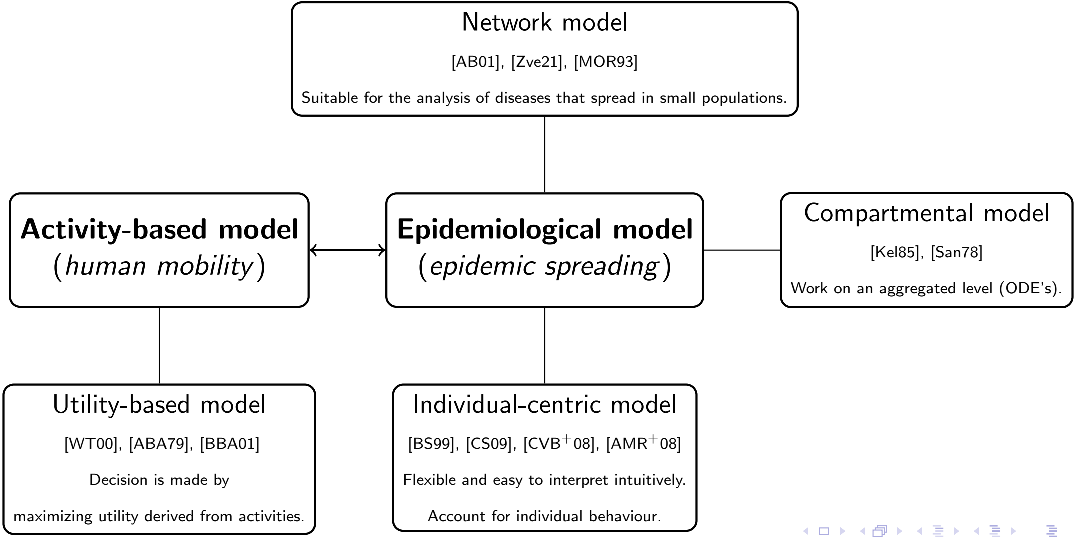
[2] S. Chang, E. Pierson, P. Koh, J. Gerardin, B. Redbird, D. Grusky, andJ. Leskovec. Mobility network models of covid-19 explain inequities and inform reopening. Nature, 589:1-6, 01 2021.

[3] M. Mancastroppa, R. Burioni, V. Colizza, and A. Vezzani. Active and inactive quarantine in epidemic spreading on adaptive activity-driven networks. Physical Review E, 102, 08 2020.

State of the Art

State of research



Compartmental models

The SIR epidemic model can be written in the following way(c.f [KMS17]):

- The transitions at each time step Δt are:

$$\frac{\partial S}{\partial t}(t) = -\lambda I(t)\frac{S(t)}{N}$$
$$\frac{\partial I}{\partial t}(t) = \lambda I(t)\frac{S(t)}{N} - \gamma I(t)$$
$$\frac{\partial R}{\partial t}(t) = \gamma I(t)$$

Notation	Parameters
λ	Contagion rate between S and I.
$1/\gamma$	Length of the infectious period for population I.

- S: Susceptible
- I: Infected
- R: Recovered

Compartmental model

[Kel85], [San78]

Work on an aggregated level (ODE's).

SIRD Disaggregated Model

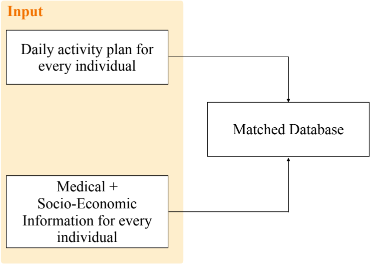
SIRD Disaggregated Model

Input

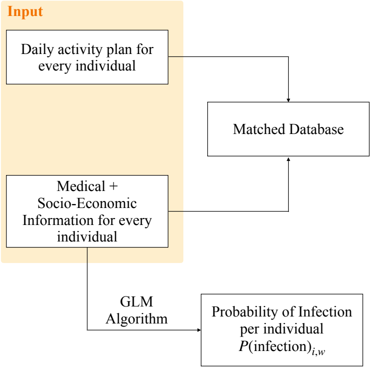
Daily activity plan for every individual

Medical + Socio-Economic Information for every individual

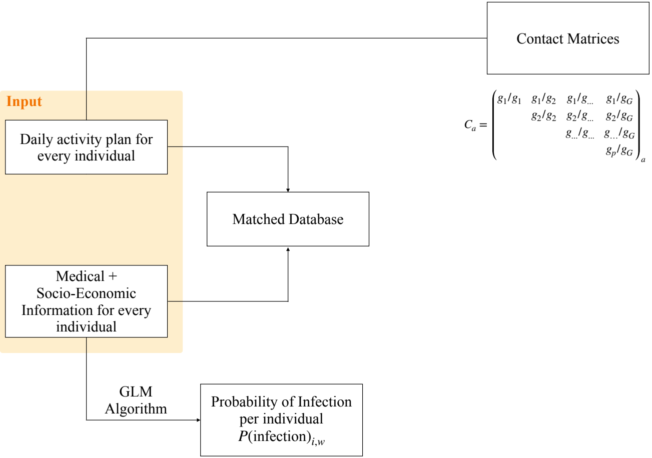
SIRD Disaggregated Model



SIRD Disaggregated Model



SIRD Disaggregated Model



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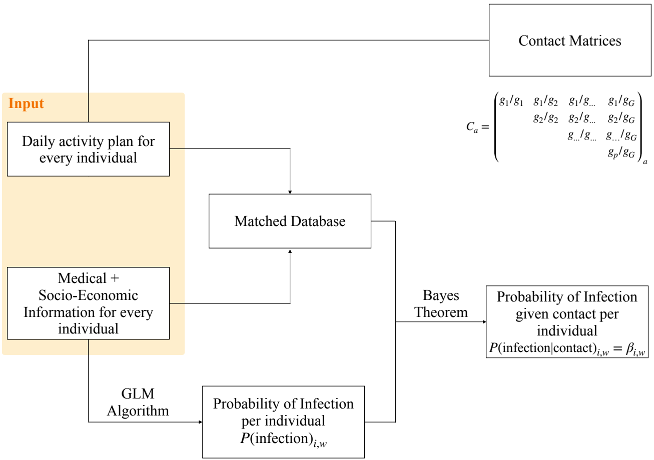

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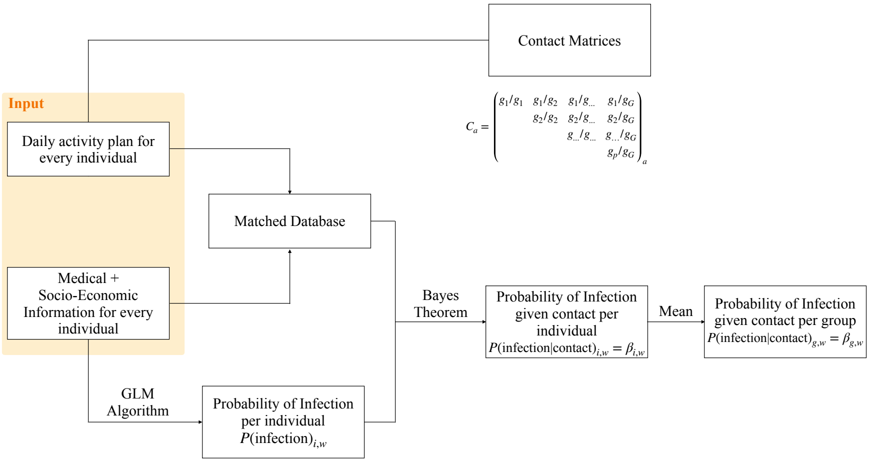

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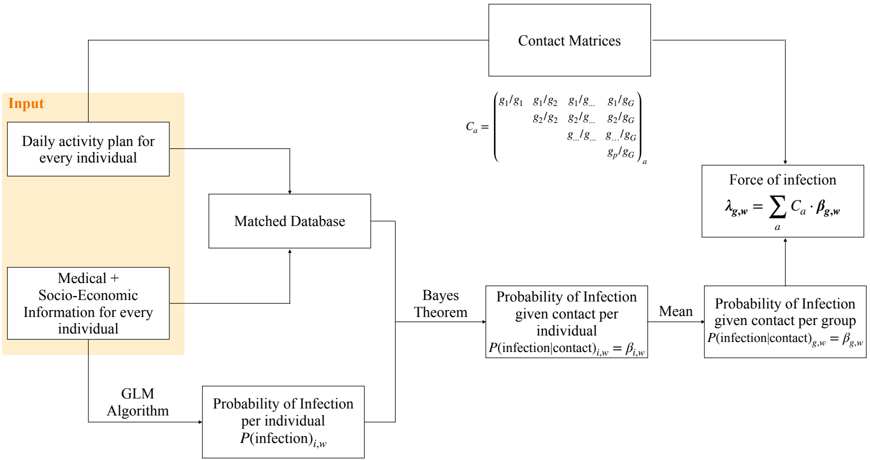

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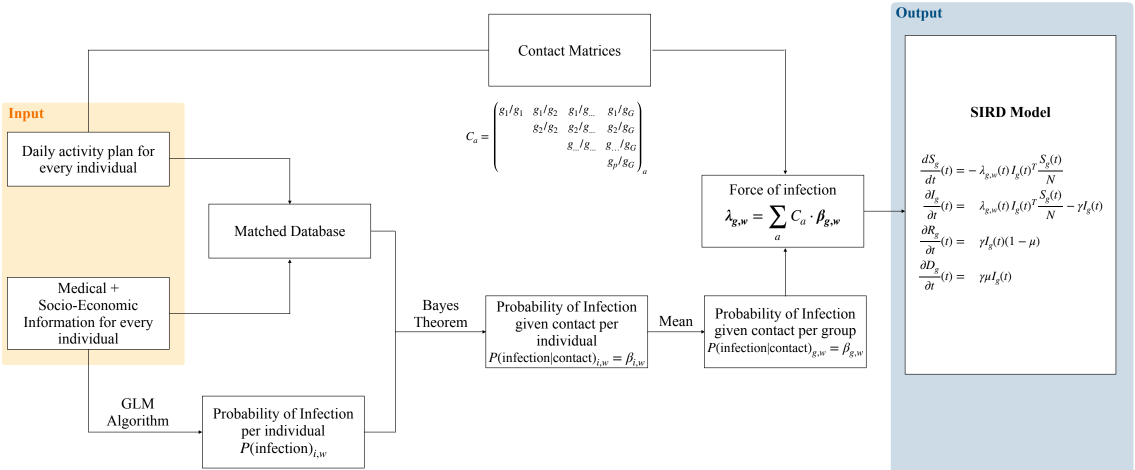

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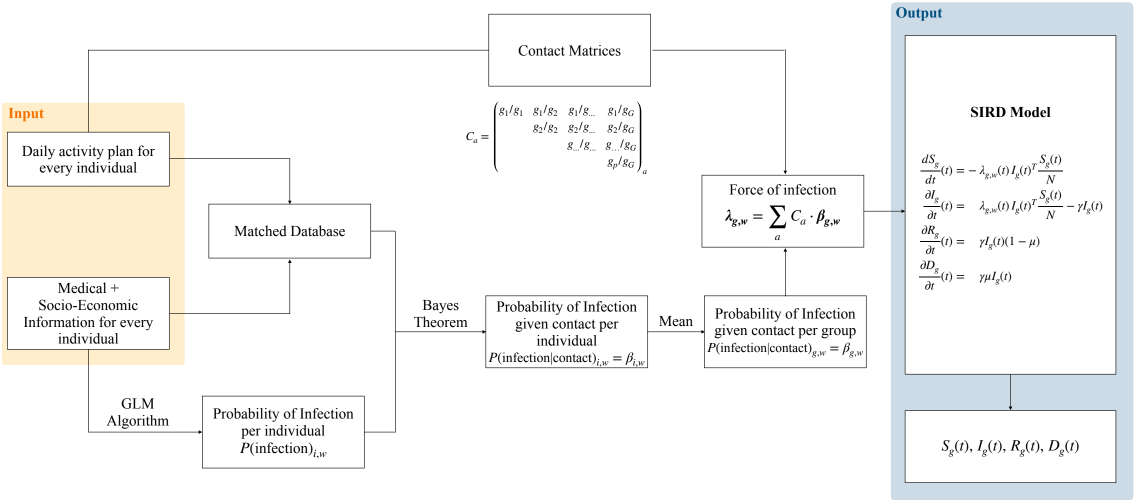
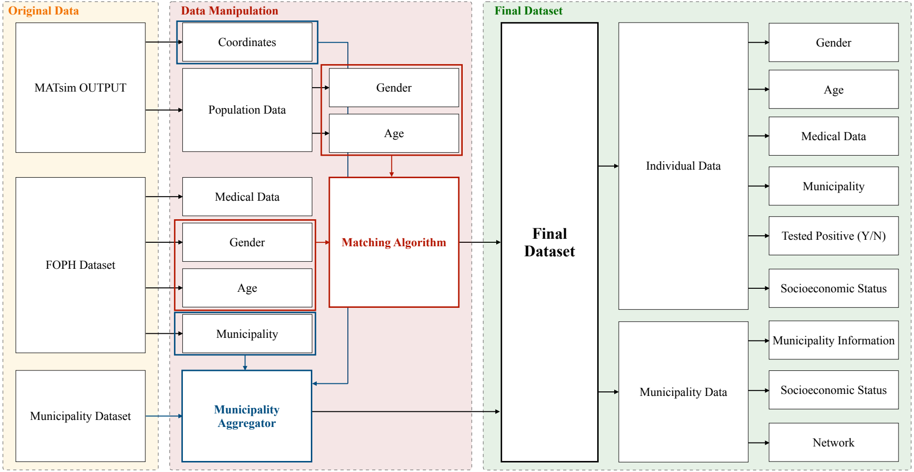
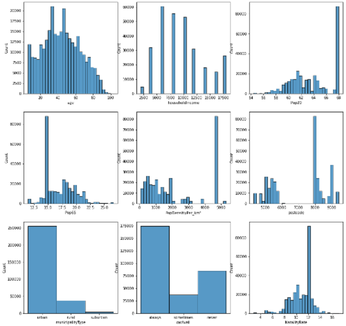


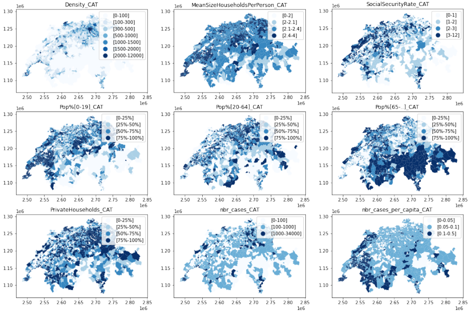
Results

Pre-process [HB21], [RPA$^+$21], [BFS22]



Pre-process





Density_CAT
[0-100]
[100-300]
[300-500]
[500-1000]
[1000-1500]
[1500-2000]
[2000-12000]
MeanSizeHouseholdsPerPerson_CAT
SocialSecurityRate_CAT
Pop%[0-19]_CAT
[0-25%]
[25%-50%]
[50%-75%]
[75%-100%]
Pop%[20-64]_CAT
PrivateHouseholds_CAT
nbr_cases_CAT
[0-100]
[100-1000]
[1000-34000]
nbr_cases_per_capita_CAT

Activity Contact Matrix

- We stratify the model into 4 age groups:
  - C = the individuals younger than 18 years old,
  - A1 = individuals between 19 and 35 years-old,
  - A2 = individuals between 36 and 55 years-old
  - E = individuals over 56 years-old

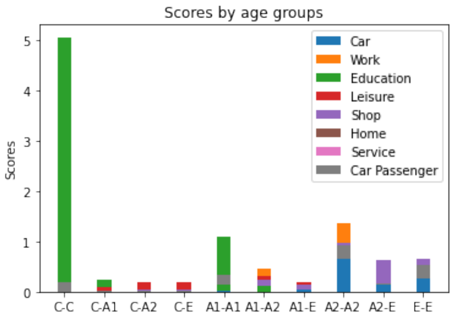
- The segmentation endows our model with high flexibility for policy testing on the different population groups. The contact matrix C_a becomes:

	child (C)	*adult1 (A1)*	*adult2 (A2)*	*elderly (E)*
child	child / child	child / adult1	child / adult2	child / elderly
adult1	-	adult1 / adult1	adult1 / adult2	adult1 / elderly
adult2	-	-	adult2 / adult2	adult2 / elderly
elderly	-	-	-	elderly / elderly

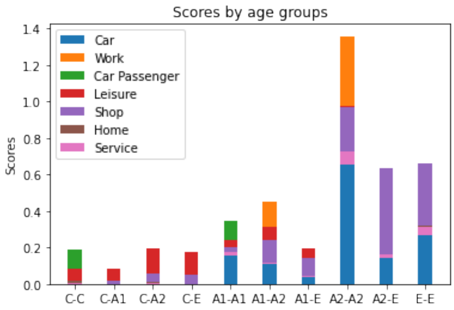
Table: Contact matrix structure for each activity

Activity Contact Matrix

All activities



Education removed



Generalized Linear Model Regression

$$P(\text{infection})_{i,1} \sim \beta_\Lambda \log(\Lambda) + \beta_\chi \log(\chi) + \beta_\Upsilon \log(\Upsilon) + \beta_\kappa \log(\kappa). \quad (1)$$

$$P(\text{infection})_{i,2} \sim \beta_\Lambda \log(\Lambda) + \beta_\chi \log(\chi) + \beta_\Upsilon \log(\Upsilon) + \beta_\kappa \log(\kappa) + \beta_\Phi \Phi. \quad (2)$$

Where:

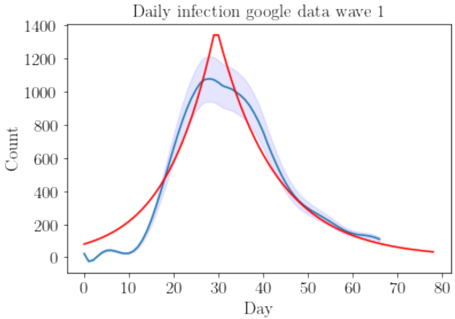
- The age of the individual: Λ.
- The percentage of the population above 65 years old for a specific municipality: χ.
- The percentage of the population between 20 and 65 years old for a specific municipality: Υ.
- The population density per km: κ.
- The income: Φ.

SIRD Disaggregated Model Output

Assumptions:

We reduce the activities the 24^{th} of March 2020 to:

- 100% Education.
- 90% Leisure and Services.
- 80% Work.
- 70% Shop.
- 60% Car and car passenger.



Conclusions and future work

- The most significant contributions are:
  - We capture how the socio-economic characteristics of an individual define the force of infection
  - We obtain a self-explanatory model, defined by the estimates of the variables that characterize the spreading event
  - We obtain high goodness of fit of our model with Google data.
- The future work includes:
  - Improve and validate the current model
  - Scale it up to more groups.
  - Include it in an optimization framework to use it for policy analysis.

Thank you

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Generalized Linear Model Regression

Summary of statistics list of covariates

Table: Summary statistics of the list of covariates

	1^{st} WAVE			2^{nd} WAVE		
Stratified by infection	0	1	SMD	0	1	SMD
n	269642	414		281576	14499	
$\Lambda(mean(SD))$	44.42 (20.99)	50.91 (20.24)	0.315	44.43(21.05)	43.33(19.68)	0.054
$\Upsilon(mean(SD))$	3.89 (3.27)	65.17 (3.07)	0.0400	63.63(3.30)	63.91(3.25)	0.086
$\kappa(mean(SD))$	2399.74 (1760.49)	3123.01 (1733.89)	0.414	2222.49(1771.15)	2401.70(1751.82)	0.102
$\chi(mean(SD))$	16.89 (2.50)	16.26 (2.29)	0.0264	17.04(2.56)	16.84(2.48)	0.077
$\Phi(mean(SD))$				0.02(0.13)	0.02(0.12)	0.002

Generalized Linear Model Regression

Summary of the estimates using Causal Inference

Table: Coefficients using Matching score algorithm

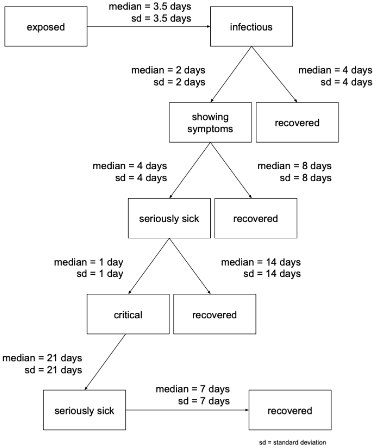
Variable	1^{st} WAVE Est.	SE	z-val.	p-val.	2^{nd} WAVE Est.	SE	z-val.	p-val.
$\log(\Lambda)$	0.641	0.101	6.321	$2.590\mathrm{e}-10$	0.0301	0.0143	2.100	0.0358
$\log(\chi)$	1.395	0.773	1.806	0.0701	-0.386	0.107	-3.608	0.000309
$\log(\Upsilon)$	7.388	2.893	2.554	0.0106	-2.0381	0.391	-5.211	$1.880e-07$
$\log(\kappa)$	0.281	0.109	2.594	0.00950	0.187	0.0141	13.246	$< 2\mathrm{e}-16$
Φ					-0.0556	0.0261	-2.131	0.0331

SIR model used in Episim, [MBC+20]

- The probability for person n to become infected by this process in a time step t in [MBC+20]:

$$P_{n,t} = 1 - \exp\left[-\Theta \sum_{m} q_{m,t} \cdot ci_{nm,t} \cdot in_{n,t} \cdot \tau_{nm,t}\right]$$

- **Main issues of this probability:**
  - Parameters unknown for COVID-19, so set to $value = 1$,
  - All multiplying so it might be independent modifying one or another,
- We want to create dependence on not only individual and time but also on the location.



Activity-based model [AG92]

- They allow more complex policies to be evaluated.
- The phenomena are understood as the result of the interaction of multiple agents, each guided by individual norms or intelligence.
- This interaction results in a complex system, consisting of many sub-systems and agents (applicable to many disciplines: ecology, economics, computer simulation...).
- It uses microscopic simulation.
- Examples: MATsim, TRANSIMS...

Epidemiological models

Issues:

- SEIR models work on an aggregate level: neglects the imperfect mixture.
- Not transferable to different epidemics.
- Crutial parameters might not be available.
- Exponential is a strong assumption.

Network models

The graph G is defined by n vertices, and m edges:

$\{G_1, G_2, \ldots, G_n\}$, where $n = \binom{M}{m}$ with $M = N(N-1)/2$.

The probability of picking each graph is the same:

$1/n$.

Network models

Issues:

- Complex to find the correct adjacency matrix.
- Difficult to use them in densely populated areas.
- Quality of the contacts between two individuals. The adjacency matrices are binary.
- Static character of network models.

Individual-centric models

If an individual is susceptible and it has contact with an infected agent, it becomes infected with a probability: p.

This probability can be defined as desired. For example in [Smi09], the probability for person n to become infected by this process in a time step t is defined as:

$$P_{n,t} = 1 - \exp\left[-\Theta \sum_{m} q_{m,t} \cdot ci_{nm,t} \cdot in_{n,t} \cdot \tau_{nm,t}\right]$$

Main issues of this probability:

- Parameters unknown for COVID-19, so set to $value = 1$,
- All multiplying so it might be independent modifying one or another,
- We want to create dependence on not only individual and time but also on the location.

Individual-centric models

- $\rightarrow$ insight on transmission and intervention that will complete what can be obtained with usual compartmental models (SIR).
- Added value of these models . . .
  - The interactions between agents are nonlinear, discontinuous or complex..
  - When the space is crucial and we do not have fixed positions.
  - Population is heterogenous with different socioeconomic characteristics.
  - Agents have complex behaviour.
  - Topology of interactions is complex.