Social Simulation of the COVID-19 Disaster

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Collaboration with

- **Infection spreading**
  Naoki Yoshioka (RIKEN Center for Computational Science), Akira Endo(London School of Hygiene & Tropical Medicine)
  Mariko Kurokawa (Metropolitan Cancer and Infectious Diseases Center Komagome Hospital)
- **Macroeconomics**
  Hiroyasu Inoue(Hyogo Univ.), Yohsuke Murase (RIKEN Center for Computational Science), Yasuyuki Todo(Waseda Univ.)
- **Corporation activities**
  Jun-Ichi Ozaki, Hideki Takayasu, Misako Takayasu(Tokyo Inst. Tech.)
- **Social sentiment**
  Yukie Sano(Tsukuba Univ.), Kenta Yamada(Ryukyu Univ.)
  Shinya Kitamura, Hayato Goto, Ryuya Oosato(Teikoku Data Bank)

Acknowledgment
use of the Fugaku (The evaluation environment in the trial phase) provided by the R-CCS

Fugaku

RIKEN R-CCS COVID-19 activities with Fugaku

RIKEN R-CCS

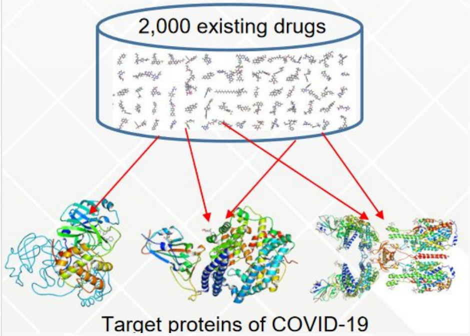
Exploring new drug candidates for COVID-19 by "Fugaku"

RIKEN / Kyoto University Yasushi OKUNO, Prof. PhD.

Research content:

...rseas to confirm the effects of existing
...e drug has shown efficacy through these
...and no effective therapeutic drug has yet
...of drugs being tested, it is possible that

...ics calculations using "Fugaku" to search
...affinity for the target proteins of COVID-19
...nited to existing antiviral drugs targeted in



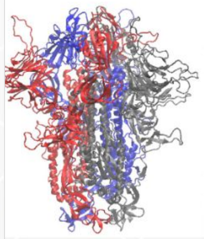
Drug search

Prediction of conformational dynamics of proteins on the surface of SARS-Cov-2 using Fugaku

RIKEN Yuji Sugita, Ph.D

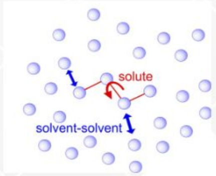
Research contents:

...e proteins that interact with virial receptor
...between the spike protein and the
...drug for COVID-19.
...determined using cryo-electron microscopy
...(MD) simulations of the spike protein in
...namic structures. We use GENESIS MD
...MD simulations on Fugaku compared to K
...art of the spike protein using a multicopy
...nal dynamics of the spike proteins.



...protein on the surface of
...RS-Cov-2

GENESIS Generalized-ensemble simulation system

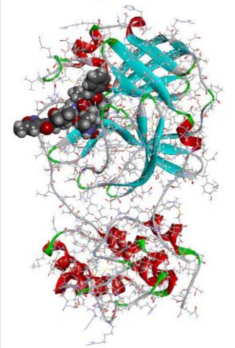


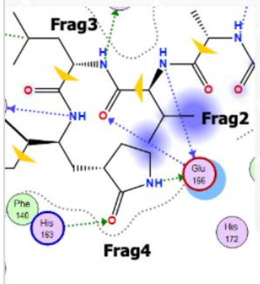
gREST can enhance motions of the solute region

MD

Fragment molecular orbital calculations for COVID-19 proteins

Yuji Mochizuki (Rikkyo University)





Simulation analysis of pandemic phenomena

RIKEN Nobuyasu Ito

Research content:

Social and economic impact is increasing globally, and Japan is now at critical bifurcation point. And challenges to make its visualization and "big data" mining have started. In this project,
...possible future of our
...e situation.
...s, and SNS text mining
...nce and
...of Hyogo, the

...nage after lockdown of Tokyo area:
...t 14th day by Dr. Inoue of the
...ne case of lockdown, but also parti...
...the "Fugaku" supercomputer.

Social step

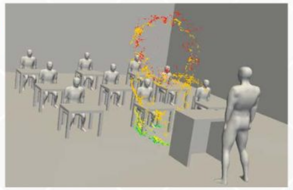
Prediction and Countermeasure for Virus Droplet Infection under the Indoor Environment

RIKEN / Kobe University Makoto TSUBOKURA

Outline of the Research:

Virus droplet infection caused by sneezing, coughing, or talking is strongly influenced by the flow, temperature and humidity of the air around an infected person and potential victims. Especially in the case of the new coronavirus, possibility of aerosol infection by atomized droplets is suggested in addition to the usual droplet infection. Because smaller aerosol particles drift in the air for a longer time, it is imperative to predict the scattering route and to estimate how surrounding airflow affects the infection so that the risk of droplet infection can be properly assessed, and effective measures to reduce infection can be proposed. In this project, massively parallel coupling simulation of virus droplet scattering, with airflow and heat transfer under the indoor environment such as inside a commuter train, offices, classrooms, and hospital rooms will be conducted. By taking into account the characteristics of the virus, its infection risk of virus droplets is assessed under various conditions. Then countermeasures to reduce the risk are proposed from a viewpoint of controlling the air flow.

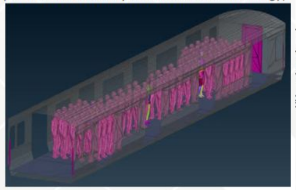
This project is a collaboration with RIKEN, Kyoto Institute of Technology, Kobe University, Osaka University, Toyohashi University of Technology, and Kajima Corporation. Complex Unified Simulation framework called CUBE, developed at RIKEN R-CCS and implemented on the supercomputer Fugaku, is mainly used, which will be the world-largest and highly accurate virus droplet simulation ever conducted.



An Example of virus droplet simulation in a classroom (By prof. Yamakawa of Kyoto Institute of Technology)

Expected Achievements:

The risk of droplet infection under the indoor environment is quantitatively evaluated, and specific countermeasures to reduce the infection risk is proposed in terms of effective ways of opening/closing windows, use of air conditioning, and placement of partitions. In addition, by creating animation of the droplet scattering and its spreading speed in the rooms from the simulation results, people can visually understand the risk of droplet infection and its countermeasures. These outputs from the simulation can protect the living and working environment from virus droplet infection, and contribute to earlier recovery of the socio-economic activities.



Simulation model of a cabin of a commuter train

Virus scattering

COVID-19 HPC Consortium | Who We Are | Collaborations | Projects | News & Press | Blo...

The COVID-19 High Performance Computing Consortium

Bringing together t...
academic leaders t...
powerful high-perf...
support of COVID-...

COVID-19: Globally

Coronavirus Cases:

35,708,182

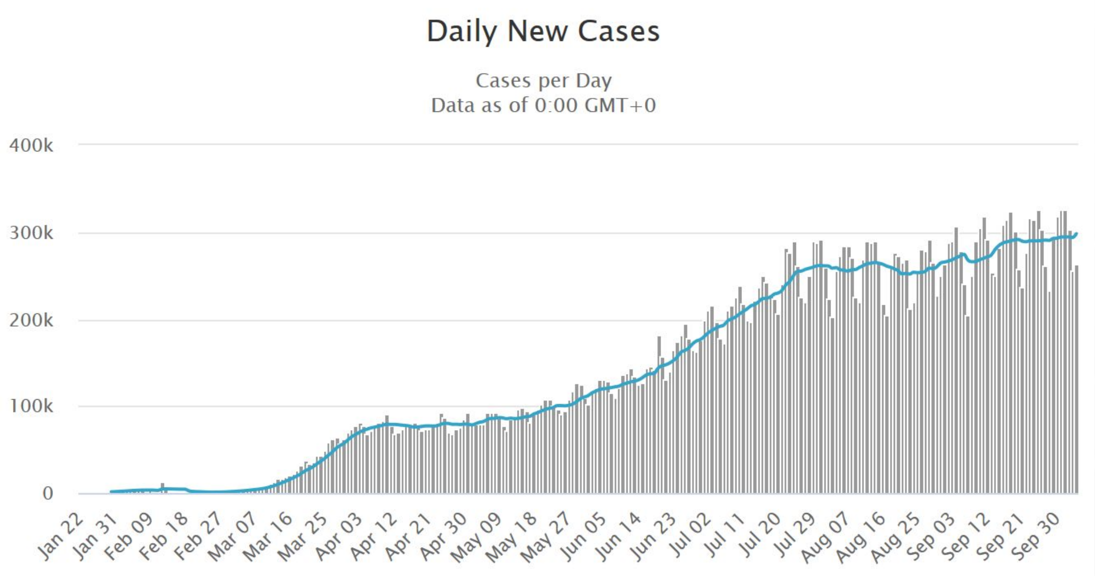
view by country

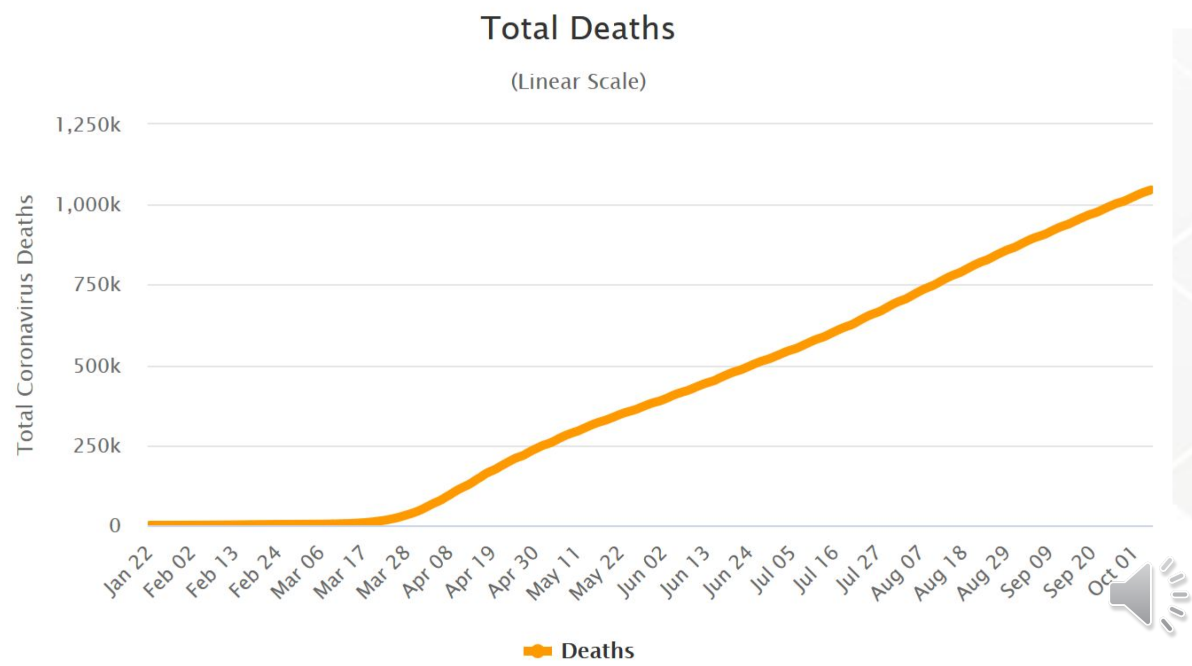
Deaths:

1,046,049

Recovered:

26,877,331





https://www.worldometers.info/coronavirus/

Fugaku

COVID-19: Japan

Japan

Coronavirus Cases:

85,739

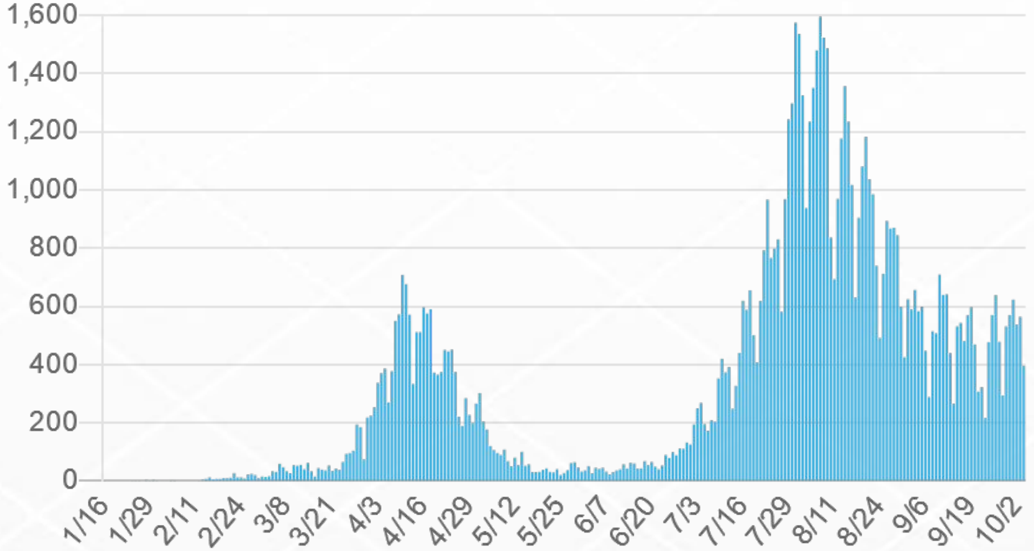
Deaths:

1,599

Recovered:

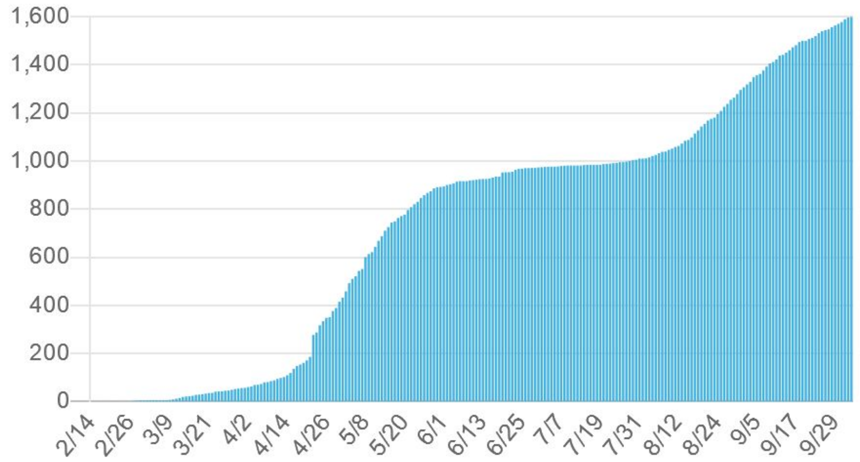
78,609

https://www.worldometers.info/coronavirus/



死亡者数（累計）

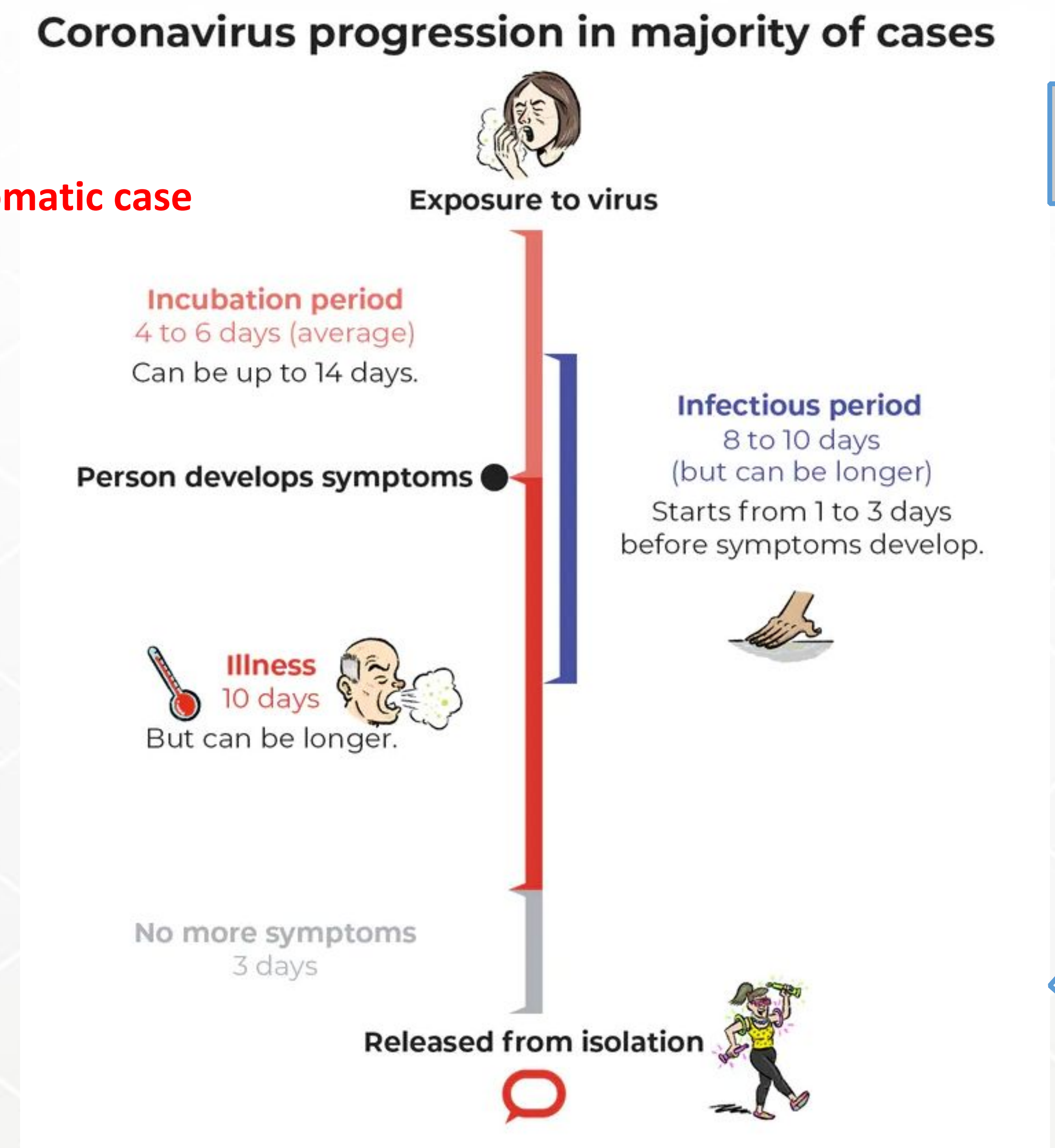
1,598 人
(前日比 +2 人)



https://www.mhlw.go.jp/stf/seisakunitsuite/bunya/0000164708_00001.html

Cases of COVID19 disease

symtomatic case



asymptomatic case

https://theconversation.com/how-long-are-you-infectious-when-you-have-coronavirus-135295;

Epidemiological characteristics of COVID (NB: this file is to be shared with third party)

感染パラメータ関係

Characteristics	Distribution	Reference
Incubation period	Lognormal distribution with right-truncation Mean: 5.6 days SD: 3.9 days [R code] plnorm(t, meanlog=1.525, sdlog=0.629)	Linton, Natalie M., et al. "Incubation period and other epidemiological characteristics of 2019 novel coronavirus infections with right truncation: a statistical analysis of publicly available case data." *Journal of clinical medicine* 9.2 (2020): 538.
Serial interval	Lognormal distribution with right-truncation Median: 4.0 days Mean: 4.7 days SD: 2.9 days [R code] plnorm(t, meanlog=1.387, sdlog=0.568)	Nishiura, Hiroshi, Natalie M. Linton, and Andrei R. Akhmetzhanov. "Serial interval of novel coronavirus (COVID-19) infections." *International journal of infectious diseases* (2020).

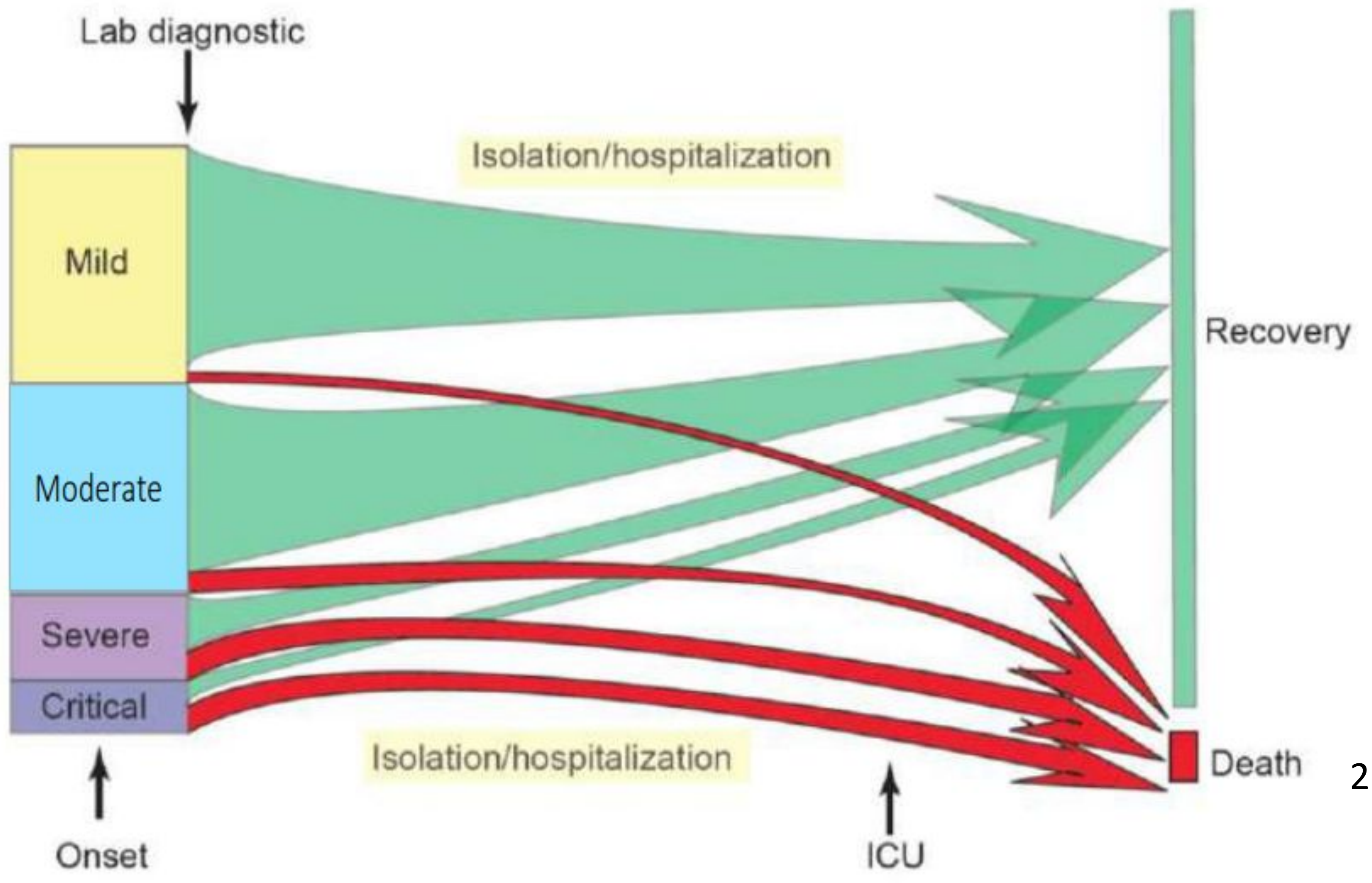
https://docs.google.com/document/d/1mRICZMjPbrqN0MDSvX6J3ZuehZO9cvU0COgicnzk4N8/edit

Fugaku

Delay distribution in reporting (date of illness onset - date of reporting)	Weibull distribution with right-truncation Mean: 7.9 days (95%CI 6.9-9.0) SD: 4.2 days (3.3-5.2) [R code] pweibull(t, shape=1.96, scale=8.91)	Akmetzhanov et al. 2020 (will soon be available on medRxiv)
Proportion of asymptomatic among infected individuals	Diamond Princess: 17.9% (95%CrI: 15.5–20.2%) Japanese evacuation flight from Wuhan: 31% (95% CI: 7.7% to 54%)	Kenji Mizumoto, et al. 2020 doi:10.2807/1560-7917.ES.2020.25.10.2000180 Hiroshi Nishiura et al 2020. doi:10.1016/j.ijid.2020.03.020

https://docs.google.com/document/d/1mRICZMjPbrqN0MDSvX6J3ZuehZO9cvU0COgicnzk4N8/edit

“Report of the WHO-China Joint Mission On Coronavirus Disease 2019(COVID-19)” (16-24 Feb. 2020)



2 ~ 3%

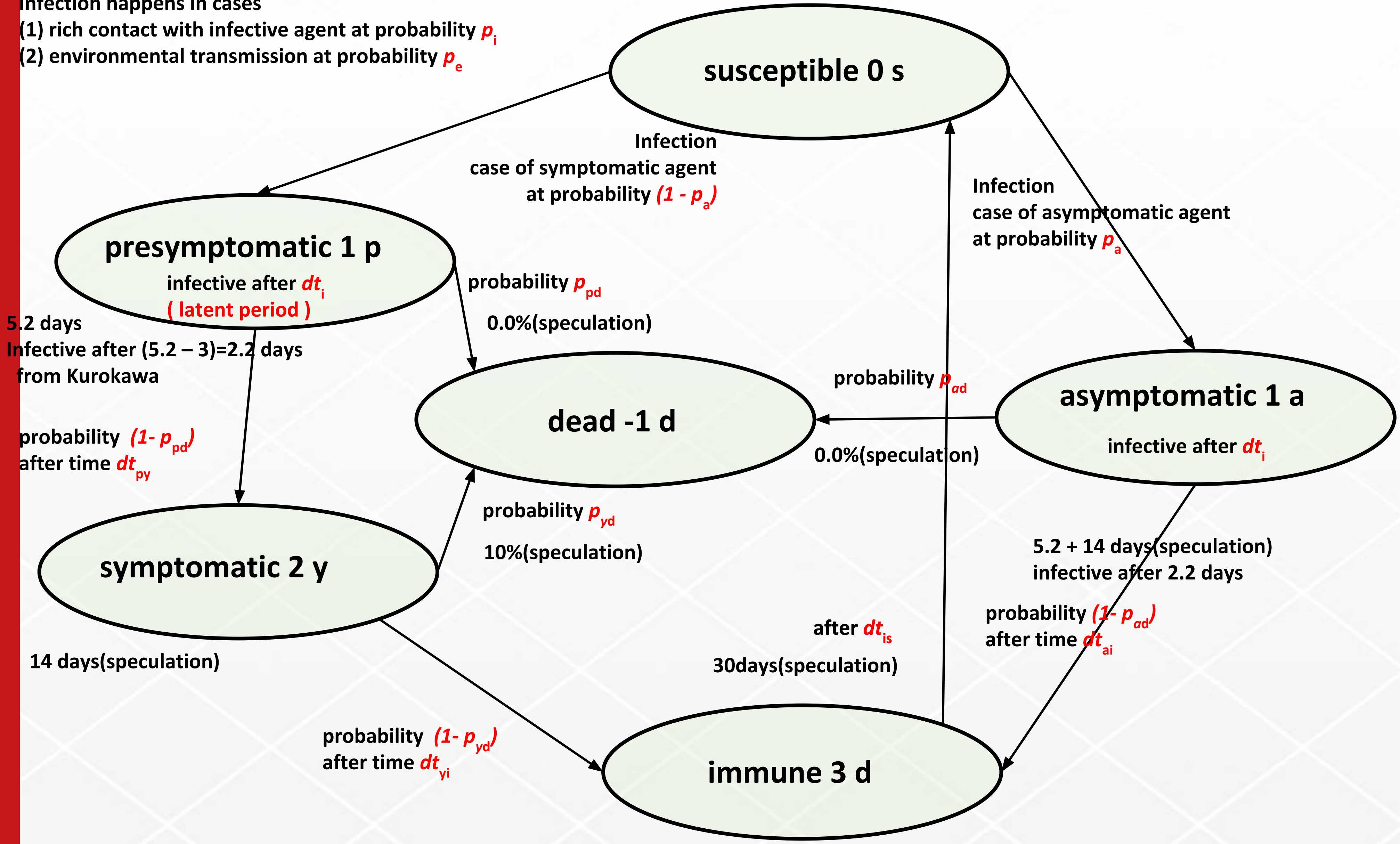
Figure 5. Pattern of disease progression for COVID-19 in China

Note: the relative size of the boxes for disease severity and outcome reflect the proportion of cases reported as of 20 February 2020. The size of the arrows indicates the proportion of cases who recovered or died. Disease definitions are described above. Moderate cases have a mild form of pneumonia.

Fugaku

An agent model
※ not a Markov model like SIR

Infection happens in cases
(1) rich contact with infective agent at probability p_i
(2) environmental transmission at probability p_e



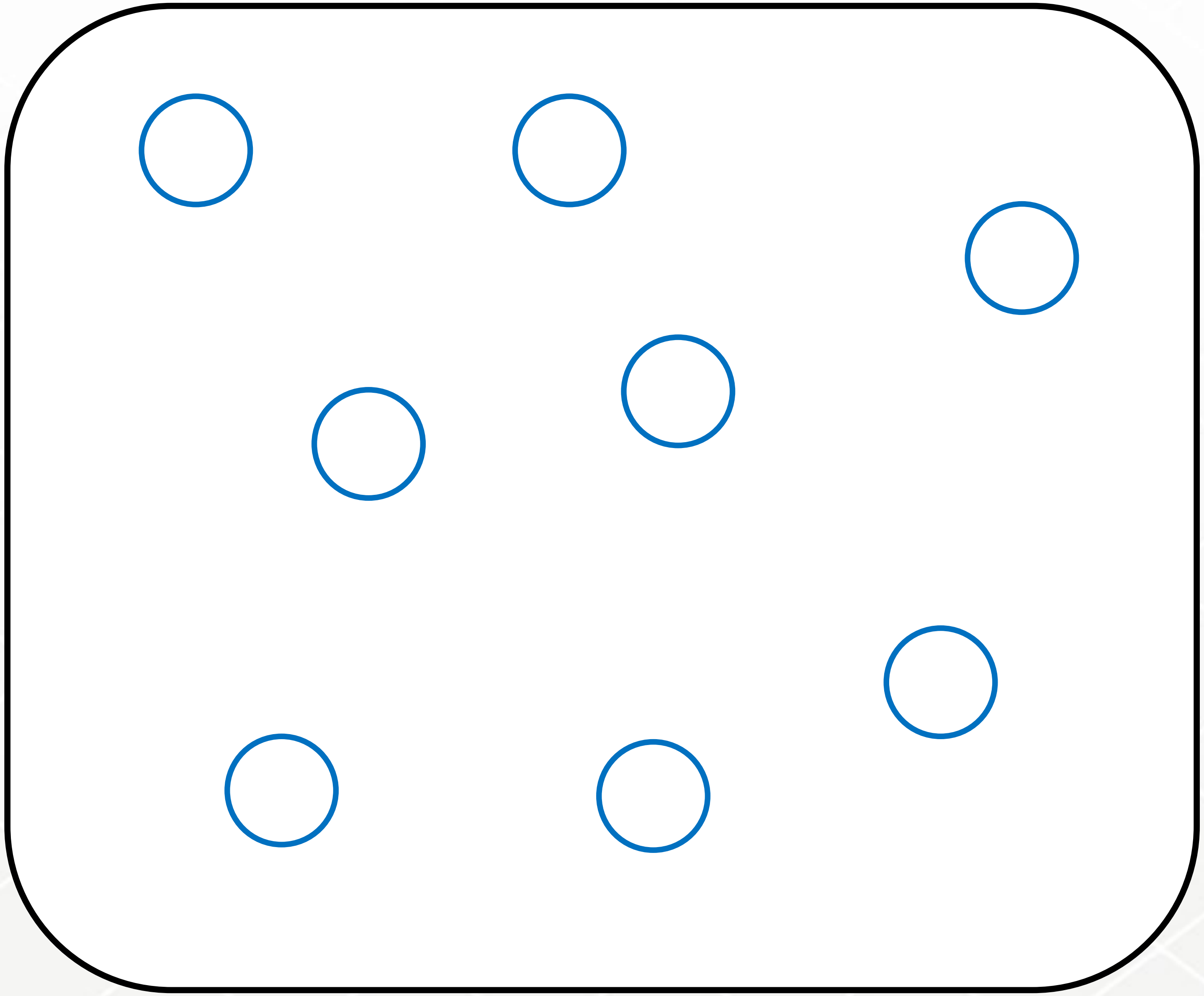
model parameters

dt_i = 0.9 days
= $(dt_{py} - dt_i)$ days (mean)
3.9 days (sd)
dt_i = 4.7 days (mean)
4.0 days (median)
2.9 days(sd)
lognormal distribution
from Endo 200420
dt_{py} = 5.6 days (mean)
3.9 days (sd)
lognormal distribution
from Endo 200420

dt_{yi} = 7 days (mean)
dt_{is} =280 days
case of β corona virus
from Endo 200420
dt_{ai} = 7 days (speculation)

p_i
p_e
p_{pd} =0.0 from Endo 200420
p_{yd} = 0.1(speculation)
p_{ad} = 0.0 from Endo 200420
p_a = 0.31 (95%[0.077 – 0.54])
Nishiura et al.(2020)
from Endo 200420

A model scenario of infection cluster formation



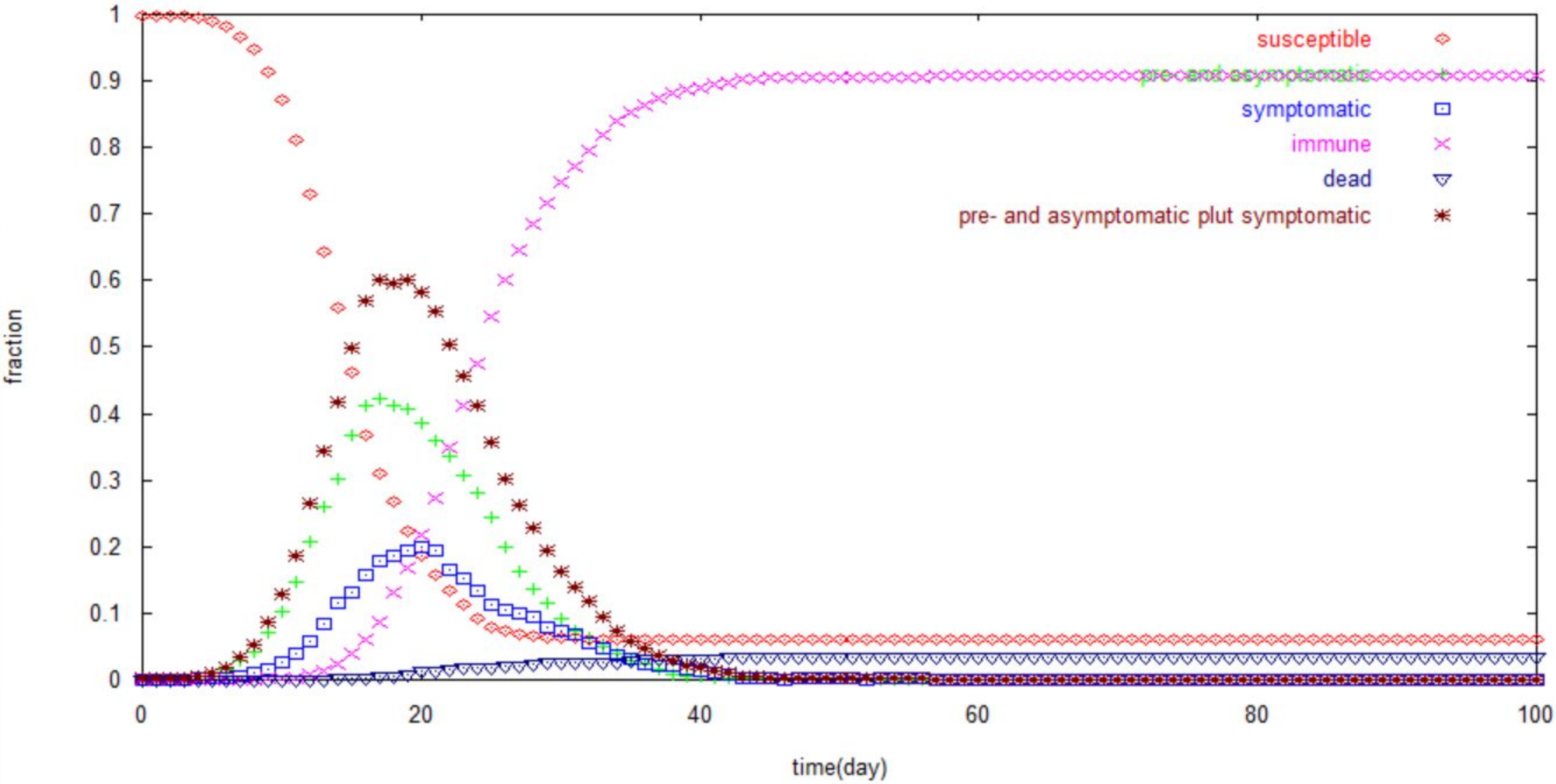
- N agents (typically 1000 for simulation)

- Non-symptomatic agents:
  meet randomly pairwisely
  with a contact probability
  meeting with infected agent,
  susceptible agent becomes infected
  with an infection probability

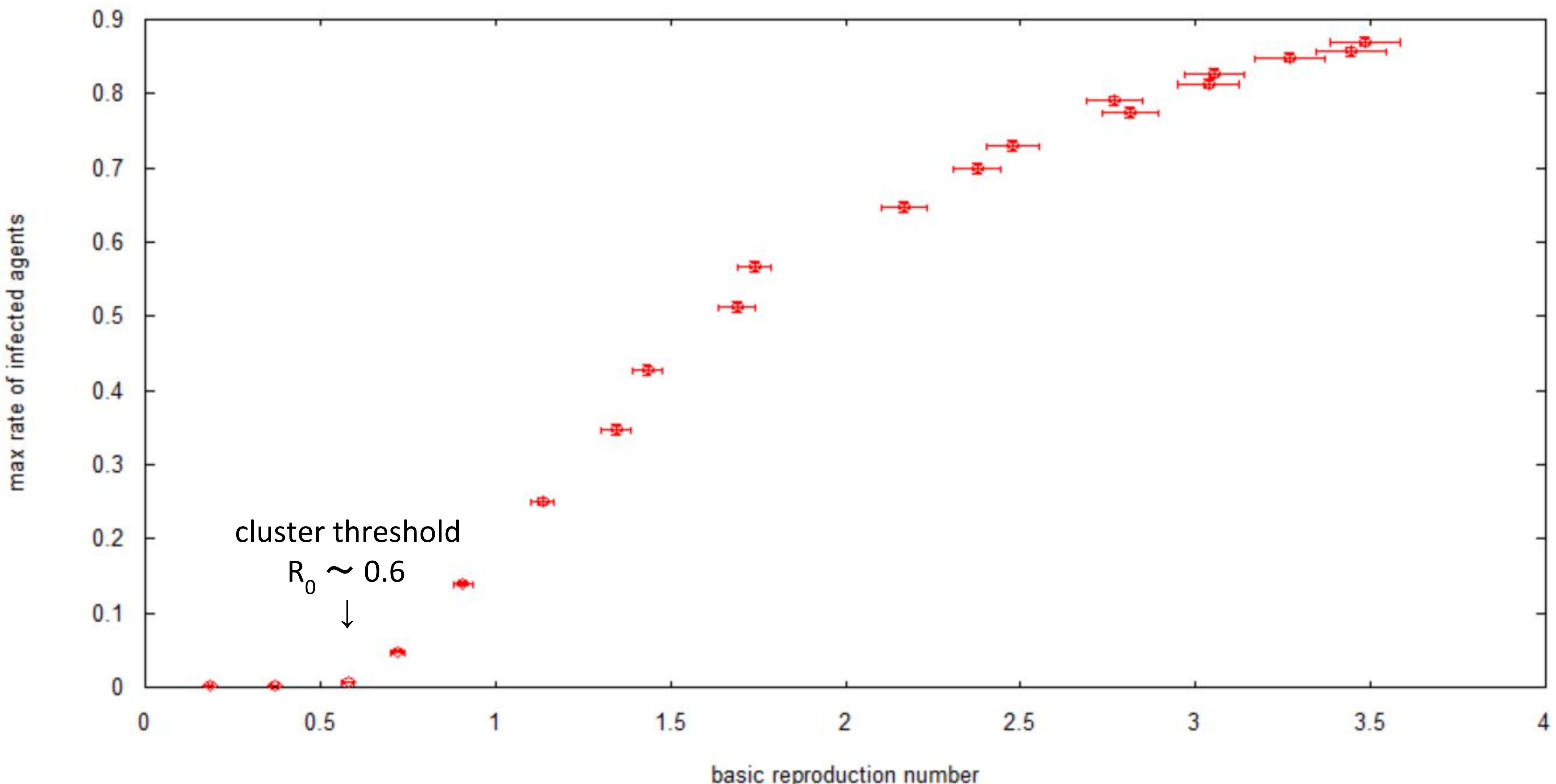
- Symptomatic agents:
  do not contact with others

200506

A typical infection-cluster formation: R_0 ~ 2



Relation between basic reproduction number and peak value of infected agent



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Disturb further infection! Contact-trace application

(1) Keep recording contact in smartphone
(2) Send alert when someone become symptomatic
(3) Stop contact when alert comes

PEPP-PT: Pan-European Privacy-Preserving Proximity Tracing

Summary

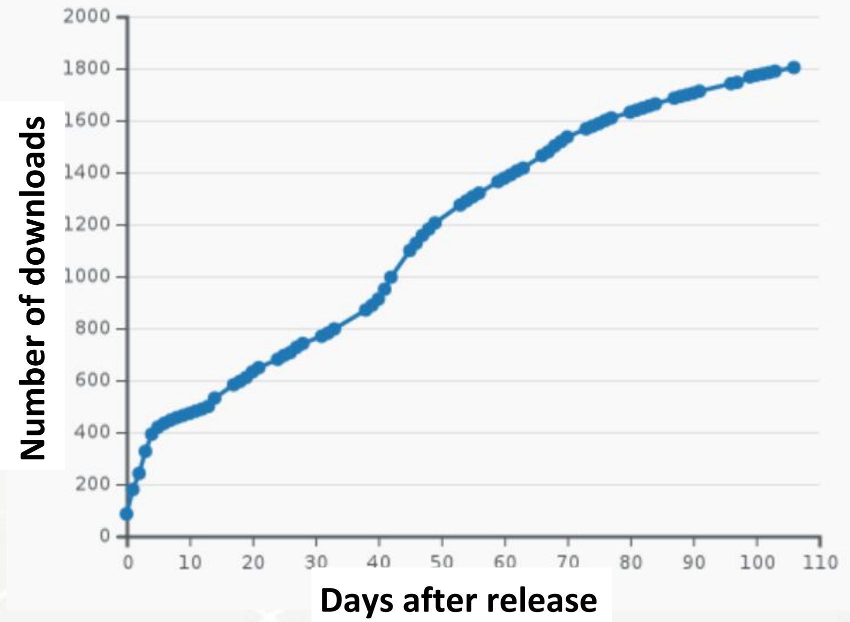
The PEPP-PT system is being created by a multi-national European team. It is an anonymous and privacy-preserving digital contact tracing approach, which is in full compliance with GDPR and can also be used when traveling between countries through an anonymous multi-country exchange mechanism. No personal data, no location, no Mac-Id of any user is stored or transmitted. PEPP-PT is designed to be incorporated in national Corona mobile phone apps as a contact tracing functionality and allows for the integration into the processes of national health services. The solution is offered to be shared openly with any country, given the commitment to achieve interoperability so that the anonymous multi-country exchange mechanism remains functional.

https://www.pepp-pt.org/

In Japan
COCOA: COVID-19 Contact-Confirming Application

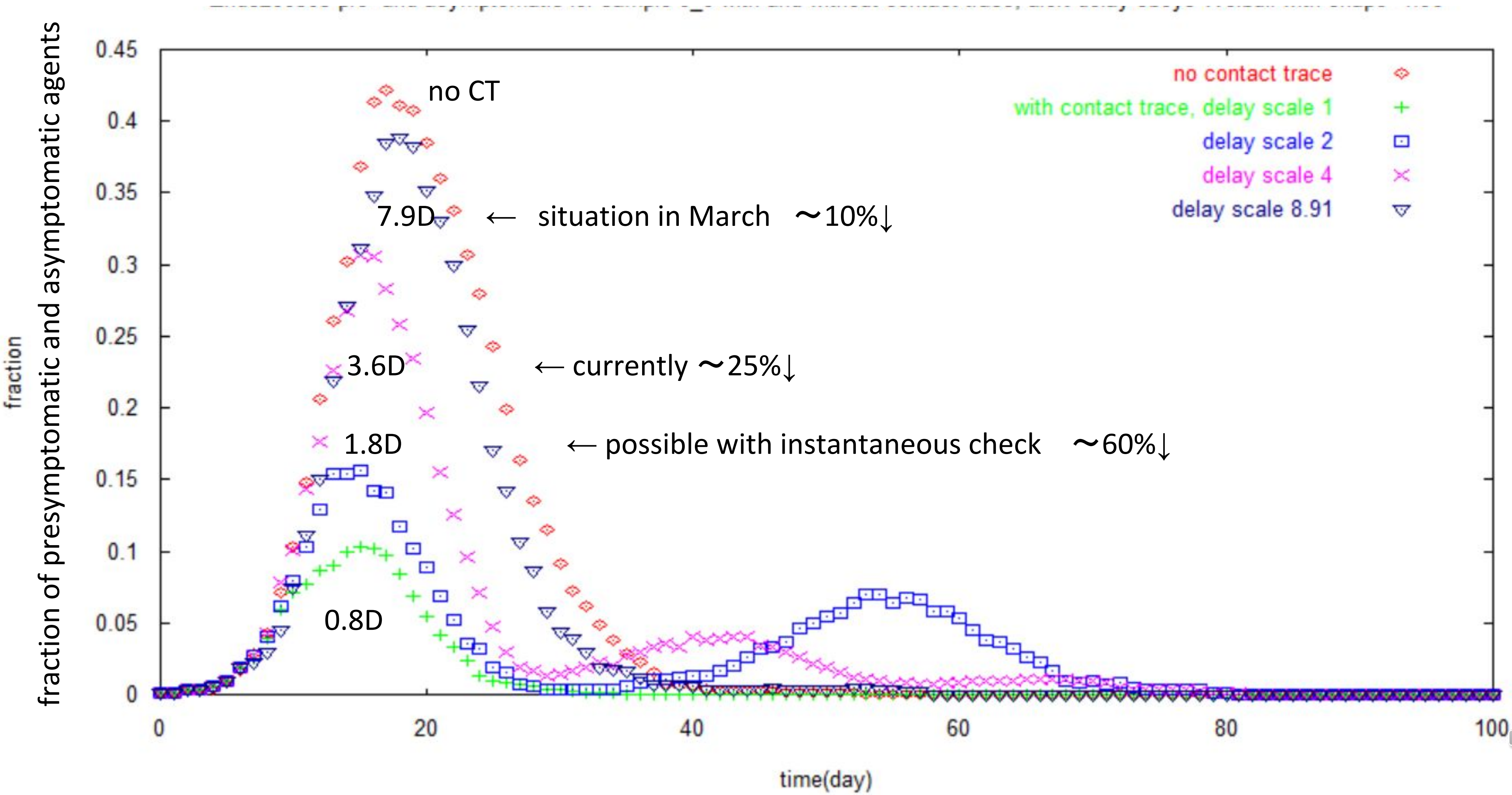
https://www.mhlw.go.jp/stf/seisakunitsuite/bunya/cocoa_00138.html

- v1.0.0 Released on June 19th
  v1.1.1 on June 30th (iOS), July 1st (Android)
  v.1.1.2 July 13th (iOS), 14th (Android), v.1.1.3 Sept. 8th (iOS), 9th (Android)
  v.1.1.4 Sept. 24th (iOS), 28th (Android)
- source code: https://github.com/cocoa-mhlw/cocoa
- 18.07 million downloads (till Oct. 6th 17:00)
  cf population: 126 million → 〜10% ?



- 1,021 positives detected and alerted(till Oct. 6th 17:00)

Supression of infection cluster with contact-trace application(100% users) with various delay time(in days) of alert



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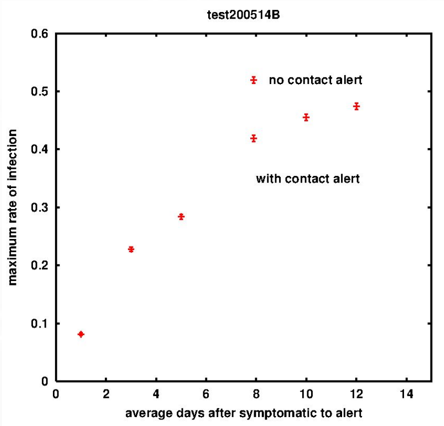
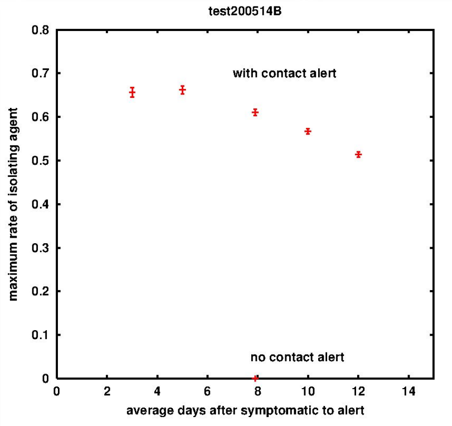
Days from symptomatic to alert

Max of infected



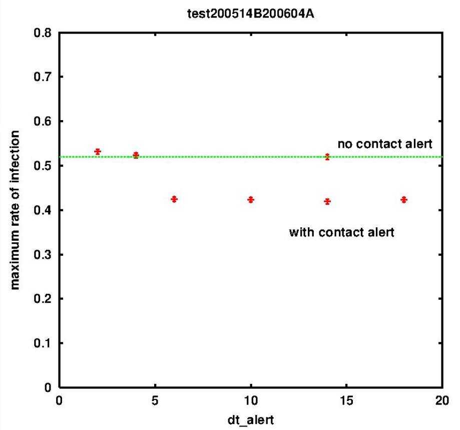
Max of isolating



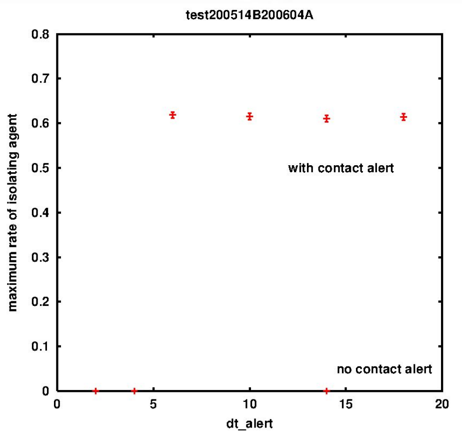
The shorter, the better

Days for target contact

Max of infected



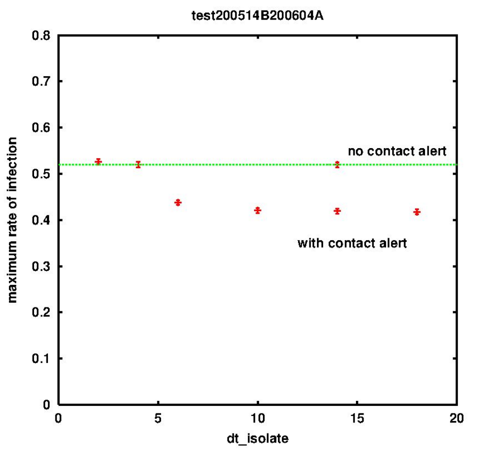
Max of isolating



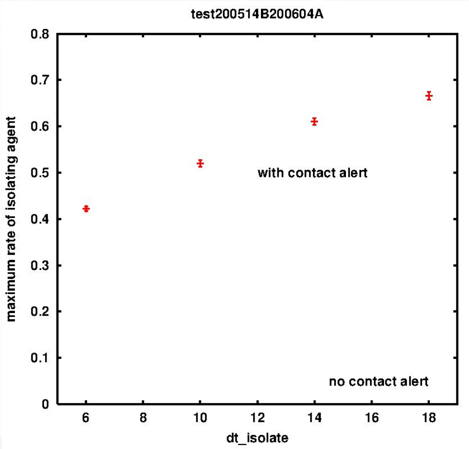
A week seems sufficient

Days for islating

Max of infected



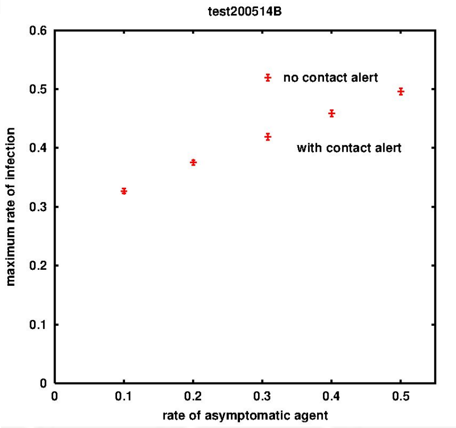
Max of isolating



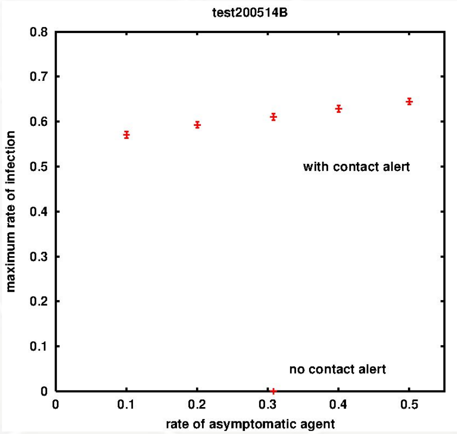
Ten days seems sufficient

Rate of asymptomatic agents

Max of infected



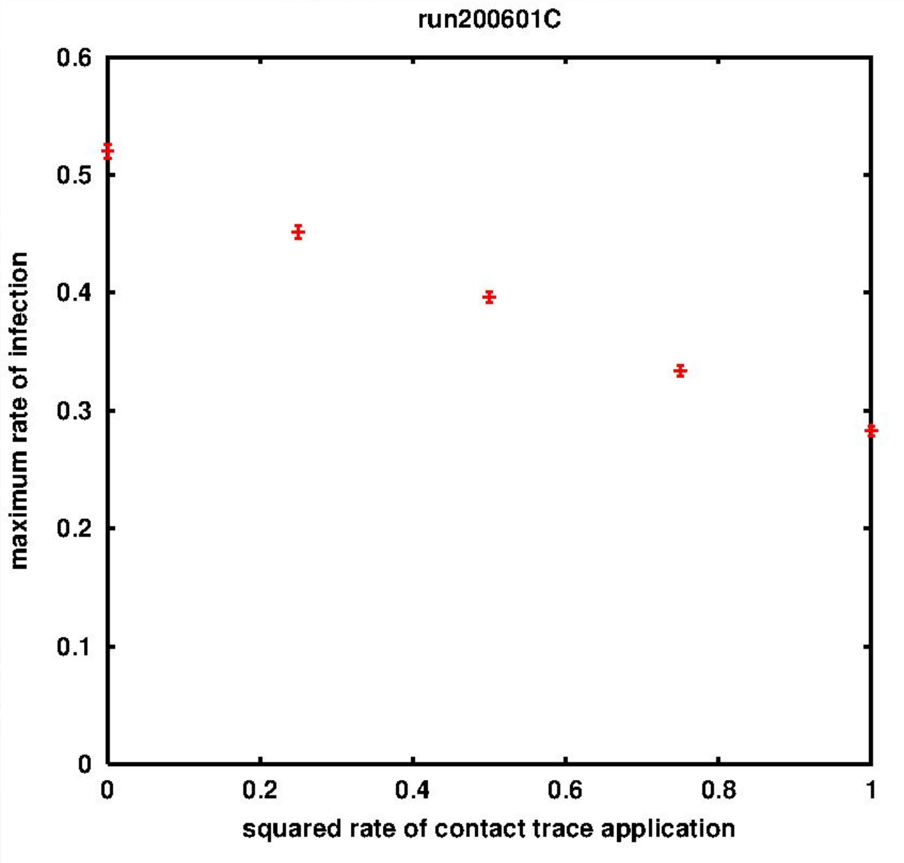
Max of isolating



The larger, a bit larger

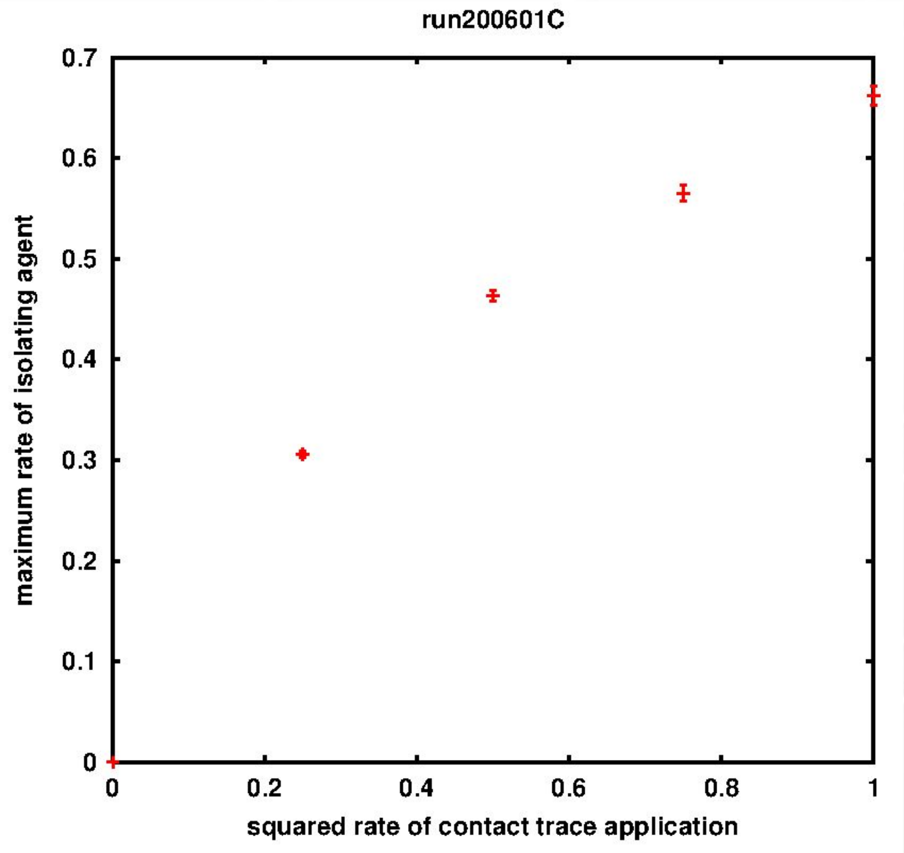
Rate of contact-trace application

Max of infected



Square of the rate

Max of isolating



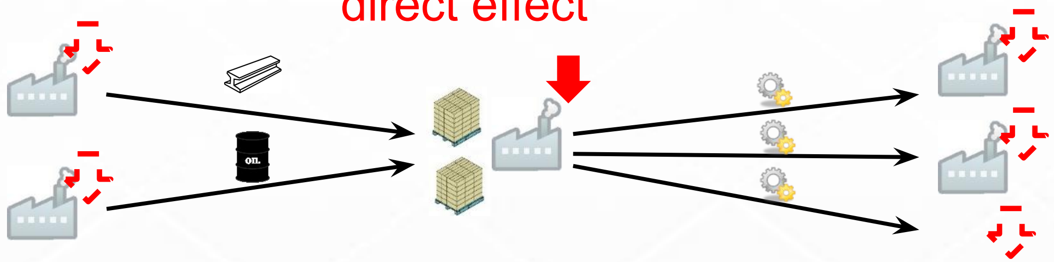
Square of the rate

Effect of the contact-trace application is proportional to its diffusion rate.

Impact on macroeconomics

indirect effect
demand side

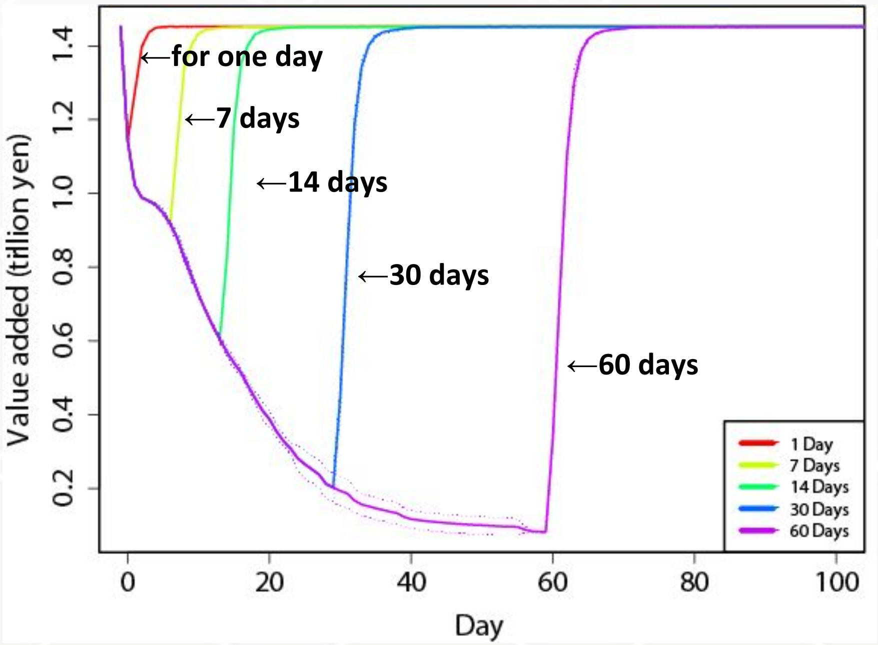
direct effect

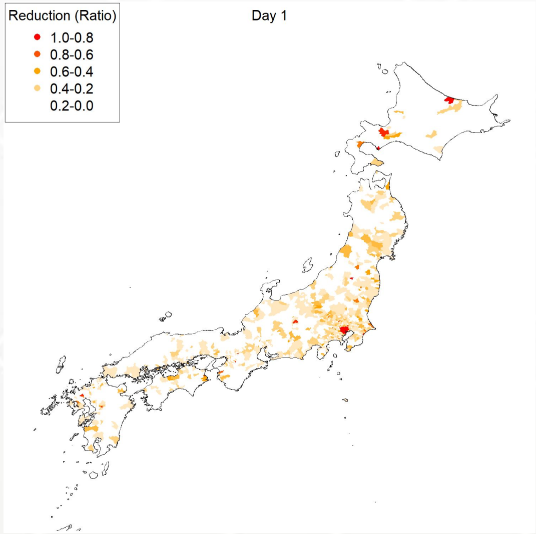


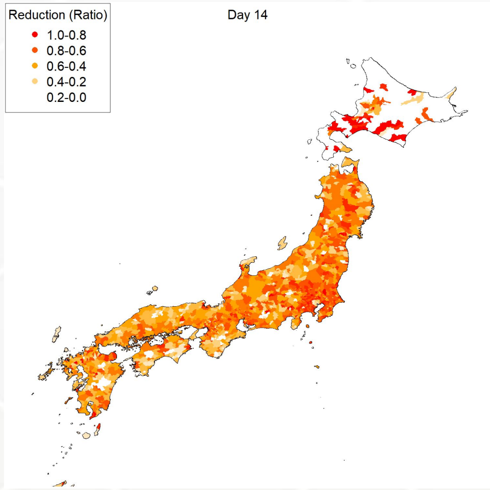
indirect effect
supply side

a model with
1.5〜2.0 million nodes

Minimize economic activities for two months all over Japan
→ estimated GDP from a supply chain model: -7.8%
in reality: -7.9%
(https://www.esri.cao.go.jp/jp/sna/data/data_list/sokuhou/gaiyou/pdf/main_1.pdf)

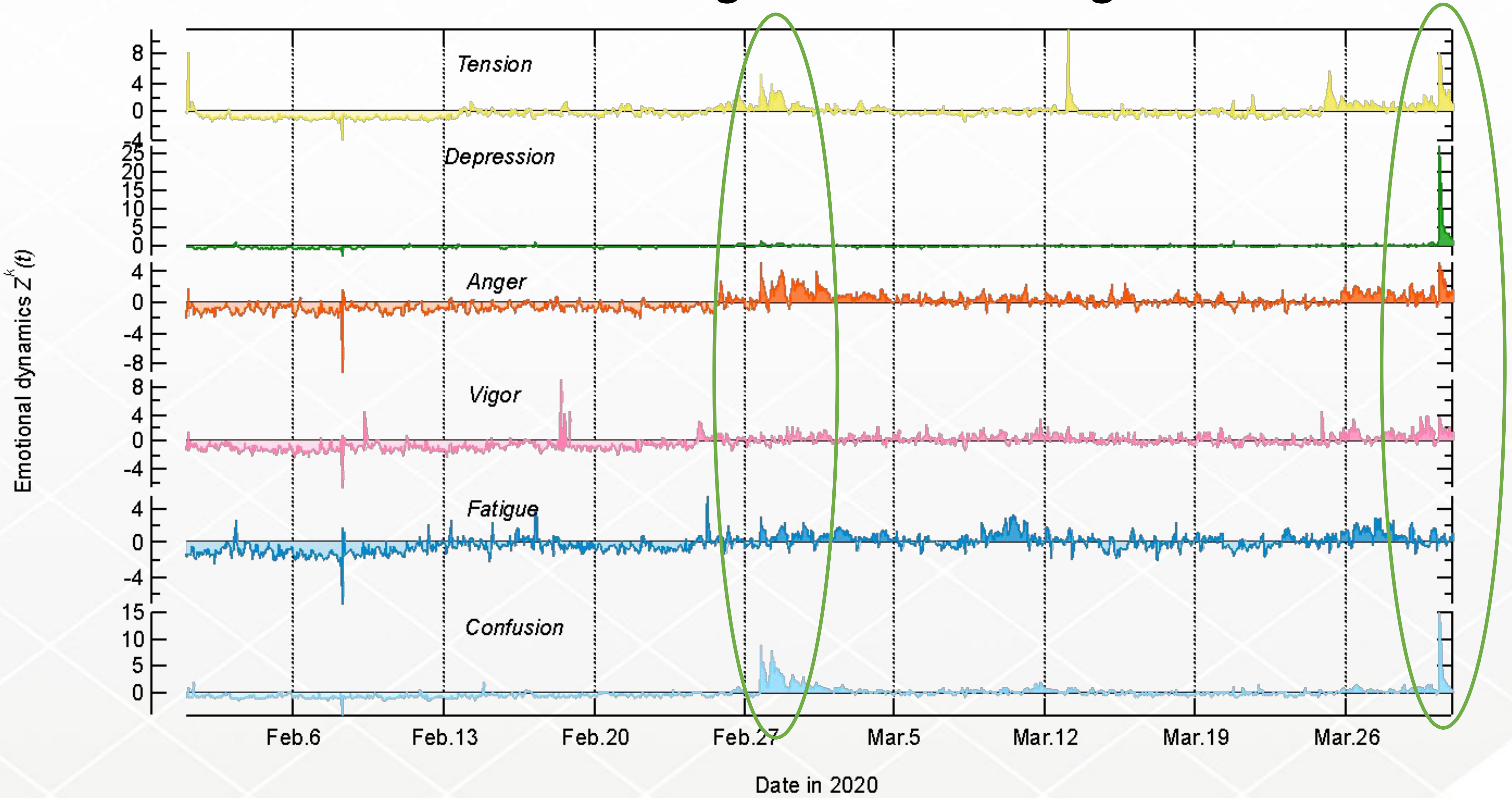






Results by Hiroyasu Inoue and Yasuyuki Todo

Social sentiment analysis from text mining of twitter messages



Results by Yukie Sano, Kenta Yamada and Misako Takayasu

Fugaku

Summary

- An agent-based model of the COVID-19 disease propagation is developed.
- Dynamics of infection-clusters are simulated.
- One approach to stop the COVID-19 pandemic, the contact-trace application, is analyzed.
- With sensitivity analysis, effective parameters to stop the disease is confirmed and determined:
    - diffusion rate > 70%
    - alert for one week
    - isolation for one week

  A hint: use the CT in office, class room and family
- Economic impact was estimated quantitatively.
- Social media analysis provides indices for social sentiment with COVID-19.

Next

- More precise deterrence of COVID-19 infection: metapolulation analysis
- Salvation planning for economic activities
- Optimization of current society
- Not only COVID-19, but also other diseases