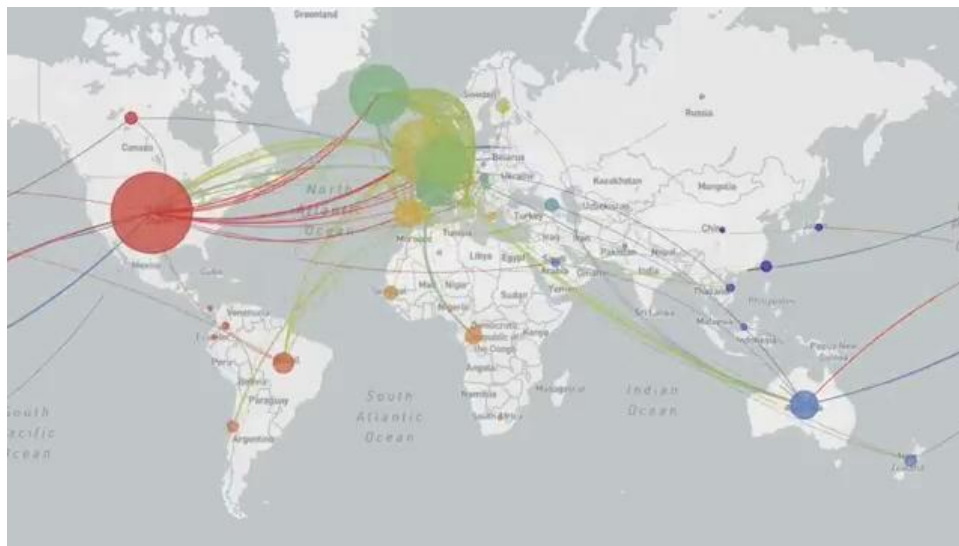




Transmission Model and COVID-19 Variants

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Motivation

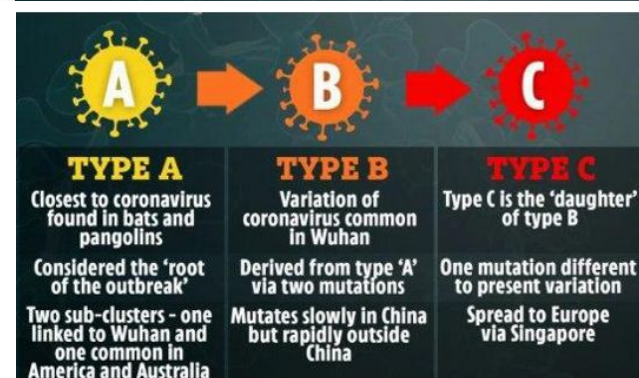
Background

Approach

Result

Next step

- phylogenetic network analysis showed there are three variants of coronavirus 2 (Covid-19), distinguished by amino acid changes named **A**, **B**, and **C**.
- The aim of this project is **to find a correlation between intrinsic characteristics of Covid-19 and the differences of the structure of transmission model of various countries.**





Motivation

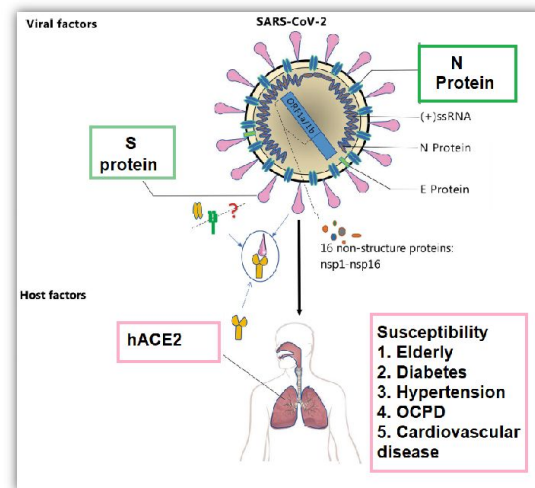
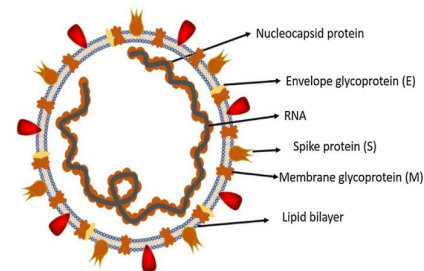
Background

Approach

Result

Next step

- Coronaviruses (SARS-CoV, MERS-CoV, H5N1, H1N1, **Covid-19**) belong to the Coronaviridae family in the Nidovirales order.
- Covid-19 emerged recently is a **highly transmittable** and pathogenic viral infection caused by severe acute respiratory syndrome.
- To prevent and implement **effective treatment strategies** for disease, knowing the **origin and transmission mechanisms** are very important.





Understanding and Exploring Network Epidemiology in the Time of Coronavirus

Motivation

Background

Approach

Result

Next step

	A	B	C	D	E
1	id	age	sex	region	date_report
2	1	55	Male	Toronto	25-01-2020
3	2	55	Female	Toronto	27-01-2020
4	3	45	Male	Vancouver Coastal	28-01-2020
5	4	25	Female	Middlesex-London	31-01-2020
6	5	55	Female	Vancouver Coastal	04-02-2020
7	6	35	Male	Vancouver Coastal	06-02-2020

<https://www.kaggle.com/>

Coronavirus Incubation Period:

Last updated: March 12, 15:00 GMT

2 - 14 days worldometer

Possible outliers: **0 - 27 days**

$$P_{\text{city}} = 1 / \text{number of regions}$$

$$K_{\text{in}} = 1$$



Lives in city X

Reported in
day 20



Lives in city X

Reported in
day 6



Lives in city X

Reported in
day 15



Lives in city Y

Reported in
day 7



Motivation

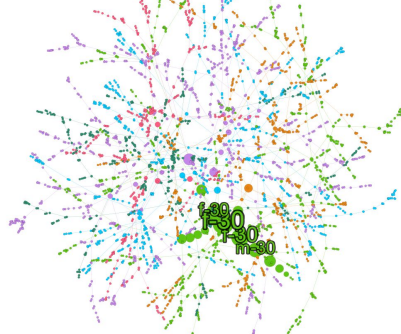
Background

Approach

Result

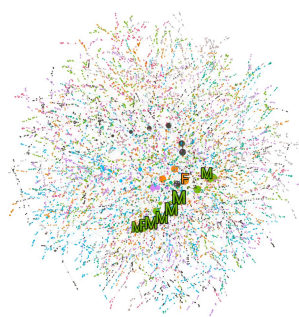
Next step

Canada



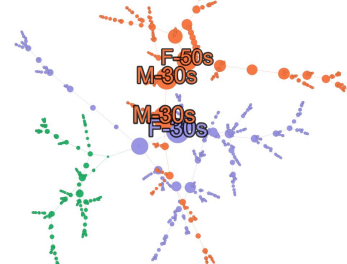
Nodes: 3409
Diameter: 29
Modularity: 0.81
Community Num. : 6
46% with 0 BC
0.1% with BC of
>13000
 $\langle K_{out} \rangle = 2.00$
Variant B

Japan



Nodes: 11033
Diameter: 44
Modularity: 0.89
Community Num. : 10
40% with 0 BC
0.1% with BC of >8000
 $\langle K_{out} \rangle = 1.00$
Variant B

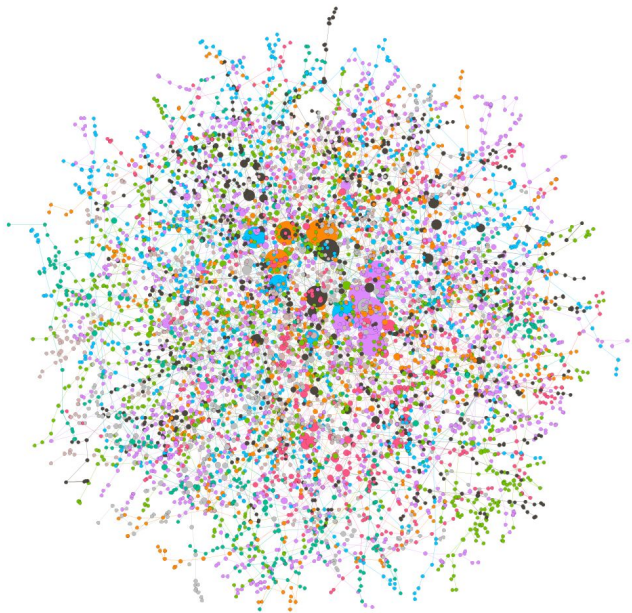
Indonesia



Nodes: 893
Diameter: 16
Modularity: 0.63
Community Num. : 3
41% with 0 BC
0.5% with BC of >800
 $\langle K_{out} \rangle = 2.00$
Variant B



Italy



Nodes: 7040
Diameter: 36
Modularity: 0.87
Community Num. : 9
38% with 0 BC
0.1% with BC of >7700
 $\langle K_{out} \rangle = 1.00$
Variant C

Immunize the
ones with high
BC

Limitation: We need more data from
more countries with specified variant
of the virus.

Modularity Algorithm: Blondel, *et al.* (2008)
Betweenness centrality: Brandes, *et al.* (2001)
Force Atlas 2 Algorithm: Jacomy, *et al.* (2014)



Motivation

Background

Approach

Result

Next step

→ Finding the assortativity of nodes with gender and age

→ Using multilayer graph with age and gender in other layers



Motivation

Background

Approach

Result

Next step

Thank you for your attention!