

CoDatMo: Creating a Common Epidemiological Framework with Bayesian Models

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Who

- Breck Baldwin: Project Manager Laplace Lab @Columbia statistics
- Andrew Gelman: @Columbia statistics
- Simon Maskell: PI Big Hypotheses Lab at U of Liverpool
- Conor Rosato, Lee Delvin, John Heap, Philip Clemson, Allesandro Varsi, Matthew Carter, Robert Moore, Vincent Beraud, Al Philips, Kelli Casidy, Jose Storypoli, Alessandra Pellini, Elias Noda, Bob Carpenter

How

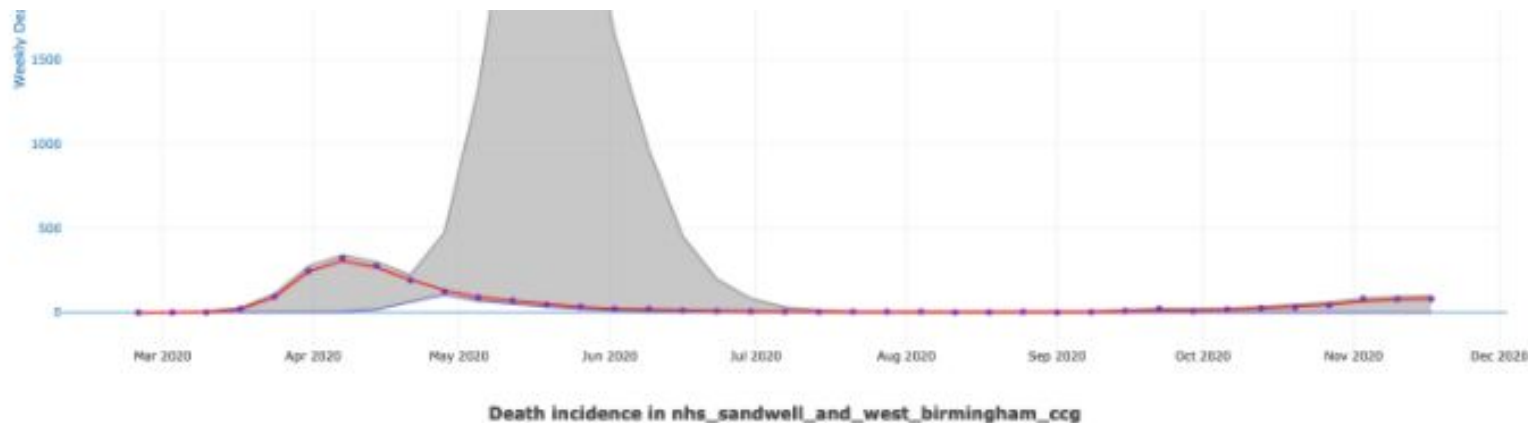
- UKRI Big Hypotheses EP/R018537/1
- NSF RAPID grant 2055251

Outline

- Overview CoDatMo
- Brief intro to Bayesian Modeling and Stan
- Go over some repositories
- Resources

CoDatMo Goals and History

1. August 2020:
 - a. Stan--a popular language for modeling COVID-19 epidemiology ~ 20 models
 - b. The UK Joint Biosecurity Center (JBC) uses many models but similarities/differences
 - c. Liverpool/Columbia decide to create an online resource for comparative COVID modeling
 - i. Improve the models
 - ii. Share ideas
2. November 15, 2020: NSF RAPID grant 2055251 for COVID awarded
3. December 2, 2020: <https://github.com/codatmo> up and running
 - a. Model example
 - b. Data
4. Submissions:
 - a. December 2, 2020: Liverpool
 - b. December 8, 2020: Ye Old Lancaster
 - c. December 20, 2020: Simple SIR
 - d.Rethinking appeal of CoDatMo to external contributors
 - e. March 14, 2020: UNINOVE Sao Paulo
5. April 14, 2020: This presentation



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Welcome to the CoDatMo site

CoDatMo (COvid DATa MOdel) exists to replicate and host COVID-19 models written in the Bayesian modeling languages like Stan or PyMC. The goals include:

- Reproduce COVID-19 models with an eye to:
 - Get the word out on important COVID-19 models by offering well documented examples approachable by statisticians, programmers and researchers.
 - Increase the impact of the original researchers and get them additional exposure.
 - Help researchers improve their models via the replication process
- Provide a common language for implementing various models.
- Facilitate information exchange between model developers.
- Provide public access to models.

CombineR

 R  BSD-3-Clause  0  0  0  0 Updated 4 hours ago

UNINOVE_Sao_Paulo

Covid Modeling work at UNINOVE Brazil

 HTML  BSD-3-Clause  1  2  0  0 Updated 3 days ago

Data

Collection of open-source data sources for the United Kingdom and the rest of the world. To be used for testing of the various models.

 HTML  BSD-3-Clause  0  0  0  0 Updated 17 days ago

Liverpool

 HTML  BSD-3-Clause  1  0  0  0 Updated 17 days ago

Top languages

 HTML  R  Stan

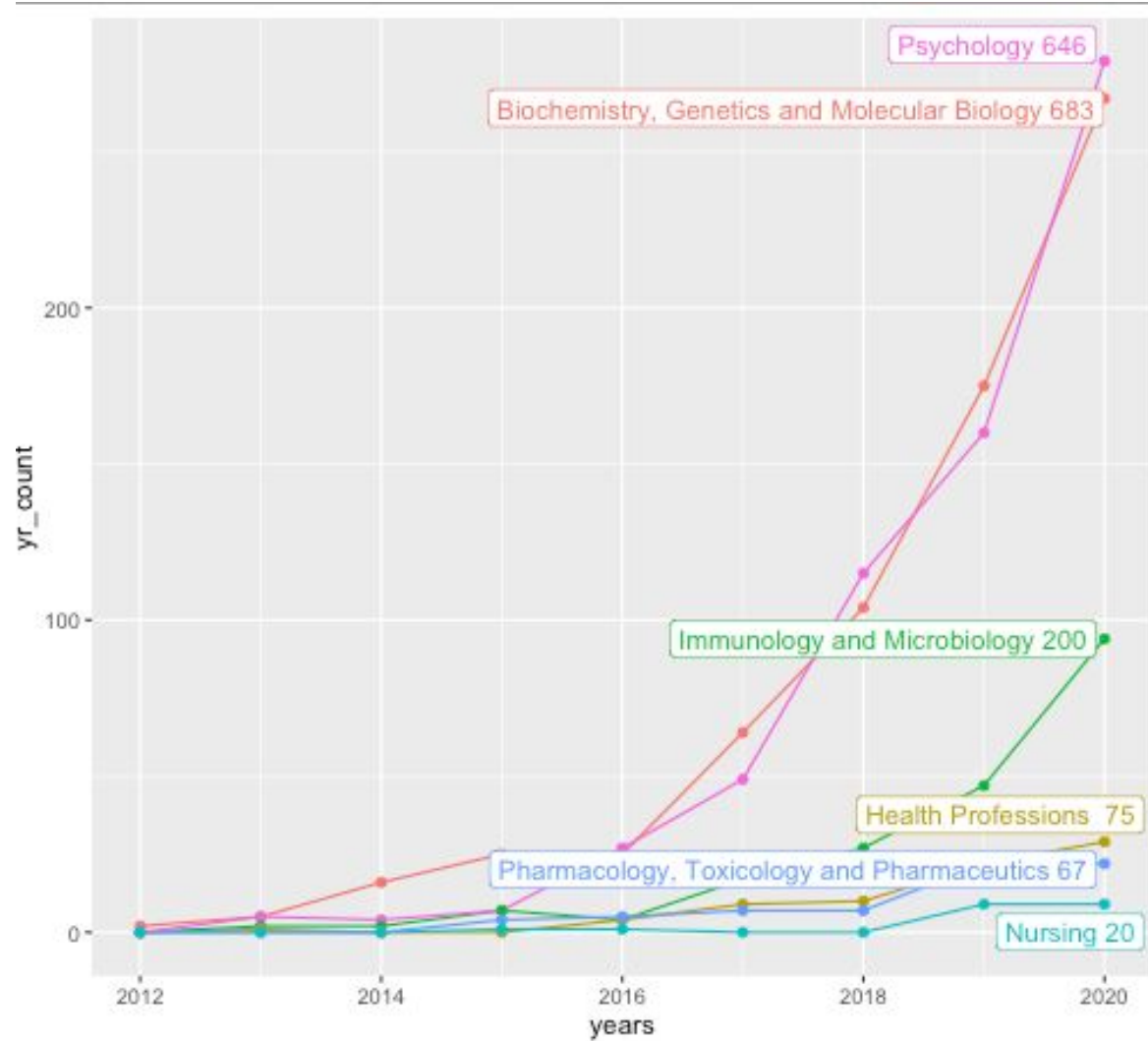
People



Invite someone

Over 50 models for COVID-19 written in Stan: Why?

- Hierarchical models
- Noise tolerant models with small to medium data sets
- Lots of room for integration of prior knowledge
- Can be very interpretable models to support counterfactual reasoning etc...
- Very robust uncertainty handling
- Huge effort on inference safety
 - Bayesian workflow
 - Inference diagnostics
 - Self monitoring gradient crawler
- Generative models
 - Mechanistic
 - Human interpretable
 - Simulation



Deep Learning

Repos in CoDatMo

https://codatmo.github.io/Simple_SIR/

https://github.com/codatmo/UNINOVE_Sao_Paulo

Resources

- Codatmo project: <https://codatmo.github.com>
 - Help us...
 - Let us help you...
- Slides: https://github.com/codatmo/documentation/blob/main/talks/CovidSymp_4_16_2021.pdf
- Modern Bayesian modeling packages:
 - Stan: <https://mc-stan.org>
 - R, Python, Scala, <https://mc-stan.org/users/interfaces/>
 - High level interfaces in lme4 tradition (R only)
 - brms: <https://paul-buerkner.github.io/brms/>
 - RStanArm: <https://mc-stan.org/rstanarm/>
 - PyMC Python HMC/NUTS: <https://pypi.org/project/pymc/>
 - TensorFlow/PyTorch
- Statistical Rethinking, Second Edition, by Richard McElreath
 - Youtube lectures <https://youtube.com/playlist?list=PLDcUM9US4XdNM4Edgs7weiyLguLSToZRI>
 - brms implementation of 1st Edition at: <https://bookdown.org/content/4857/>
- Bayesian Statistics for the Social Sciences GR5065 in <http://www.qmss.columbia.edu/>:
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