

Methods of Applied Statistics I

STA2101H F LEC9101

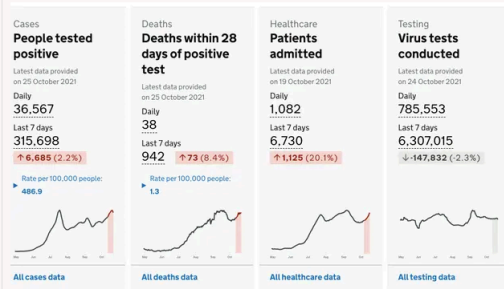
Week 10

November 24 2021

On Covid, we need to be careful when we talk about numbers

David Spiegelhalter and Anthony Masters

A recent wave of mistakes shows how misinterpreting data risks misrepresenting the impact of the virus



1. Upcoming events
2. In the News
3. Theory of GLMs
4. Reminder: HW10 ready Nov 25, due Dec 2, is the final HW for the term
5. Reminder: Final Project due Dec 17 23.59 PhD Dec 20 09.00
6. Office Hour Nov 24 16.30 – 18.00 this week only

- Monday Nov 29 3.30 Data Science ARES series
Policy Questions, Messy Data: Three approaches to turning messy data into information for public policy [Link](#)



- Friday Nov 26 Toronto Data Workshop



Kieran Campbell U of T

Dear friends,

Toronto Data Workshop this Friday, 26 November, at noon (Toronto time) hosts Professor Kieran Campbell on the intersection of biomedical data and data science.

Dr. Kieran Campbell is an investigator at the Lunenfeld-Tanenbaum Research Institute and an assistant professor at the Departments of Molecular Genetics and Statistical Sciences, University of Toronto. His research focusses on Bayesian models and machine learning for high dimensional biomedical data, including single-cell and cancer genomics. Recently, he has led efforts to develop statistical machine learning methodology to integrate single-cell RNA and DNA sequencing data to uncover the effects of tumour clonal identity on gene expression, as well as methods to automatically delineate the tumour microenvironment from single-cell RNA-sequencing data. Such findings can improve our understanding of cancer progression and of why certain tumours are resistant to therapies, leading to relapse. <https://www.camlab.ca>

- Thursday Nov 4 3.30
Diffusion Schrödinger Bridges with Applications
to Score-Based Generative Modelling

Arnaud Doucet, U Oxford



[Zoom Link](#)

- **Part I 3–5 pages, non-technical**
 1. a description of the scientific problem of interest
 2. how (and why) the data being analyzed was collected
 3. preliminary description of the data (plots and tables)
 4. non-technical summary for a non-statistician of the analysis and conclusions
- **Part II 3–5 pages, technical**
 1. models and analysis
 2. summary for a statistician of the analysis and conclusions
- **Part III Appendix**

R script or .Rmd file; additional plots; additional analysis; References

- 40 points total
- Part I:
 - description of data and scientific problem 5
 - suitability of plots and tables 5 clear, non-technical, concise but thorough
 - quality of the presentation 5
- Part II:
 - summary of the modelling and methods 5 justification for choices
 - suitability and thoroughness of the analysis 10 model checks, data checks
- Part III:
 - relevance of additional material 5
 - complete and reproducible submission 5

- binomial regression: deviance residuals, Pearson residuals, Pearson X^2 , non-canonical link functions
- Poisson regression: deviance residuals, Pearson residuals, Pearson X^2 , non-canonical link functions
- overdispersion, quasi-Poisson, quasi-Binomial
- measures of risk: odds ratio, risk ratio, risk difference, prospective/retrospective sampling
- glm theory Part I

HW 8

I managed to compute the residuals following the formula on the slides and got results which agree exactly with R. I used the formula

$$r_{DI} = \text{sign}(y_i - \hat{p}_i) \sqrt{2[y_i \log\{y_i/n_i\hat{p}_i\} + (n_i - y_i) \log\{(n_i - y_i)/(n_i - n_i\hat{p}_i)\}]}$$

The only difference just being substituting the " \pm " with " $\text{sign}(y_i - \hat{y}_i)$ ". Since the data is bernoulli, I used $n_i =$ and $\hat{p}_i = \hat{y}_i$.

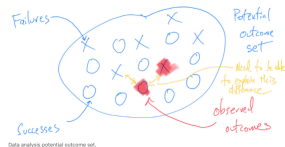
- Guardian, Nov 14 Spiegelhalter & Masters
“On Covid we need to be careful when we talk about numbers”

On Covid, we need to be careful when we talk about numbers
David Spiegelhalter and Anthony Masters

A recent wave of mistakes shows how misinterpreting data risks misrepresenting the impact of the virus



- Simply Statistics, Nov 10 Peng
Thinking about failure in data analysis



Nature Behaviour, Nov Wagenmakers et al.

Seven steps towards more transparency in statistical practice

nature
human behaviour

PERSPECTIVE
<https://doi.org/10.1038/s41562-021-01211-8>



Seven steps toward more transparency in statistical practice

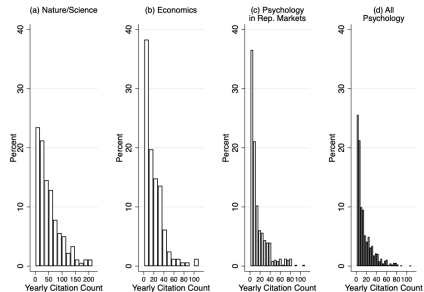
Eric-Jan Wagenmakers^{1,2}, Alexandra Sarafoglou¹, Sil Aarts², Casper Albers³, Johannes Algermissen⁴, Štěpán Bahník⁵, Noah van Dongen¹, Rink Hoekstra⁶, David Moreau⁷, Don van Ravenzwaaij⁸, Aljaž Sluga⁹, Franziska Stanke¹⁰, Jorge Tendeiro^{8,11} and Balazs Aczel¹²

We argue that statistical practice in the social and behavioural sciences benefits from transparency, a fair acknowledgement of uncertainty and openness to alternative interpretations. Here, to promote such a practice, we recommend seven concrete statistical procedures: (1) visualizing data; (2) quantifying inferential uncertainty; (3) assessing data preprocessing choices; (4) reporting multiple models; (5) involving multiple analysts; (6) interpreting results modestly; and (7) sharing data and code. We discuss their benefits and limitations, and provide guidelines for adoption. Each of the seven procedures finds inspiration in Merton's ethos of science as reflected in the norms of communalism, universalism, disinterestedness and organized scepticism. We believe that these ethical considerations—as well as their statistical consequences—establish common ground among data analysts, despite continuing disagreements about the foundations of statistical inference.

Science Advances May 2021 Serra-Garcia & Gneezy

Nonreplicable publications are cited more than replicable ones

FIGURE S1. Distribution of yearly citation counts by replication project



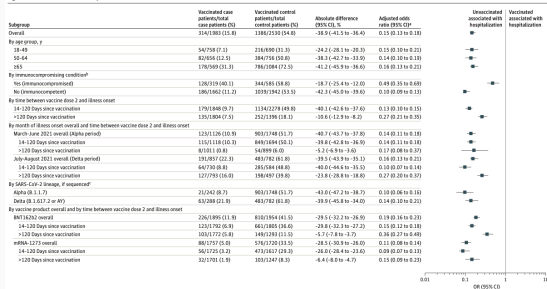
Notes: This figure shows distribution of yearly citation counts of each replicated study, across the three replication projects. Panel (a) for (7), Panel (b) for (6), and Panel (c) for (5), including those studies in replication markets. Panel (d) includes all papers in the psychology RP (5), that featured a significant result in the replicated paper.

“the distribution of citation counts is highly right-skewed. We hence use **Poisson regression models** for the main specification in the paper.”

J Am. Medical Assoc. Nov 4, 2021 Tenforde et al.

Association Between mRNA Vaccination and COVID-19 Hospitalization and Disease Severity

Figure 2. Association Between Hospitalization for COVID-19 and Prior Vaccination With a 2-Dose mRNA Vaccine

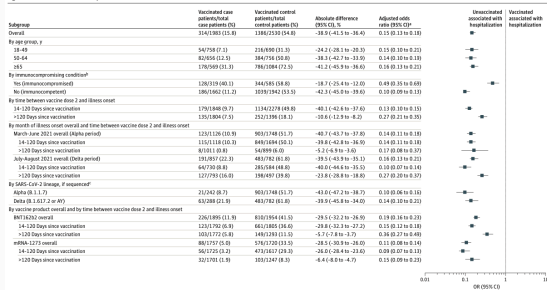


“We used a test-negative **case-control** design to assess the association between hospitalization for COVID-19 and prior vaccination with an mRNA COVID-19 vaccine. In this analysis, **case patients** were those hospitalized with COVID-19 and **control patients** were those hospitalized for other reasons.”

medRxiv preprint; Roessler et al.

Post COVID-19 in children, adolescents and adults: results of a matched cohort study

Figure 2. Association Between Hospitalization for COVID-19 and Prior Vaccination With a 2-Dose mRNA Vaccine



“We used a test-negative **case-control** design to assess the association between hospitalization for COVID-19 and prior vaccination with an mRNA COVID-19 vaccine. In this analysis, **case patients** were those hospitalized with COVID-19 and **control patients** were those hospitalized for other reasons.”

- $f(y_i; \mu_i, \phi_i) = \exp\left\{\frac{y_i\theta_i - b(\theta_i)}{\phi_i} + c(y_i; \phi_i)\right\}$
- $E(y_i | x_i) = b'(\theta_i) = \mu_i$ defines μ_i as a function of θ_i
- $g(\mu_i) = x_i^T \beta = \eta_i$ links the n observations together via covariates
- $g(\cdot)$ is the **link** function; η_i is the **linear predictor**
- $\text{Var}(y_i | x_i) = \phi_i b''(\theta_i) = \phi_i V(\mu_i)$
- $V(\cdot)$ is the **variance function**

GLM Models: Examples

- Normal: $f(y_i; \mu_i, \sigma^2) = \frac{1}{\sqrt{(2\pi)\sigma}} \exp\left\{-\frac{1}{2\sigma^2}(y_i - \mu_i^2)\right\}$ $\exp\left\{\frac{y_i\theta_i - b(\theta_i)}{\phi_i} + c(y_i; \phi_i)\right\}$

- Binomial: $f(r_i; p_i) = \binom{m_i}{r_i} p_i^{r_i} (1 - p_i)^{m_i - r_i}; \quad y_i = r_i/m_i$

- ELM (p.115) uses $a_i(\phi)$ in place of ϕ_i , later (p.117) $a_i(\phi) = \phi/w_i$;
SM uses ϕ_i , later (p. 483) $\phi_i = \phi a_i$

GLM Models: Examples

- Normal: $f(y_i; \mu_i, \sigma^2) = \frac{1}{\sqrt{(2\pi)\sigma}} \exp\left\{-\frac{1}{2\sigma^2}(y_i - \mu_i^2)\right\}$
 $= \exp\left\{\frac{y_i\mu_i - (1/2)\mu_i^2}{\sigma^2} - (1/2)\log \sigma^2 - y_i^2/2\sigma^2 - (1/2)\log \sqrt{(2\pi)}\right\}$

$$\phi_i = \sigma^2, \quad \theta_i = \mu_i, \quad b(\mu_i) = \mu_i^2/2, \quad b'(\mu_i) = \mu_i, \quad b''(\mu_i) = 1$$

- Binomial: $f(r_i; p_i) = \binom{m_i}{r_i} p_i^{r_i} (1 - p_i)^{m_i - r_i}; \quad y_i = r_i/m_i$
 $= \exp[m_i y_i \log\{p_i/(1 - p_i)\} + m_i \log(1 - p_i) + \log \binom{m_i}{m_i y_i}]$

$$\phi_i = 1/m_i, \quad \theta_i = \log\{p_i/(1 - p_i)\}, \quad b(p_i) = -\log(1 - p_i), \quad p_i = E(y_i)$$

- ELM (p.115) uses $a_i(\phi)$ in place of ϕ_i , later (p.117) $a_i(\phi) = \phi/w_i$;
SM uses ϕ_i , later (p. 483) $\phi_i = \phi a_i$

Family	Canonical link	Variance function	ϕ_i
Normal	$\eta = \mu$	1	σ^2
Binomial	$\eta = \log\{\mu/(1 - \mu)\}$	$\mu(1 - \mu)$	$1/m_i$
Poisson	$\eta = \log(\mu)$	μ	1
Gamma	$\eta = 1/\mu$	μ^2	$1/\nu$
Inverse Gaussian	$\eta = 1/\mu^2$	μ^3	ξ

$$\begin{aligned}
 \text{Gamma: } f(y_i; \mu_i, \nu) &= \frac{1}{\Gamma(\nu)} \left(\frac{\nu}{\mu_i}\right)^\nu y_i^{\nu-1} \exp\left(-\frac{\nu}{\mu_i}\right) y_i \\
 &= \exp\left[-\frac{\nu}{\mu_i} y_i - \nu \log\left(\frac{1}{\mu_i}\right) + (\nu - 1) \log(y_i) + \nu \log(\nu) - \log\{\Gamma(\nu)\}\right] \\
 &= \exp\left\{\nu\left(\frac{y_i}{\mu_i} - \log\left(\frac{1}{\mu_i}\right) + (\nu - 1) \log(y_i) - \log \Gamma(\nu) + \nu \log(\nu)\right)\right\}
 \end{aligned}$$

- $\ell(\beta; \mathbf{y}) = \sum \left\{ \frac{y_i \theta_i - b(\theta_i)}{\phi_i} + c(y_i, \phi_i) \right\} \quad b'(\theta_i) = \mu_i; \quad b''(\theta_i) = V(\mu_i)$

- $g(\mu_i) = g\{b'(\theta_i)\} = \eta_i = \mathbf{x}_i^\top \beta$

- $\frac{\partial \ell(\beta; \mathbf{y})}{\partial \beta_j} = \sum \frac{\partial \ell_i}{\partial \theta_i} \frac{\partial \theta_i}{\partial \beta_j} = \sum \frac{y_i - b'(\theta_i)}{\phi_i} \frac{\partial \theta_i}{\partial \beta_j}$

- $g'(b(\theta_i)) b''(\theta_i) \frac{\partial \theta_i}{\partial \beta_j} = g'(\mu_i) V(\mu_i) \frac{\partial \theta_i}{\partial \beta_j} = x_{ij}$

- $\frac{\partial \ell(\beta; \mathbf{y})}{\partial \beta_j} = \sum \frac{y_i - \mu_i}{\phi_i g'(\mu_i) V(\mu_i)} x_{ij} = \sum \frac{y_i - \mu_i}{a_i \phi g'(\mu_i) V(\mu_i)} x_{ij}$

when $\phi_i = a_i \phi$

ELM has $\phi_i = \phi / w_i$

- matrix notation:

$$\frac{\partial \ell(\beta)}{\partial \beta} = \mathbf{X}^\top \mathbf{u}(\beta), \quad \mathbf{X} = \frac{\partial \eta}{\partial \beta^\top}, \quad \mathbf{u} = (u_1, \dots, u_n), \quad u_i = \frac{y_i - \mu_i}{\phi_i g'(\mu_i) V(\mu_i)}$$

- $\ell(\beta; \mathbf{y}) = \sum \left\{ \frac{y_i \theta_i - b(\theta_i)}{\phi_i} + c(y_i, \phi_i) \right\} \quad b'(\theta_i) = \mu_i; \quad b''(\theta_i) = V(\mu_i)$
- $g(\mu_i) = g\{b'(\theta_i)\} = \eta_i = \mathbf{x}_i^\top \beta$
- $\frac{\partial \ell(\beta; \mathbf{y})}{\partial \beta_j} = \sum \frac{\partial \ell_i}{\partial \theta_i} \frac{\partial \theta_i}{\partial \beta_j} = \sum \frac{y_i - b'(\theta_i)}{\phi_i} \frac{\partial \theta_i}{\partial \beta_j}$
- $g'(b(\theta_i)) b''(\theta_i) \frac{\partial \theta_i}{\partial \beta_j} = g'(\mu_i) V(\mu_i) \frac{\partial \theta_i}{\partial \beta_j} = x_{ij}$
- $\frac{\partial \ell(\beta; \mathbf{y})}{\partial \beta_j} = \sum \frac{y_i - \mu_i}{\phi_i g'(\mu_i) V(\mu_i)} x_{ij} = \sum \frac{y_i - \mu_i}{a_i \phi g'(\mu_i) V(\mu_i)} x_{ij}$

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Scale parameter ϕ_i

- in most cases, either ϕ_i is known, or $\phi_i = \phi a_i$, where a_i is known
- Normal distribution, $\phi = \sigma^2$
- Binomial distribution $\phi_i = m_i^{-1}$
- Gamma distribution, $\phi = 1/\nu$

Family	Canonical link	Variance function	ϕ_i
Normal	$\eta = \mu$	1	σ^2
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Inverse Gaussian	$\eta = 1/\mu^2$	μ^3	ξ

$$\bullet \frac{\partial \ell(\beta; \mathbf{y})}{\partial \beta_j} = \sum \frac{y_i - \mu_i}{\phi_i g'(\mu_i) V(\mu_i)} \mathbf{x}_{ij} = \sum \frac{y_i - \mu_i}{a_i \phi g'(\mu_i) V(\mu_i)} \mathbf{x}_{ij}$$

when $\phi_i = a_i \phi$

- if $\theta_i = g(\mu_i)$ **canonical link**, then $g'(\mu_i) = 1/V(\mu_i)$, and

$$\sum \frac{y_i \mathbf{x}_{ij}}{a_i} = \sum \frac{y_i \hat{\mu}_i \mathbf{x}_{ij}}{a_i}$$

Solving maximum likelihood equation

- Newton-Raphson: $\ell'(\hat{\beta}) = \mathbf{0} \approx \ell'(\beta) + (\hat{\beta} - \beta)\ell''(\beta)$

defines iterative scheme

- $\hat{\beta}^{(t+1)} = \hat{\beta}^{(t)} - \{\ell''(\hat{\beta}^{(t)})\}^{-1}\ell'(\hat{\beta}^{(t)})$

- Fisher scoring: $-\ell''(\beta) \leftarrow \mathbf{E}\{-\ell''(\beta)\} = \mathbf{i}(\beta)$

many books use $\mathbf{I}(\beta)$

- $\hat{\beta}^{(t+1)} = \hat{\beta}^{(t)} + \{\mathbf{i}(\hat{\beta}^{(t)})\}^{-1}\ell'(\hat{\beta}^{(t)})$

- applied to matrix version: $\mathbf{X}^T \mathbf{u}(\hat{\beta}) = \mathbf{0} \doteq \mathbf{X}^T \mathbf{u}(\beta) + (\hat{\beta} - \beta) \mathbf{X}^T \frac{\partial \mathbf{u}(\beta)}{\partial \beta^T}$

- change to Fisher scoring: $\mathbf{X}^T \mathbf{u}(\hat{\beta}) = \mathbf{0} \doteq \mathbf{X}^T \mathbf{u}(\beta) + (\hat{\beta} - \beta) \mathbf{X}^T \mathbf{E} \left\{ \frac{\partial \mathbf{u}(\beta)}{\partial \beta^T} \right\}$

$$\hat{\beta} = \beta + \mathbf{i}(\beta)^{-1} \mathbf{X}^T \mathbf{u}(\beta)$$

... maximum likelihood equation

$$\hat{\beta} = \beta + i(\beta)^{-1} X^T u(\beta)$$

- $\frac{\partial^2 \ell(\beta; y)}{\partial \beta_j \partial \beta_k} = \sum \frac{-b''(\theta_i)}{\phi_i} \left(\frac{\partial \theta_i}{\partial \beta_j} \right) \left(\frac{\partial \theta_i}{\partial \beta_k} \right) + \sum \frac{y_i - b'(\theta_i)}{\phi_i} \frac{\partial^2 \theta_i}{\partial \beta_j \partial \beta_k}$
- $E \left(-\frac{\partial^2 \ell(\beta; y)}{\partial \beta_j \partial \beta_k} \right) = \sum \frac{V(\mu_i)}{\phi_i} \frac{x_{ij}}{g'(\mu_i)V(\mu_i)} \frac{x_{ik}}{g'(\mu_i)V(\mu_i)} = \sum \frac{x_{ij}x_{ik}}{\phi_i \{g'(\mu_i)\}^2 V(\mu_i)}$
-

$$\begin{aligned}\hat{\beta} &= \beta + (X^T W X)^{-1} X^T u(\beta) = (X^T W X)^{-1} \{X^T W X \beta + X^T u(\beta)\} \\ &= (X^T W X)^{-1} \{X^T W (X \beta + W^{-1} u(\beta))\} \\ &= (X^T W X)^{-1} X^T W z\end{aligned}$$

- does not involve ϕ_i iteratively re-weighted least squares W, z both depend on β
- **derived response** $z = X\beta + W^{-1}u$ linearized version of y

Summary

Model:

$$\mathbb{E}(y_i) = \mu_i; \quad g(\mu_i) = \mathbf{x}_i^T \boldsymbol{\beta}; \quad \text{Var}(y_i) = \phi_i \mathbf{V}(\mu_i) \quad \phi_i = \mathbf{a}_i \boldsymbol{\phi}$$

Estimation:

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{W} \mathbf{X})^{-1} \mathbf{X}^T \mathbf{W} \mathbf{z}; \quad \mathbf{z} = \mathbf{X} \boldsymbol{\beta} + \mathbf{W}^{-1} \mathbf{u}; \quad \mathbf{z}(\boldsymbol{\beta}) = \mathbf{X} \boldsymbol{\beta} + \mathbf{W}^{-1}(\boldsymbol{\beta}) \mathbf{u}(\boldsymbol{\beta})$$

Variance:

$$\text{Var}(\hat{\boldsymbol{\beta}}) \doteq (\mathbf{X}^T \mathbf{W} \mathbf{X})^{-1} \quad \mathbf{W} \text{ is diagonal}$$

On pp. 118-119 of ELM, this iteration is carried out in R on the `bliss` data

Summary 2

$$\begin{aligned}\hat{\beta} &= (X^T W X)^{-1} X^T W z; & z &= X\beta + W^{-1}u; & z(\beta) &= X\beta + W^{-1}(\beta)u(\beta) \\ \text{Var}(\hat{\beta}) &\doteq (X^T W X)^{-1} & & & W &\text{ is diagonal}\end{aligned}$$

$$W_{ii} =$$

$$u_i =$$

Note $\hat{\beta}$ is free of ϕ because of W and W^{-1} , but $\text{Var}(\hat{\beta})$ depends on ϕ

Warning: in ELM W is defined slightly differently (no ϕ), so he has $\text{Var}(\hat{\beta}) = (X^T W X)^{-1} \hat{\phi}$

Summary 2

$$\begin{aligned}\hat{\beta} &= (X^T W X)^{-1} X^T W z; & z &= X\beta + W^{-1}u; & z(\beta) &= X\beta + W^{-1}(\beta)u(\beta) \\ \text{Var}(\hat{\beta}) &\doteq (X^T W X)^{-1} & & & W &\text{ is diagonal}\end{aligned}$$

$$W_{ii} = \frac{1}{\phi a_i \{g'(\mu_i)\}^2 V(\mu_i)}$$

$$u_i = \frac{y_i - \mu_i}{\phi a_i g'(\mu_i) V(\mu_i)}$$

Note $\hat{\beta}$ is free of ϕ because of W and W^{-1} , but $\text{Var}(\hat{\beta})$ depends on ϕ

Warning: in ELM W is defined slightly differently (no ϕ), so he has $\text{Var}(\hat{\beta}) = (X^T W X)^{-1} \hat{\phi}$
Further, the w_i on p.117 is not the same as the w_i on p. 118; SM uses a_i instead which would have been better for ELM

Analysis of data using GLMs: overview

- choose a model, often based on type of response or on mean/variance relationship
- fit a model, using maximum likelihood estimation convergence (almost) guaranteed
- inference for individual coefficients $\hat{\beta}_j$ from summary
- inference for groups of coefficients by analysis of deviance
- estimation of ϕ based on Pearson's Chi-square

typo in ELM p.121: cross out = $\text{var}(\hat{\mu})$

$$\hat{\phi} = \frac{1}{n-p} \sum_{i=1}^n \frac{(y_i - \hat{\mu}_i)^2}{V(\hat{\mu}_i)}$$

- analysis of deviance: see p. 121 (near bottom) likelihood ratio tests
- diagnostics: same as for `lm` ELM p.124; SM p.477
 - residuals: deviance or Pearson; can be standardized ELM likes 1/2 normal plots
 - influential observations: uses hat matrix `SMPracticals` has very good GLM diagnostics

`glm.diag`, `plot.glm.diag`

The last slide about GLM theory

- special to `glm`
- two models, Poisson and Binomial, have no ϕ parameter
- this has two consequences
- the **residual deviance** can be used as a test of fit of the model
- two pseudo-models are available called `quasibinomial`, `quasipoisson`
- quasi-binomial: $\text{var}(y_i) = \phi p_i(1 - p_i)$
- quasi-Poisson: $\text{var}(y_i) = \phi \mu_i$
- quasi- is a quick way to fit proportion or count responses, but allow the variance to be bigger (or rarely, smaller) than it would be under the binomial or Poisson model
- caveat – none of this works for **binary** data, only **binomial** $n_i \geq 5$, approx



Vaccinated English adults under 60 are dying at twice the rate of unvaccinated people the same age

And have been for six months. This chart may seem unbelievable or impossible, but it's correct, based on weekly data from the British government.

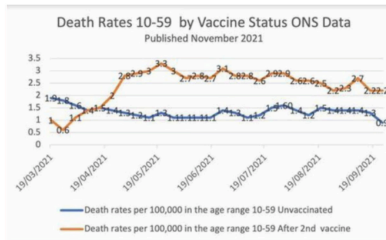


Alex Berenson

Nov 20 1,137 627

The brown line represents weekly deaths from all causes of vaccinated people aged 10-59, per 100,000 people.

The blue line represents weekly deaths from all causes of unvaccinated people per 100,000 in the same age range.



I have checked the underlying dataset myself and this graph is correct. Vaccinated people under 60 are twice as likely to die as unvaccinated people. And overall deaths in Britain are running well above normal.

I don't know how to explain this other than vaccine-caused mortality.

Is watching the 1984 Ghostbusters movie killing people? A Statistician's Perspective

Is watching the 1984 Ghostbusters movie killing people?

English adults under 60 who have watched the 1984 Ghostbusters movie are dying at twice the rate of people who have watched the 2021 Ghostbusters movie the same age.

And have been for six months. The chart may seem unbelievable or impossible but it is correct, based on weekly data from the British government.

The brown line represents weekly deaths from all causes of people aged 10-59 who have watched the 1984 Ghostbusters movie but not the 2021 Ghostbusters movie, per 100,000 people.

The blue line represents weekly deaths from all causes of unvaccinated people per 100,000 in the same age range.

Is watching the 1984 Ghostbusters movie killing people?



I have checked the underlying dataset myself and the graph plotted above is correct. People under 60 who watched the 1984 Ghostbusters movie are twice as likely to die as people who watched the 2021 Ghostbusters movie. The overall deaths in Britain are running well above normal.

→ [casestudies.pdf](#)