

Observational evidence on vaccine effectiveness against delta variant – latest results and risk of bias considerations

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Joint work led by

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with

- Cochrane Response (led by Nicholas Henschke and Gemma Villanueva)
- University of Bristol (led by Julian Higgins)
- WHO (particularly Fatema Kazi)



The screenshot shows the home page of the COVID-NMA website. The navigation bar is blue with a home icon, and links for 'About us', 'Living Mapping', 'COVID-19 treatments', 'Vaccines', and 'Preventive treatments'. Social media icons for Twitter and email are also present. The main content area features the COVID-NMA logo, which includes the text 'COVID-19 OPEN LIVING EVIDENCE SYNTHESIS TO INFORM DECISION'. Below the logo is the heading 'The COVID-NMA initiative' and the sub-heading 'A living mapping and living systematic review of Covid-19 trials'. A central text box contains the following information:

COVID-NMA is an international research initiative supported by the WHO and Cochrane.

We provide a [living mapping](#) of COVID-19 trials. We are also conducting living evidence synthesis on [preventive interventions, treatments and vaccines](#) for COVID-19 to assist decision makers.

See the description of our model [here](#) and our living review protocol [here](#).



The screenshot shows a page titled 'COVID-19 VACCINE EFFECTIVENESS ON VARIANTS OF CONCERN'. The navigation bar is blue with a home icon, and links for 'About us', 'Living Mapping', 'COVID-19 treatments', and 'Vaccines'. The 'Preventive treatments' link is highlighted. Social media icons for Twitter and email are also present. The main content area features the heading 'OBSERVATIONAL STUDIES' and the sub-heading 'PROTOCOL'. The text below reads:

Our protocol is available on Zenodo [here](#) .

VARIANTS OF CONCERN

We identified observational studies assessing vaccine effectiveness on variant from the studies identified by [Krause P et al. Lancet 2021](#) and the process described in our [protocol](#) .

Vaccine effectiveness is based on direct evidence but also indirect evidence (i.e., variant exposure extrapolated the prevalence of the variant in the population) reported in the manuscript or in secondary sources.

Risk of bias assessment is ongoing and may be missing on the forest plots.

Analyses for variant delta and Beta were updated, some studies are awaiting classification (last search date 24 sep, 2021).

- We look for:
 - comparative observational studies in any population
 - must account for at least some confounders in the design or analysis
 - involving any COVID-19 vaccine or vaccine schedule
 - that report **severe disease**, infection (after 1 or 2 doses), symptomatic disease (after 1 or 2 doses), mortality or long COVID

Trial	Design	Variant	Participants	Type	In
<p>Bajema K, MMWR, 2021</p> <p>Full text</p> <p>Commentary</p>	Test-negative	Delta	U.S. veterans hospitalized at five Veterans Affairs Medical Centers (VAMCs) in USA.	RNA based vaccine	n
				RNA based vaccine	
				RNA based vaccine	B n
<p>Bar-On Y, N Engl J Med, 2021</p> <p>Full text</p> <p>Commentary</p>	Cohort	Delta	Israel residents 60 years of age or older who had been fully vaccinated at least 5 months earlier	RNA based vaccine	
				RNA based vaccine	n

Study registration: *

Publication Bajema K, MMWR, 2021

Dates: 2021-07-01 to 2021-08-06

Funding: Not reported/unclear

Conflict of interest: no COI (Vincent C. Marconi reports research grants from Eli Lilly and Co., Gilead Sciences, and ViiV Healthcare. No other potential conflicts of interest were disclosed.)

Study design: Test-negative

Description of participants: U.S. veterans hospitalized at five Veterans Affairs Medical Centers (VAMCs) in USA.

Inclusion criteria:

- Adults aged ≥ 18 years
- hospitalized at five VAMCs (in Atlanta, Georgia
- Bronx, New York
- Houston, Texas
- Los Angeles, California
- and Palo Alto, California)
- Patients were eligible for inclusion if they had COVID-19–like illness (i.e., fever, new or worsened cough or shortness of breath, loss of taste or smell, oxygen saturation on room air $< 94\%$, requirement for noninvasive ventilation or endotracheal intubation with mechanical ventilation, or chest radiograph or computed tomography pulmonary findings consistent with pneumonia) and a molecular test (reverse transcription–polymerase chain reaction [RT-PCR] or isothermal nucleic acid amplification test) for SARS-CoV-2 performed within 14 days before admission or during the first 72 hours of hospitalization.

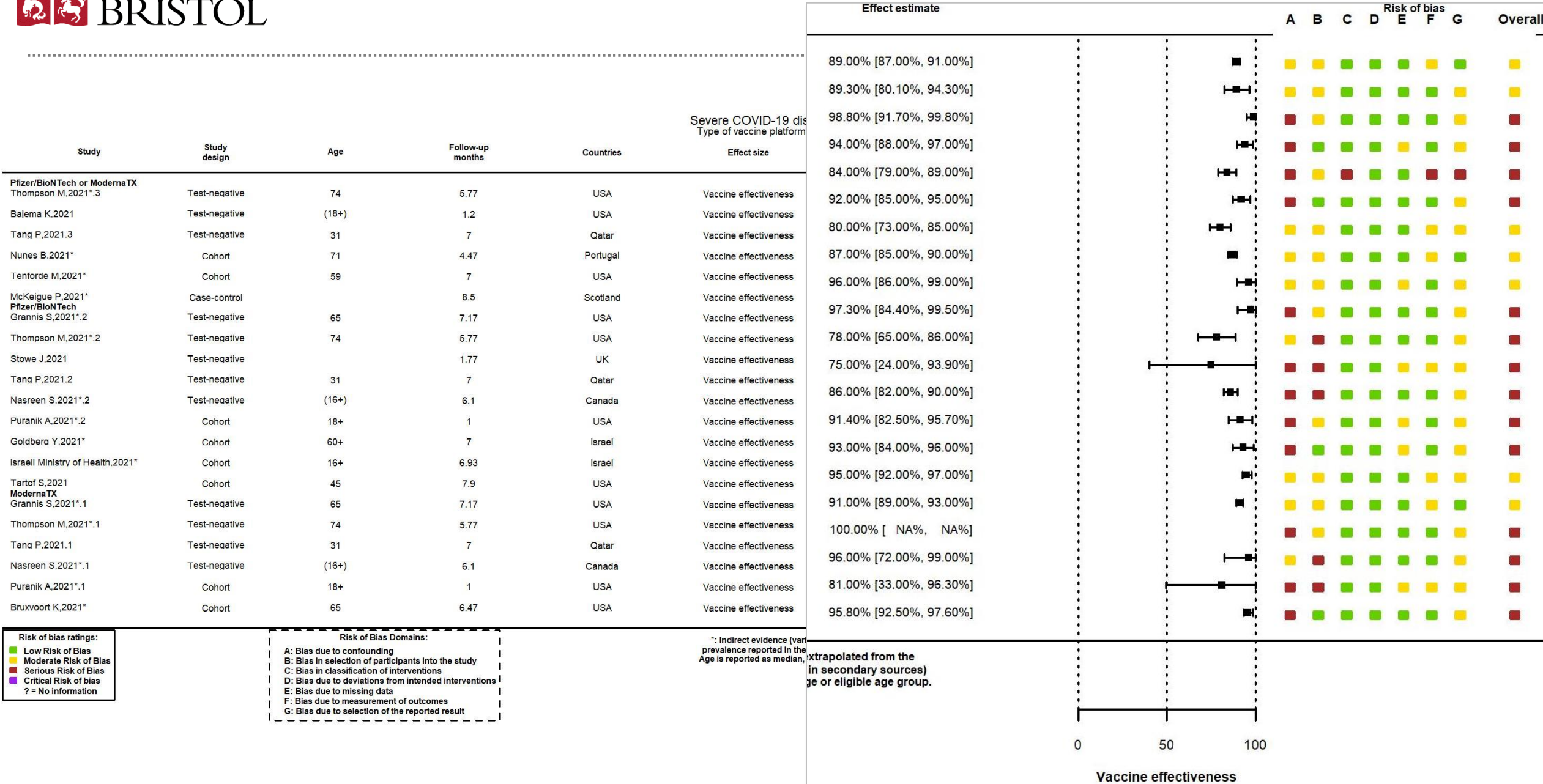
Exclusion criteria:

- Participants who received only 1 dose of an mRNA COVID-19 vaccine, 2 mRNA doses with receipt of the second dose < 14 days before the qualifying SARS-CoV-2 test, mixed mRNA vaccine products (i.e., a different product for each dose), or the Janssen (Johnson & Johnson) COVID-19 vaccine

Follow-up duration (months): 1.2

Methods

Results for RNA-based vaccines against Delta variant:



Risk of bias ratings:
 ■ Low Risk of Bias
 ■ Moderate Risk of Bias
 ■ Serious Risk of Bias
 ■ Critical Risk of bias
 ? = No information

Risk of Bias Domains:
 A: Bias due to confounding
 B: Bias in selection of participants into the study
 C: Bias in classification of interventions
 D: Bias due to deviations from intended interventions
 E: Bias due to missing data
 F: Bias due to measurement of outcomes
 G: Bias due to selection of the reported result

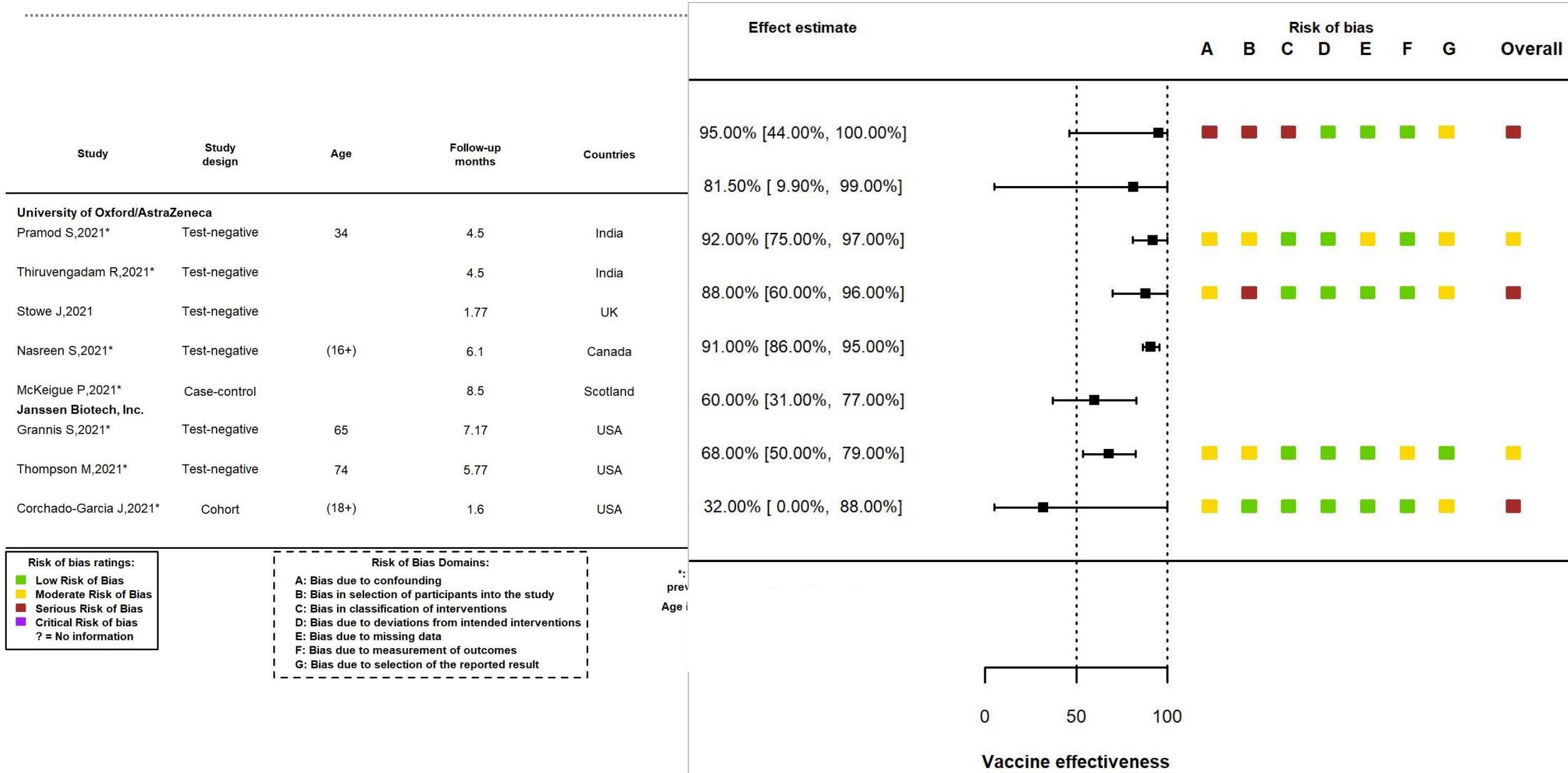
*: Indirect evidence (var prevalence reported in the Age is reported as median,

extrapolated from the in secondary sources) age or eligible age group.

0 50 100

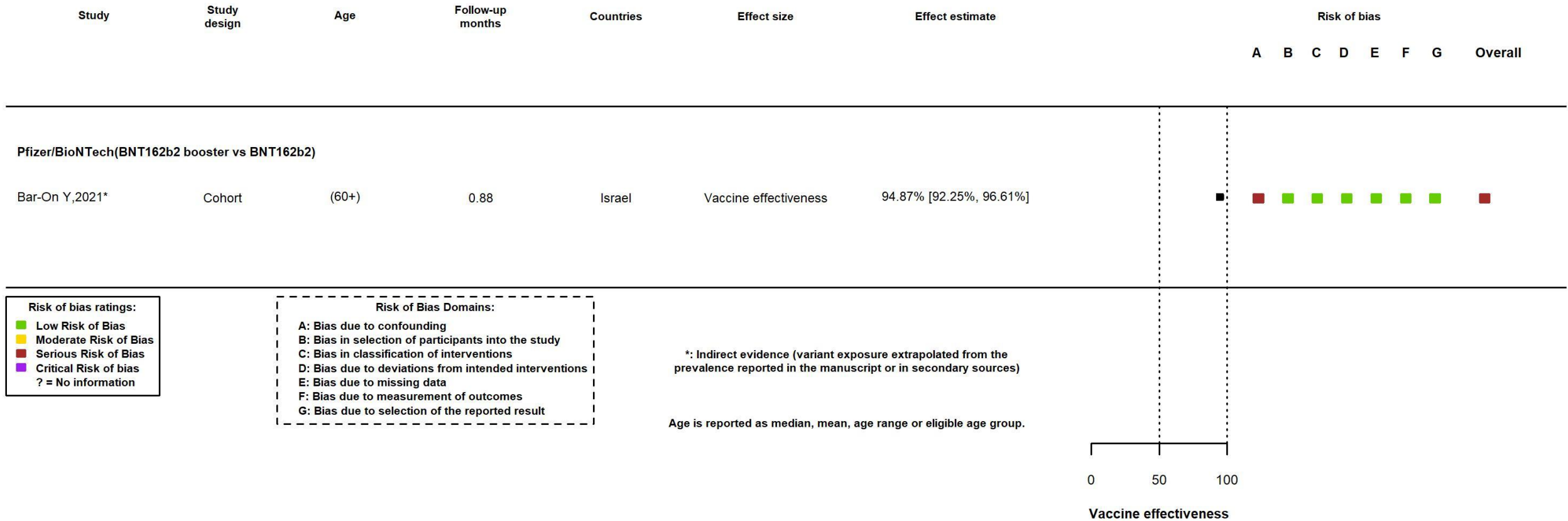
Vaccine effectiveness

Results for non-replicating viral vector vaccines against Delta variant: Severe disease



Results for **booster dose** of RNA-based vaccine against Delta variant: **Severe disease**

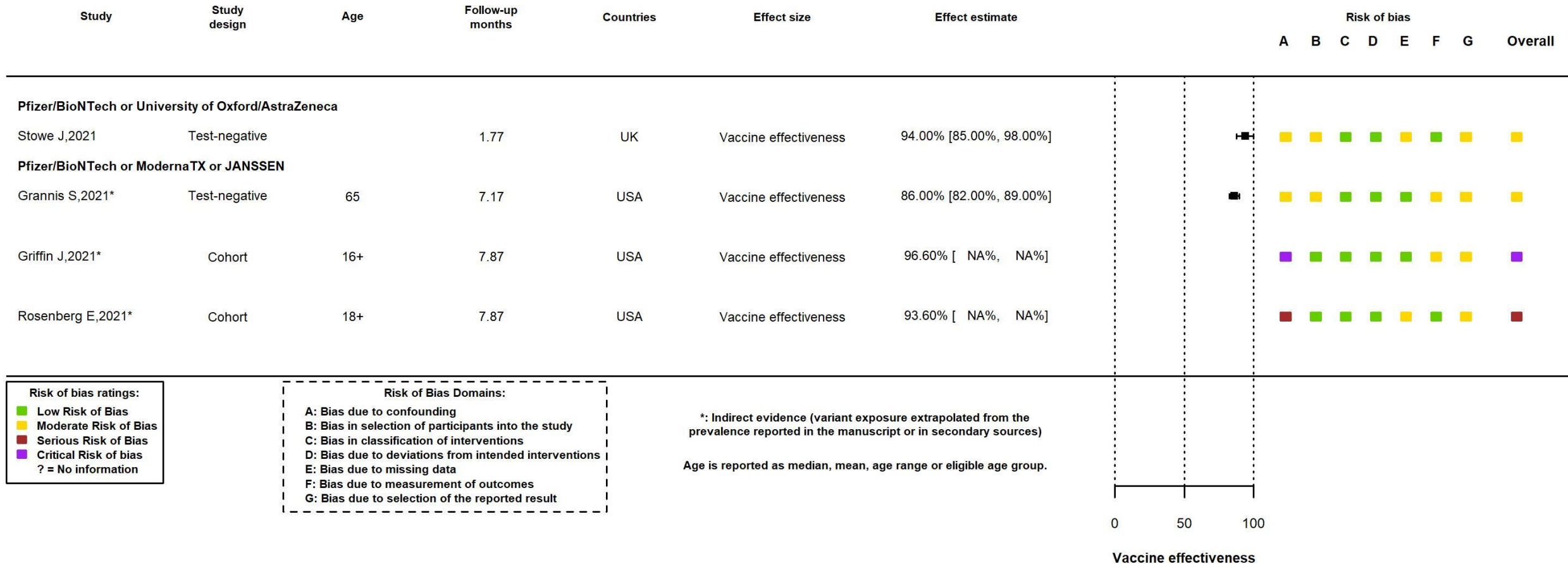
Severe COVID-19 disease, Variant: Delta



Results for **various** vaccines (inseparable) against Delta variant: **Severe disease**

Severe COVID-19 disease, Variant: Delta

Type of vaccine platform: Any COVID-19 vaccine



Quality of the evidence: assessing **risk of bias** in each result

RESEARCH METHODS AND REPORTING

ROBINS-I: a tool for assessing risk of bias in non-randomised studies of interventions

Jonathan AC Sterne,¹ Miguel A Hernán,² Barnaby C Reeves,³ Jelena Savović,^{1,4} Nancy D Berkman,⁵ Meera Viswanathan,⁶ David Henry,⁷ Douglas G Altman,⁸ Mohammed T Ansari,⁹ Isabelle Boutron,¹⁰ James R Carpenter,¹¹ An-Wen Chan,¹² Rachel Churchill,¹³ Jonathan J Deeks,¹⁴ Asbjørn Hróbjartsson,¹⁵ Jamie Kirkham,¹⁶ Peter Jüni,¹⁷ Yoon K Loke,¹⁸ Theresa D Pigott,¹⁹ Craig R Ramsay,²⁰ Deborah Regidor,²¹ Hannah R Rothstein,²² Lakhbir Sandhu,²³ Pasqualina L Santaguída,²⁴ Holger J Schünemann,²⁵ Beverly Shea,²⁶ Ian Shrier,²⁷ Peter Tugwell,²⁸ Lucy Turner,²⁹ Jeffrey C Valentine,³⁰ Hugh Waddington,³¹ Elizabeth Waters,³² George A Wells,³³ Penny F Whiting,³⁴ Julian PT Higgins³⁵

BMJ 2016
(undergoing update 2021)

Bias domains

Bias due to confounding

Bias in selection of participants into the study

Bias in classification of interventions

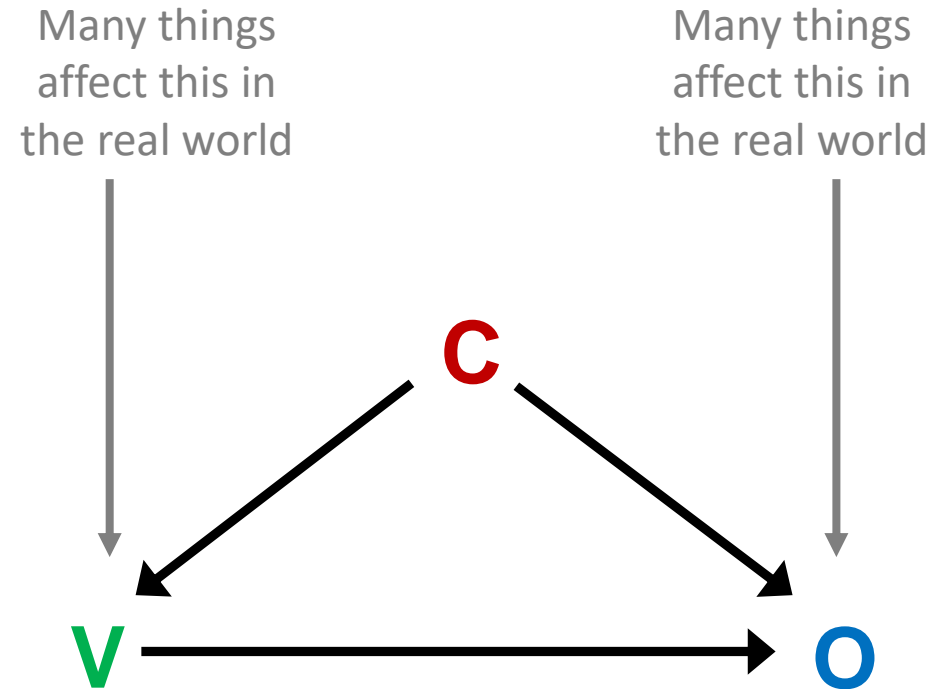
Bias due to departures from intended interventions

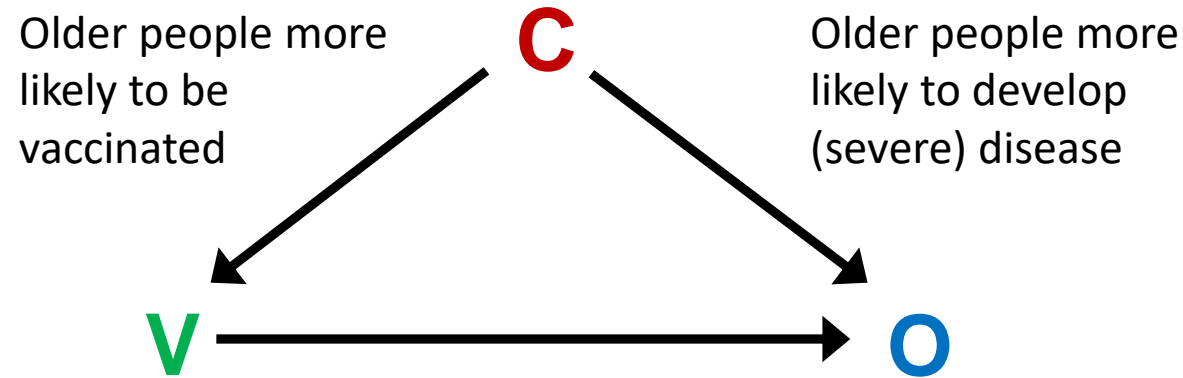
Bias due to missing data

Bias in measurement of outcomes

Bias in selection of the reported result

Confounding occurs when
there is a **common cause (C)**
of BOTH
whether someone is
vaccinated (V)
AND
whether someone has an
outcome event (O)





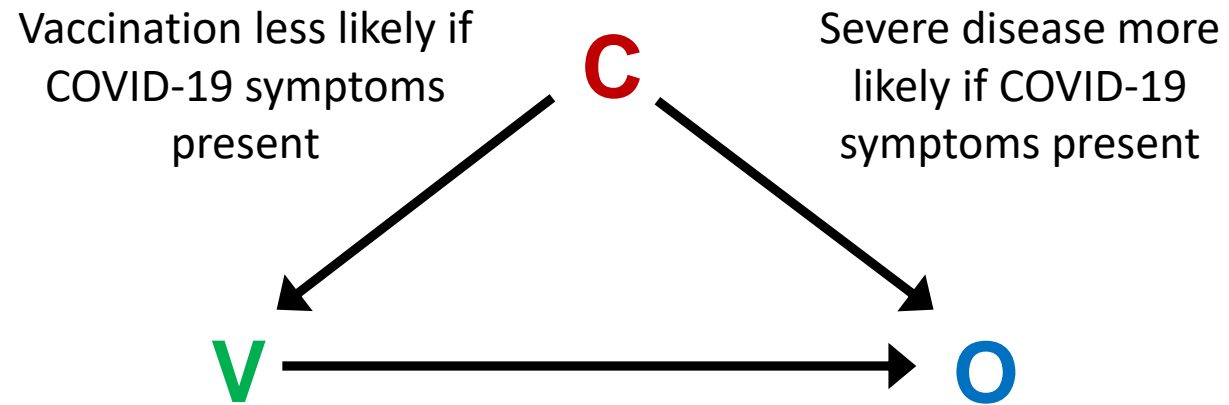
Leads to association between vaccination and disease even if the vaccine is ineffective

We can address this by *adjusting for age*

We examine a fixed list of potential confounding factors

- Age
- Sex
- Socioeconomic status
- Ethnicity
- Comorbidities
- Geographic location
- Specific populations (e.g. healthcare worker/elderly in institution)
- **Calendar time** (to reflect changing incidence of virus)
- Hospitalization and need for health care
- **Symptoms at time of planned vaccination**
- **Health-seeking behaviour** (e.g. frequency of consultation, flu vaccine history)

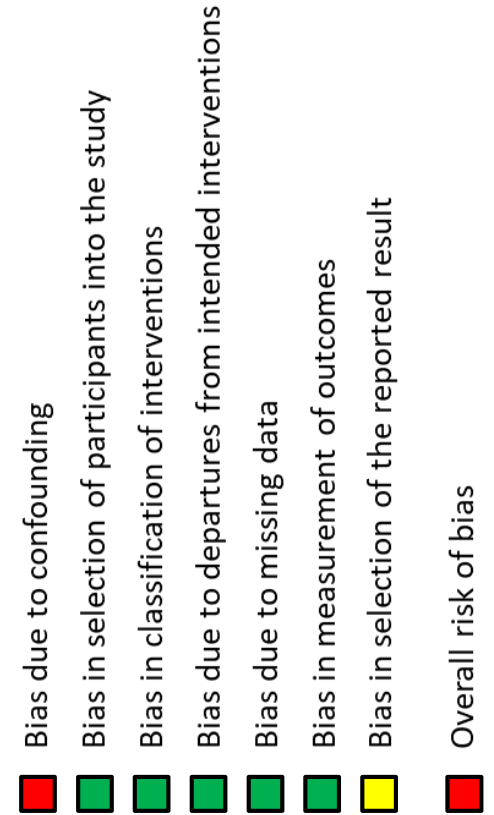
Confounding: COVID-19 symptoms



More difficult to address

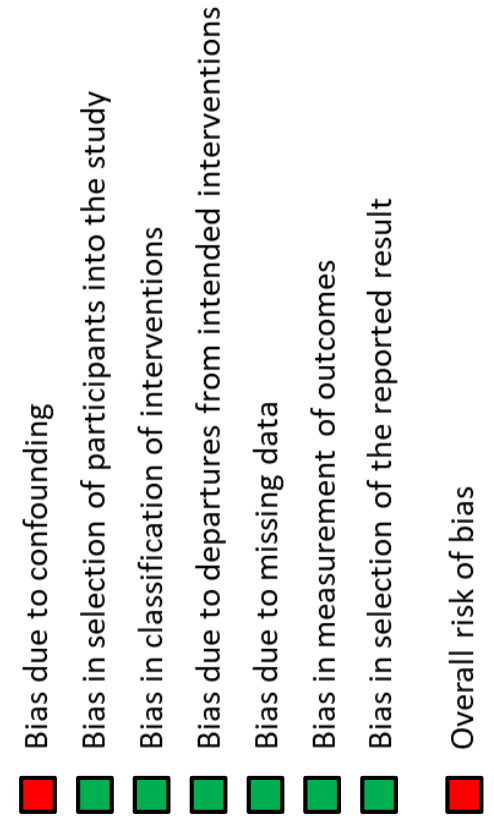
Example 1: Bruxvoort et al (Kaiser Permanente, Southern California)

- Cohort study
- Did not control for symptoms at the time of potential vaccination (judged to be at serious risk of bias due to confounding)
- No evidence of a protocol (very common in these studies) – so possibility of cherry picking of results
- Moderna, VE 95.8% (95% CI 92.5% to 97.6%) against severe disease



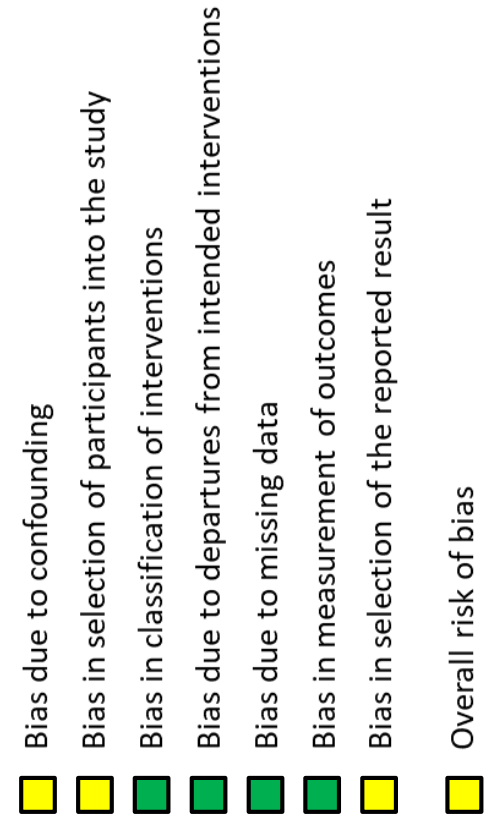
Example 2: Bar-On et al (Israel)

- Cohort study
- Did not control for potential confounding due to socioeconomic status, health seeking behaviour, specific populations, comorbidities, calendar time, COVID-19 symptoms at time of planned vaccination
- Otherwise seems quite strong
 - and a protocol is available (unusual for these studies)
- Pfizer booster, VE 94.9% (95% CI 92.5% to 96.6%)



Example 3: Bajema et al (US Veterans)









- Test-negative design
 - restricts the investigation to those who provide a test result
 - compare vaccination history in those who test positive with those who test negative
 - reduces confounding due to health-seeking behaviour
 - but this is not a panacea...
 - there is a risk of introducing spurious associations between vaccination and disease
 - (because these may both cause people to get tested)
 - risk of **selection bias**



- Pfizer or Moderna, VE 89.3% (95% CI 80.1% to 94.3%)









Example 4: Grannis et al (multiple USA sites)

- Another test-negative design
- In addition, possible bias in determination of severe COVID-19 due to knowledge of vaccination status of hospital patients

	Bias due to confounding
	Bias in selection of participants into the study
	Bias in classification of interventions
	Bias due to departures from intended interventions
	Bias due to missing data
	Bias in measurement of outcomes
	Bias in selection of the reported result
	Overall risk of bias

Example 5: Thompson et al (multiple USA sites)

- Another test-negative design
- A protocol is available (unusual for these studies)

	Bias due to confounding
	Bias in selection of participants into the study
	Bias in classification of interventions
	Bias due to departures from intended interventions
	Bias due to missing data
	Bias in measurement of outcomes
	Bias in selection of the reported result
	Overall risk of bias

- There are **risks of bias** in all the studies, although in general we think most large studies have done a good job
- **Magnitudes and directions** of the combined effects of different sources biases of bias are extremely **difficult to predict**
- But we **do not think that the biases are large** in comparison with the observed vaccine effectiveness estimates
- **Conclusion:** there is **robust evidence of high effectiveness**, substantially beyond 50% VE in most cases

Full results and details of methods are available from covid-nma.com



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Preventive treatments

COVID-NMA
COVID-19 OPEN LIVING EVIDENCE SYNTHESIS
TO INFORM DECISION

The COVID-NMA initiative
A living mapping and living systematic review
of Covid-19 trials

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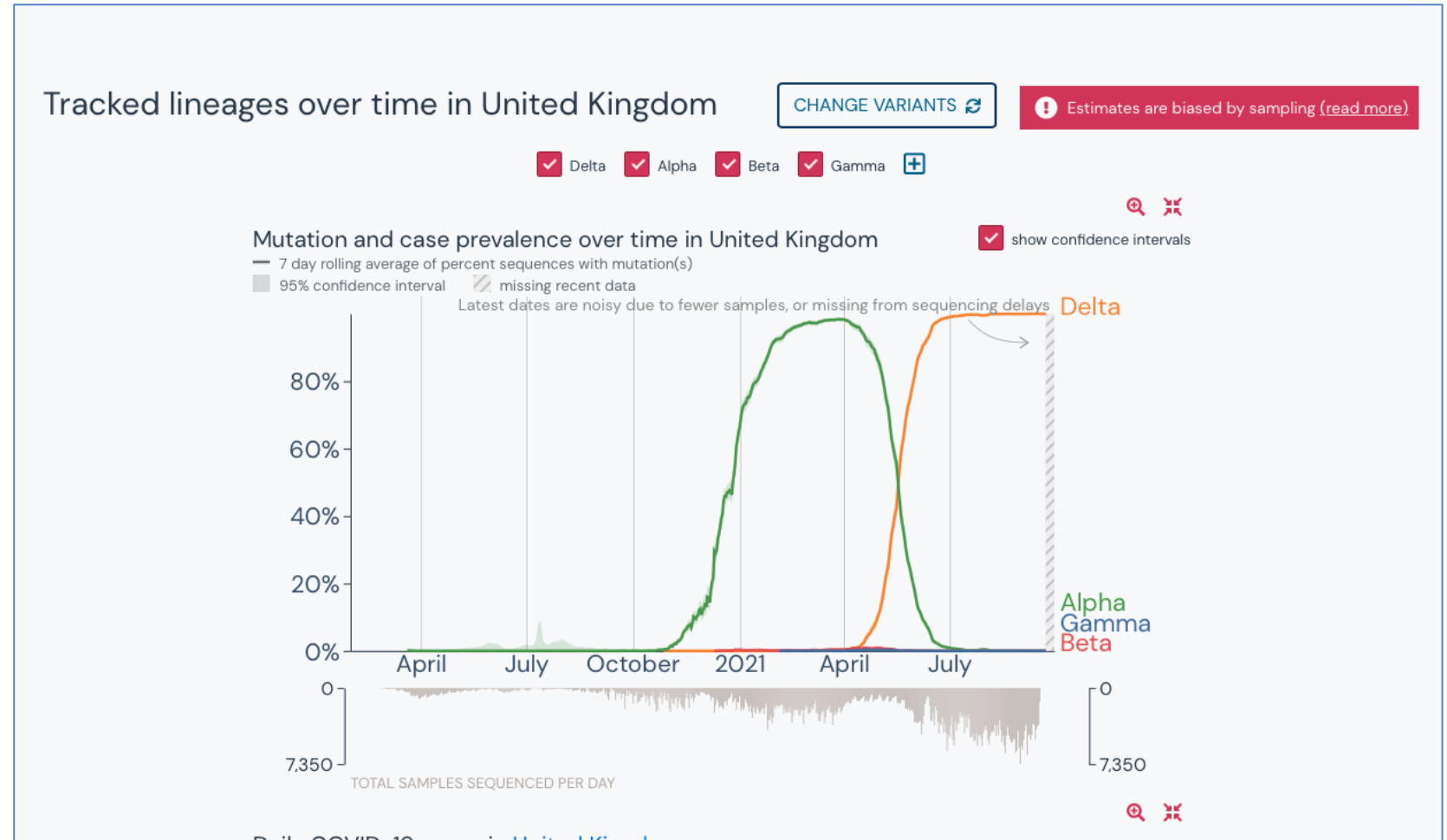
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Vaccines

- Living mapping
- Living evidence synthesis (Vaccine RCTs)
- Living evidence synthesis (Vaccine RCTs - Variants)
- Living evidence synthesis (Observational studies - Variants)

- **Direct evidence:** effectiveness against variant determined by sequencing all cases
- **Indirect evidence:** study performed while variant of concern was >50% prevalent in the population



<https://outbreak.info/location-reports>