

# Assessing the evidentiary value of secondary data analyses: A commentary on Gangestad, Dinh, Grebe, Del Giudice, and Thompson (2019)

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Secondary data analyses (analyses of open data from published studies) can play a critical role in hypothesis generation and in maximizing the contribution of collected data to the accumulation of scientific knowledge. However, assessing the evidentiary value of results from secondary data analyses is often challenging because analytical decisions can be biased by knowledge of the results of (and analytical choices made in) the original study and by unacknowledged exploratory analyses of open data sets (Scott & Kline, 2019; Weston, Ritchie, Rohrer, & Przybylski, 2018). Using the secondary data analyses reported by Gangestad et al. (this issue) as a case study, we outline several approaches that, if implemented, would allow readers to assess the evidentiary value of results from secondary data analyses with greater confidence.

<https://doi.org/10.1016/j.evolhumbehav.2019.08.004>

*Keywords:* secondary data analyses; menstrual cycle; replication; confirmatory; exploratory

Word count: X

Jünger et al. (2018) reported results of a longitudinal study testing for evidence that women's preferences for masculine men's body shapes track changes in fertility. They found no evidence for significant effects of fertility on preferences for markers of masculinity, such as muscularity and height, adding to a growing literature comprising recent large-scale longitudinal studies that found little evidence that within-subject changes in women's preferences for putative male cues of good genes reliably track within-woman changes in conception risk or steroid hormone levels (Dixson et al., 2018; Jones et al., 2018; Jünger, Motta-Mena, et al., 2018; Urszula M. Marcinkowska et al., 2018a, 2018b; Marcinkowska, Helle, Jones, & Jasienska, 2019; Stern, Gerlach, & Penke, 2018).

Gangestad et al. (2019 this issue) recently published alternative analyses of Junger et al.'s (2018) open data. They argued that the results of these reanalyses suggest that women's preferences for muscularity track changes in sex hormones (specifically, progesterone). They highlighted that their secondary analyses were closely modelled on their preregistered analysis plans for an ongoing study by their lab that has a similar design to the study reported by Jünger et al. (2018). However,


since Jünger et al.'s (2018) paper was cited in Gangestad et al.'s preregistration (<https://osf.io/zbktu/>), that preregistration was not blind to the results and analytical choices reported in Jünger et al.'s (2018) paper. In addition, Gangestad et al.'s preregistration cites Jünger et al. (2018) for the same effect of progesterone on body shape preferences that Gangestad et al. reported in their reanalyses, but that was not seen in Jünger et al.'s original analyses.


Because of the above, using Gangestad et al.'s preregistration as the basis for their reanalyses of Jünger et al.'s (2018) data would not have sufficiently guarded against biases that may have been introduced by knowledge of Jünger et al.'s (2018) analytical choices and results. In other words, the claim that Gangestad et al.'s results have high evidentiary value because their analyses were closely modelled on a preregistered analysis plan, is circular. Therefore, locating Gangestad et al.'s reanalyses on the continuum between confirmatory (where statistical significance can be interpreted as indicating that a given result has high evidentiary value) and exploratory (where statistical significance cannot be interpreted as indicating that a given result has high evidentiary value) is not straightforward.

As is the case in many other areas, open data and analysis code are becoming the standard in research on menstrual cycle and mate preferences. How can the field ensure that readers can assess the evidentiary value of secondary data with confidence? Below, we highlight four possible solutions to this problem. The solutions we outline are not intended as an exhaustive list and are also not necessarily mutually exclusive.

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The first solution is to use open data for hypothesis generation. In such cases, the results should be clearly labelled as exploratory if published (see Weston et al., 2018 for a discussion of the importance of this type of transparency when reporting secondary data analyses). Alternatively, authors could wait until confirmatory analyses have been carried out on a newly collected data set before publication. That the preregistration Gangestad et al. modelled their reanalyses on includes a direct reference to the results of their reanalyses of Jünger et al.'s (2018) data means it is misleading to imply that preregistering their analysis plan increases the evidentiary value of Gangestad et al.'s secondary data analyses. However, it is encouraging that Gangestad and colleagues plan to replicate their reanalysis of Jünger et al.'s data on a new data set that they are currently collecting. Importantly, the open analysis code they have included with their reanalysis means it will be relatively straightforward for readers of this forthcoming work to directly compare those with the ones reported by Gangestad et al. (this issue).

The second solution is to use open data for direct replication of new results (i.e., to confirm results of other studies by replicating their analyses on other open data). A recent example of this approach comes from DeBruine, Hahn, and Jones (2019), who used open data from Jones et al. (2018) to directly replicate Marcinkowska et al.'s (2018b) analyses of (and results for) combined effects of average progesterone levels and partnership status on women's preferences for male facial masculinity.

The third solution is to use specification curve analyses (Simonsohn, Simmons, & Nelson, 2015) or the closely related technique multiverse analyses (Stegen, F.Tuerlinckx, A. Gelman, & Vanpaemel, 2016). These methods indicate how robust results are across a range of reasonable analytical plans. For example, this approach has recently proven effective in analyses of the possible effects of social media use on life satisfaction (Orben, Dienlin, and Przybylski (2019)), demonstrating that such effects are typically small and very sensitive to the specific analytical choices made. Indeed, Stern et al.'s (this issue) analyses demonstrate that the significance of the effects that Gangestad et al. reported is extremely sensitive to specific analytical decisions made, suggesting they are not robust and have low evidentiary value.

A fourth potential solution is for the field to create a data management infrastructure that would allow large data sets to be made open in phases (Scott and Kline (2019)). With this solution, some of the data from a study would be made open for exploratory analyses immediately. The remainder (i.e., an independent or "hold out" sample) would then be made open at a later date for preregistered confirmatory analyses based on the earlier exploratory analyses. This approach has been employed successfully in other research areas (e.g., physics) and is being adopted by some large-scale multisite research

initiatives (e.g., recent developments with the Psychological Science Accelerator or the Attitudes, Identities, and Individual Differences Study). Indeed, combining this approach with specification curve analyses may be optimal for guarding against biases.

We reiterate that secondary data analyses are essential for hypothesis generation and maximizing the contribution that published data can make to the accumulation of scientific knowledge. However, to make a substantial contribution requires that people are able to assess the evidentiary value of secondary data analyses, both accurately and confidently. We encourage researchers, readers, and editors to carefully consider how secondary data analyses reported in papers and presented at conferences were conducted, described, and interpreted when assessing the evidentiary value of their results. We believe that considering the solutions described above would allow the evidentiary value of further secondary analyses of data to be assessed more confidently.

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