The prevalence of polycystic ovary syndrome in reproductive-aged women of different ethnicity: a systematic review and meta-analysis

SUPPLEMENTARY MATERIALS

The model includes several modules. Suppose there are I studies in total for the White, and for each studies $i = 1,...,I$ we observed the number of PCOS cases out of the total unselected female population. A Binomial distribution was used to model these studies:

$$x_i \sim Binomial(\beta_i, m_i) \quad (1)$$

β_i represents the probability of developing PCOS for White in study. *i.* Because the outcome is binary, which means that individuals can either be a PCOS case or not, we used logistic regression to model the pooled mean probability of developing PCOS for the White population (study-specific probability). We further assumed that random variables obtained after logit scale transformation follows a normal distribution:

$$logit(\beta_i) = \gamma_i\ Normal(\mu_\gamma, \sigma_\gamma^2) \quad (2)$$

μ_γ represents the pooled mean probability of developing PCOS on the logit scale for White population. In order to calculate the probability of PCOS, we need to rescale it to estimate:

$$p = \frac{\exp(\mu_\gamma)}{1+\exp(\mu_\gamma)} \quad (3)$$

where p is the pooled mean probability of PCOS for White population as a whole

This module is completed by including some reasonable prior distributions to μ_γ and σ_γ Markov Chain Monte Carlo methods were then performed in JAGS (interfaced with R) so the prior distributions can be updated by the observed data to generate some posterior distributions from which random samples of parameters of interest (i.e. prevalence of PCOS) can be drawn.

We tested several versions of prior distributions for this model by attempting a range of values for p and k in the following formula:

$$\mu_\gamma \sim Normal(p\ , \sigma_\gamma^2) \quad (4)$$

$$\sigma_\gamma \sim Uniform(0, k) \quad (5)$$

The prior distribution we included are based on some reasonable subjective belief. Given thatwe do not expect very high risk of developing PCOS for women, i.e. >20% in the general population. The values of were chosen to be within a reasonable range, i.e. 2-20% and different values were tested in a descending order (from largest value to smallest value). For example, we may start from 15% and go down to 12%, 9%, 6%, 3% to see which values of p produce better model fit statistics. It should be noted that μ_γ and σ_γ are on a logit scale, so even k= 2 represents a large variance.

However, as previously, we assumed that σ_γ follows a uniform distribution, it potentially indicates a problem that the simulation processes tend to be largely influenced by k where k is the upper bound of the uniform distribution, i.e.*Uniform* (0, k) Therefore, we decided to attempt half-Cauchy distribution for :

$$\mu_\gamma \sim Normal(p, \sigma_\gamma^2) \quad (6)$$

$$\sigma_\gamma = \frac{|Z_r|}{\sqrt{\varepsilon_r}} \quad (7)$$

$$Z_r \sim Normal(0, \sigma_{z_r}^2) \quad (8)$$

$$\varepsilon_r \sim Gamma(0.5, 0.5) \quad (9)$$

$$\sigma_{z_r}^2 = \frac{1}{B_r^2} \quad B_r \sim Uniform(0, 0.5) \quad (10)$$

The half-Cauchy distribution is advantageous in terms of allowing for outliers and accommodating small variances close to zero.

The statistical software provided deviance information criterion (DIC) of each model, which is a measurement of the goodness of fit of the model to the data, with lower values indicating a better fit. We attempted different versions of priors and then integrated results from various models by model averaging. Models with smaller DIC were weighted up while models with larger DIC were weighted down. The following formula was used to compute the weight of each model we included after statistical reasoning:

$$w_h = \frac{exp(-0.5\Delta DIC_h)}{\sum_{h=1}^{H} exp(-0.5\Delta DIC_h)} \quad (11)$$

where $\Delta DIC_h = min_h(DIC_h) - DIC_h$ and $h = 1,...H$, indicating the set of models

The same statistical principles were applied to obtain estimates of prevalence for other ethnic groups.

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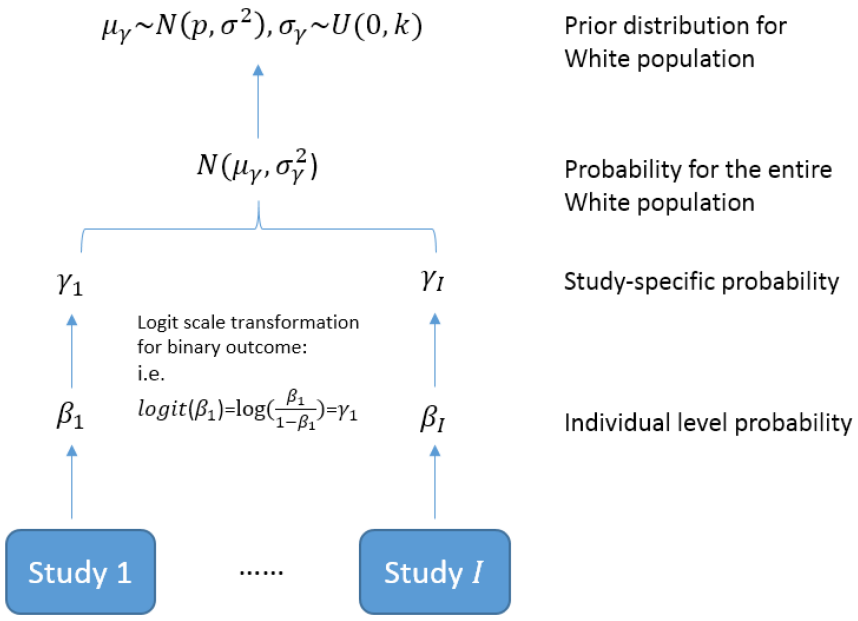
Supplementary Table 1: Results of prevalence studies (42 studies in total). See Supplementary_ Table_1

Supplementary Table 2: Evaluation of methodological quality of the 42 prevalence studies (score equals the total number of stars). See Supplementary_Table_2



Supplementary Figure 1: The modelling approach is discussed by using an explicit example of the White (Caucasian) population. The results of the rest of ethnic groups were estimated based on the same method. The graphic representation of this model is shown in Figure 1.