Brief summary of IWAS results

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About

Here I summarize some of the results shared by IWAS paper https://www.sciencedirect.com/science/article/pii/S1053811920308338.

I focused on structural and diffusion IDPs from UKB part (supplementary table).

Load data

```
kk = rbind(
  read.csv('../iwas_s1_structural.csv')[-1, ],
  read.csv('../iwas_s1_diffusion.csv')[-1, ]
)
ff = rbind(
  read.csv('../iwas_s1_structural.csv')[1, ] %>% mutate(type = 'structural'),
  read.csv('../iwas_s1_diffusion.csv')[1, ] %>% mutate(type = 'diffusion')
)
kk %>% ggplot() + geom_point(aes(x = beta_MVIWAS, y = beta_MVIWAS_Egger)) + coord_equal()
```
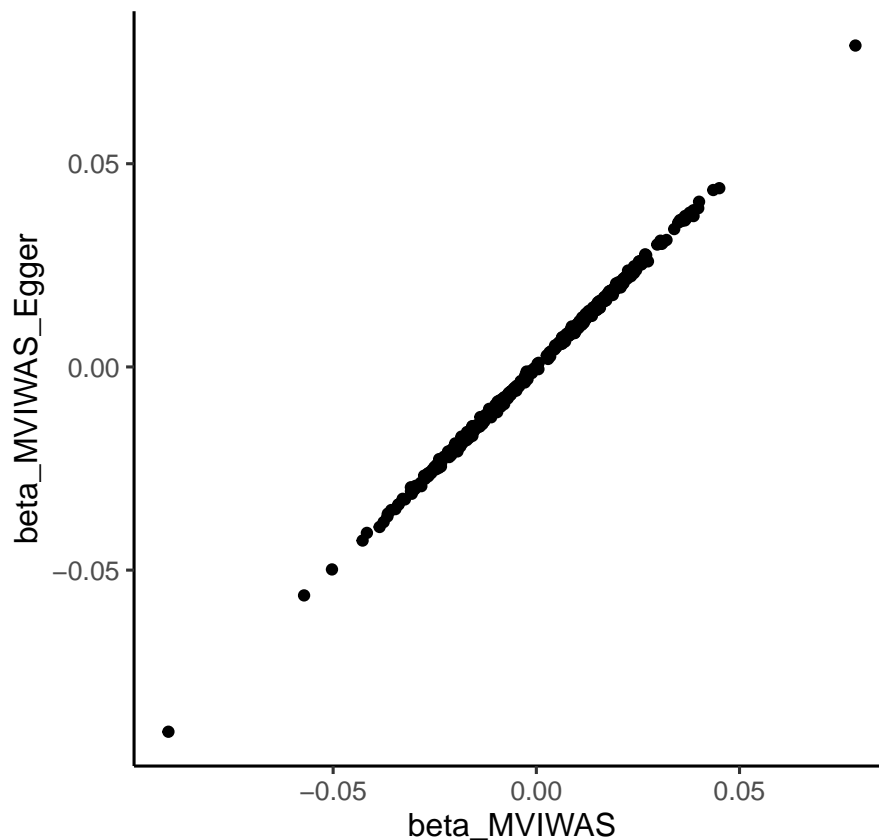
```
kk %>% ggplot() + geom_point(aes(x = -log(p_MVIWAS), y = -log(p_MVIWAS_Egger))) + coord_equal()
```
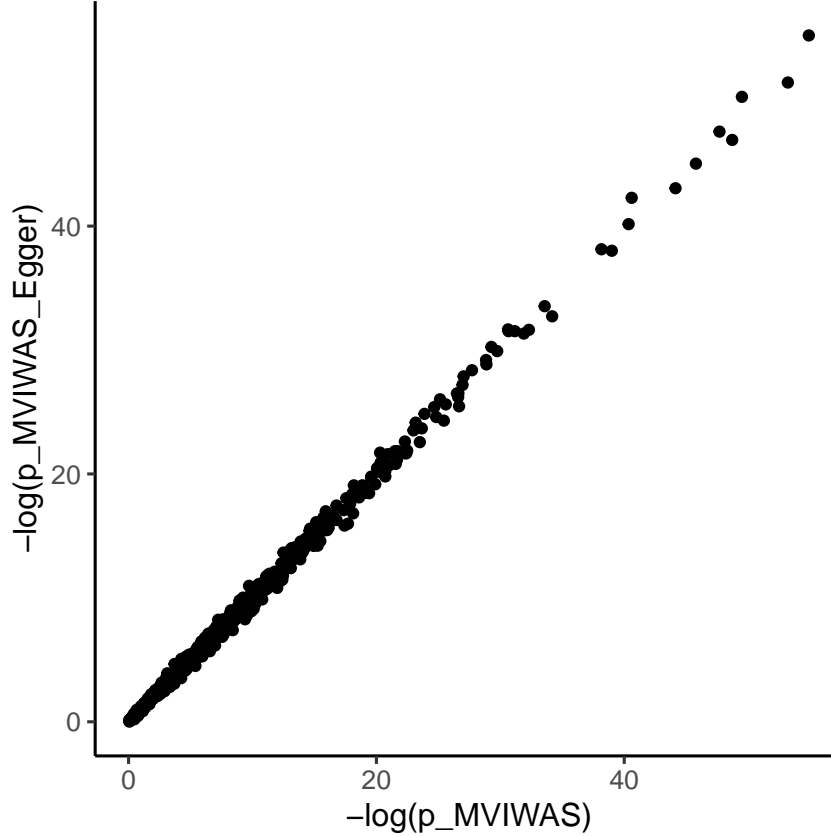


```
ff[, c(-2:-7, -11)] %>% pander(caption = 'Mu in Egger')
```

Table 1: Mu in Egger

IDP	beta_MVIWAS_Egger	se_MVIWAS_Egger	p_MVIWAS_Egger	MVIWAS.Egger.Sig.	type
mu	0.000158	2.059e-05	1.708e-14	Yes	structural
mu	0.0001737	2.041e-05	1.782e-17	Yes	diffusion

A brief summary

Differences between BrainXcan and IWAS:

- They did not do decomposition (PCA for obtaining region-specific and common factors).
- They proposed MV-IWAS which fit multiple IDPs jointly.
- They also proposed MV-IWAS-Egger which considers the direct effect of SNPs.
  - But the Egger version does not change the result much (see Figures above).

Pitfalls of IWAS:

- They did not use up-to-date UKB IDP GWAS.
- The joint model is sensitive to LD.
- The MV-IWAS was done for significant IDPs which is subject to selective bias and they do not account for this bias.