A community wiki for best practices when analysing iPSYCH data

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About me

- PhD in predictive human genetics

- Just started as a postdoc at NCRR, Aarhus University

- Involved in the R community

Community

A **community share 3 characteristics**:

- Participants have a common product or purpose that they work on or toward,

- They are mutually engaged, i.e., they assist and mentor one another,

- They develop shared resources and domain knowledge.

$\implies$ It is **faster to build together instead of reinventing the wheel**.

- Lave & Wenger (1991). Situated Learning: Legitimate Peripheral Participation.
- Wenger (1998). Communities of Practice: Learning, Meaning, and Identity.
- Sholler et al. (2019). Ten simple rules for helping newcomers become contributors to open projects.

You already benefit from many communities

If you

- use open-source programming languages such as ⦿R and 🐍,

- google problems and find solutions:

    - in blog posts and tutorials (relayed by e.g. R Bloggers and R Weekly)

    - on Stack Overflow

    - on Biostars

People invest time in this, often as they want to **give back to the community**.

Many analyses in Genetics

- Genome-Wide Association Study (GWAS)

- Principal Component Analysis (PCA)

- Heritability estimation

- Genetic correlation

- Mendelian Randomisation (MR)

- Polygenic Risk Scores (PRS)

- etc.

$\Longrightarrow$ It is hard to know about everything, and **it can be overwhelming**.

My example: after 3 years of thesis, I am an "expert" in PCA and PRS, but still know too little about analyses such as MR and genetic correlation.

Create a community wiki for best practices when analysing iPSYCH data

- Build a common knowledge and best practices about genetic analyses

- Share your analysis code to be used by others (e.g. for other phenotypes)

- Recall some particularities about iPSYCH data (e.g. "wave effect", data security, etc.)

In practice, we could simply create wiki pages on GitHub.

And possibly have a communication tool (e.g. Slack).

But, we would need people to get involved in this.

Thanks

Feedback and help welcome

(we can talk here or by email at fp@econ.au.dk)

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Slides created via R package **xaringan**.