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.

$\Longrightarrow$ 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 Python,
- 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

- GWAS
- Principal Component Analysis (PCA)
- Genetic correlation
- Mendelian Randomization (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 communtiy 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.

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**.