

# Approaches to imaging (epi-) genetics and to life in general

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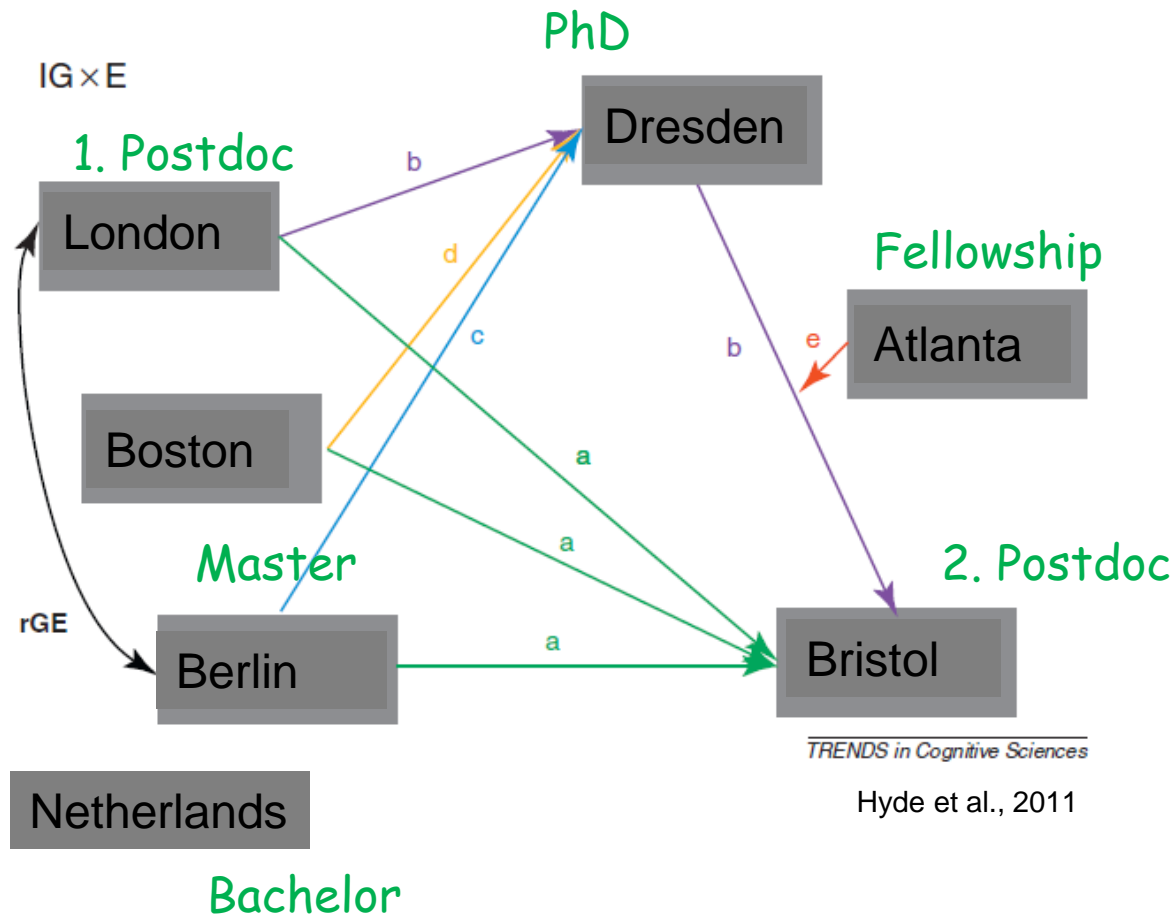
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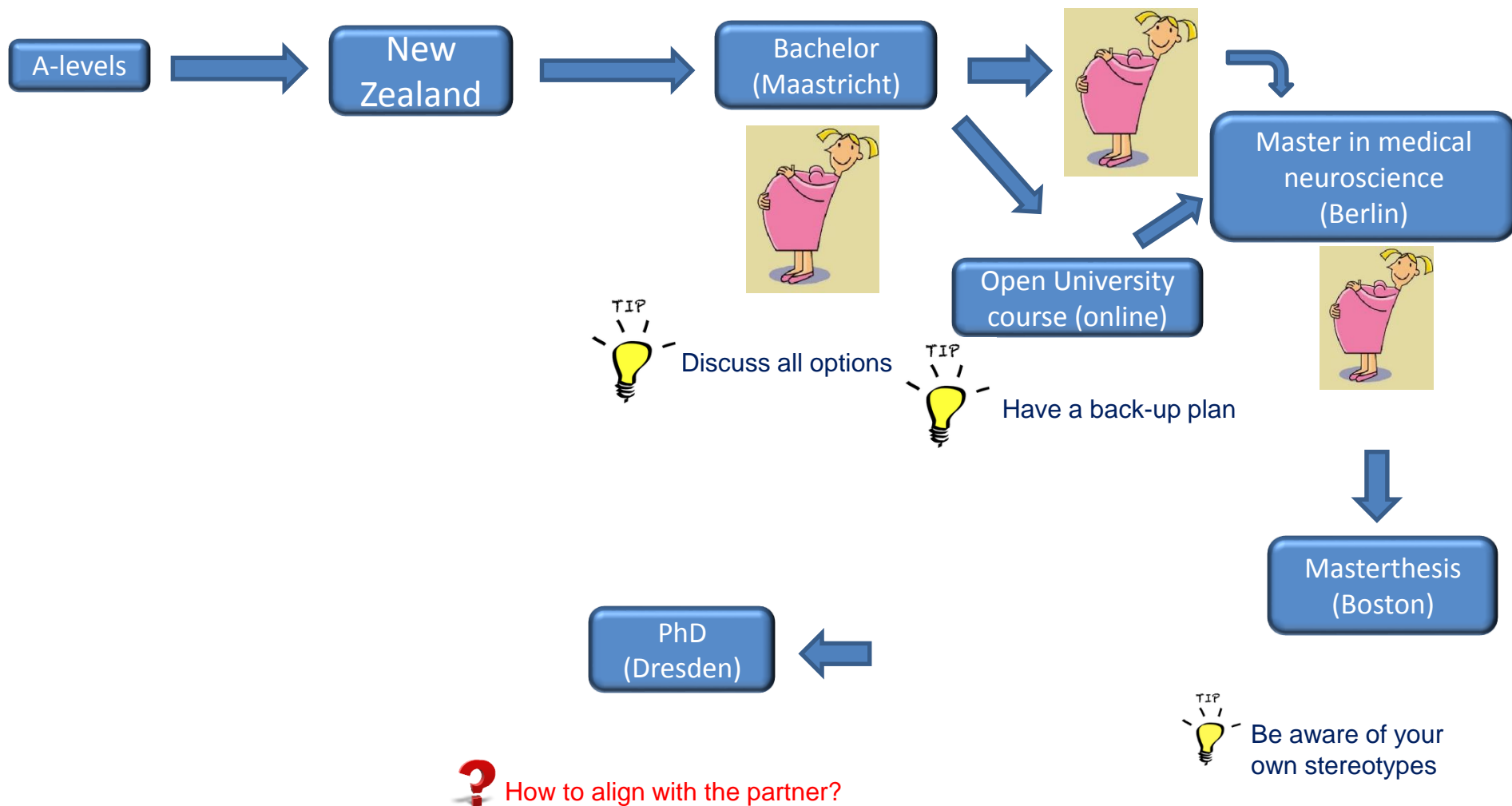
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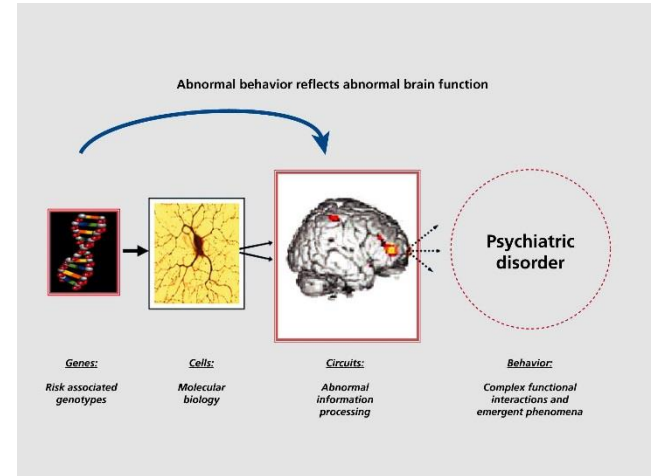


# Gene – Environment Interactions



- Genetic variants either
  - (too) rare or
  - of small effect or
  - not replicated...to explain schizophrenia etiology

⇒ Use polygenic scores or/and epigenetics

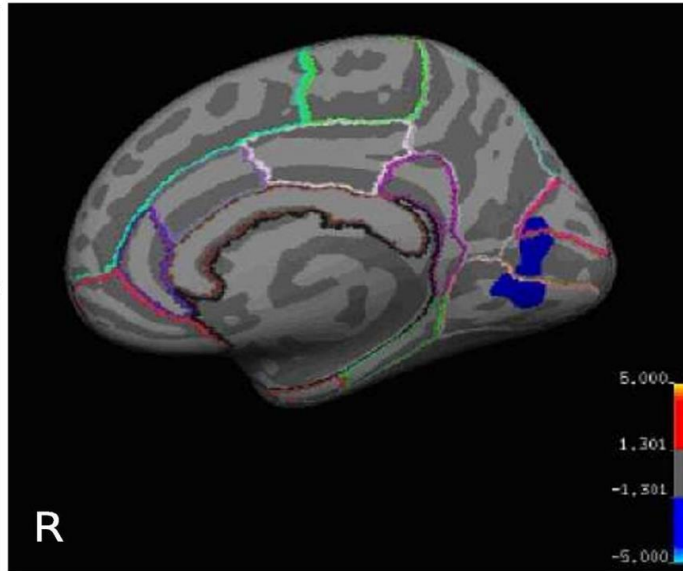
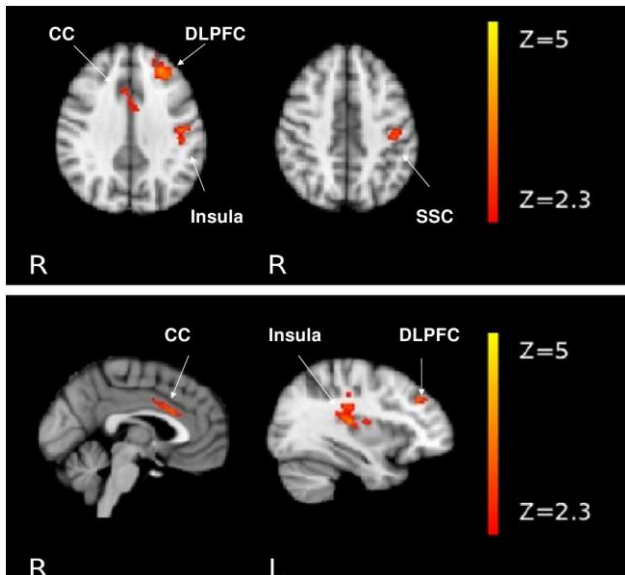


[dialogues-cns.org](http://dialogues-cns.org)

- Dichotomous outcome variable (disease status)
  - Explains little variance
  - Not continuous
  - Does not allow to study risk effect on a brain networks

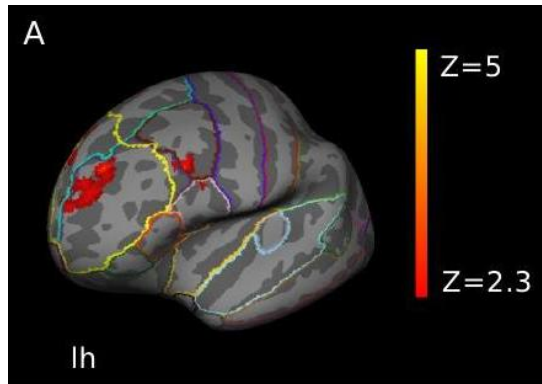
⇒ Use intermediate phenotypes

- No genotype effect of either SNP on diagnosis, but on brain function  
(rs12541) and structure (rs12807809)
- No diagnosis\*SNP interaction
- No effect on performance
- => Components in the **NMDA-signalling pathway** contribute to subtle changes in neural functioning and anatomy linked to schizophrenia



Walton et al., 2013a

# Polygenic Risk Score



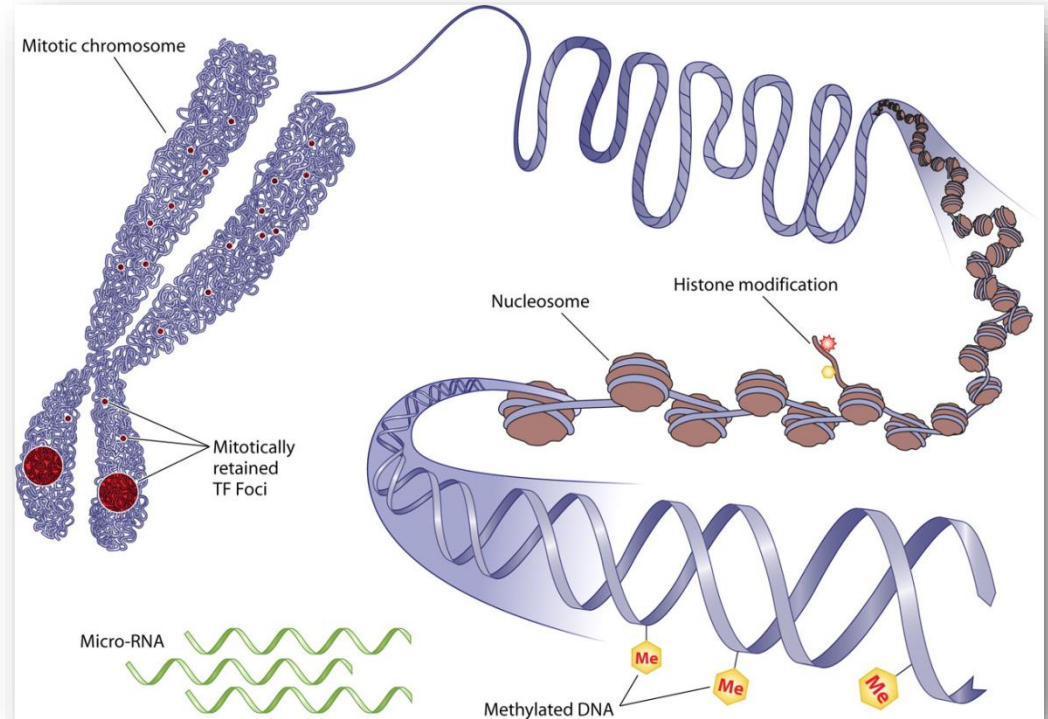
Walton et al., 2013b

Cluster	Functional annotation	Enrichment score	Number of associated genes
1	axonogenesis neuron projection development	4.58	21
2	ion binding cell motility and migration	2.98	73
3		2.78	12
4	channel activity GTPase regulator	2.32	13
5	activity	2.23	13

- No PGRS effect on diagnosis, but on brain function
- No PGRS\*diagnosis interaction
- No correlation with performance
- Accounted for 4.3% of the total variance
- => combined impact of **many common genetic variants** of small effect reveal etiologic mechanisms of the disorder better than single common genetic variants

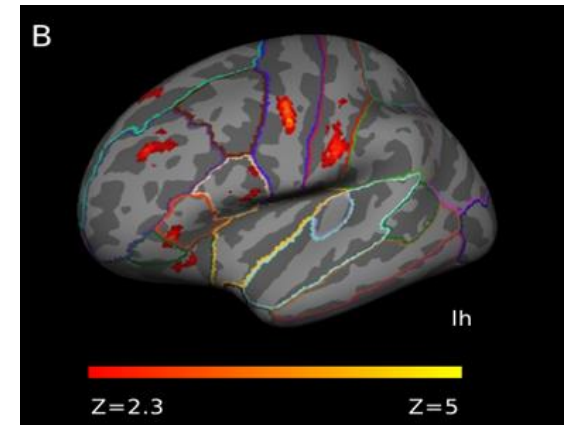
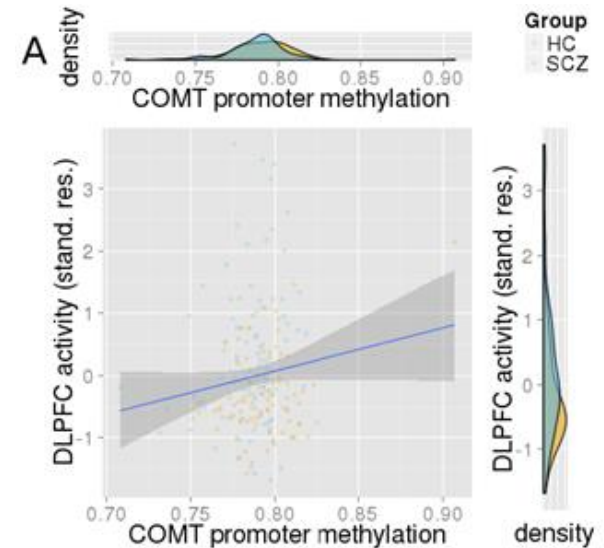
## Epigenetic processes

- DNA methylation
- chromatin remodelling
- RNA transcripts
- microRNAs
- prions
- ...



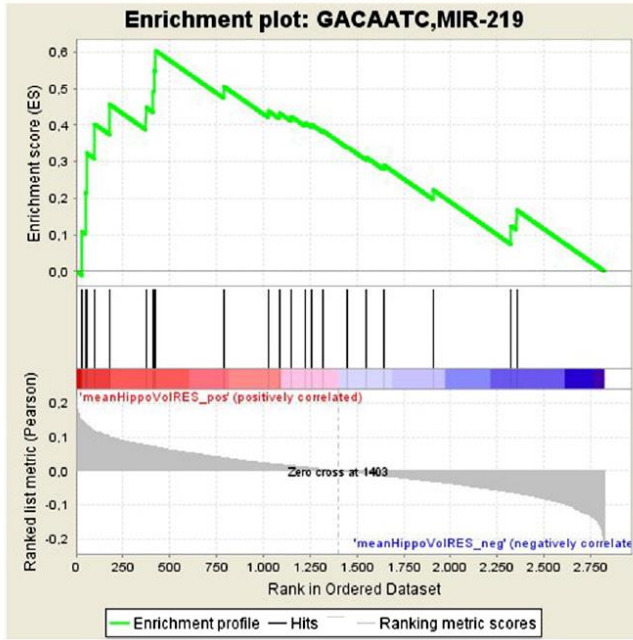
Zaidi et al., 2010

- MB-COMT promoter methylation effects on diagnosis and brain function
- No methylation\*diagnosis interaction
- trend correlation with performance ( $p=0.06$ )
- => importance of **COMT** and **epigenetic risk mechanisms** in schizophrenia



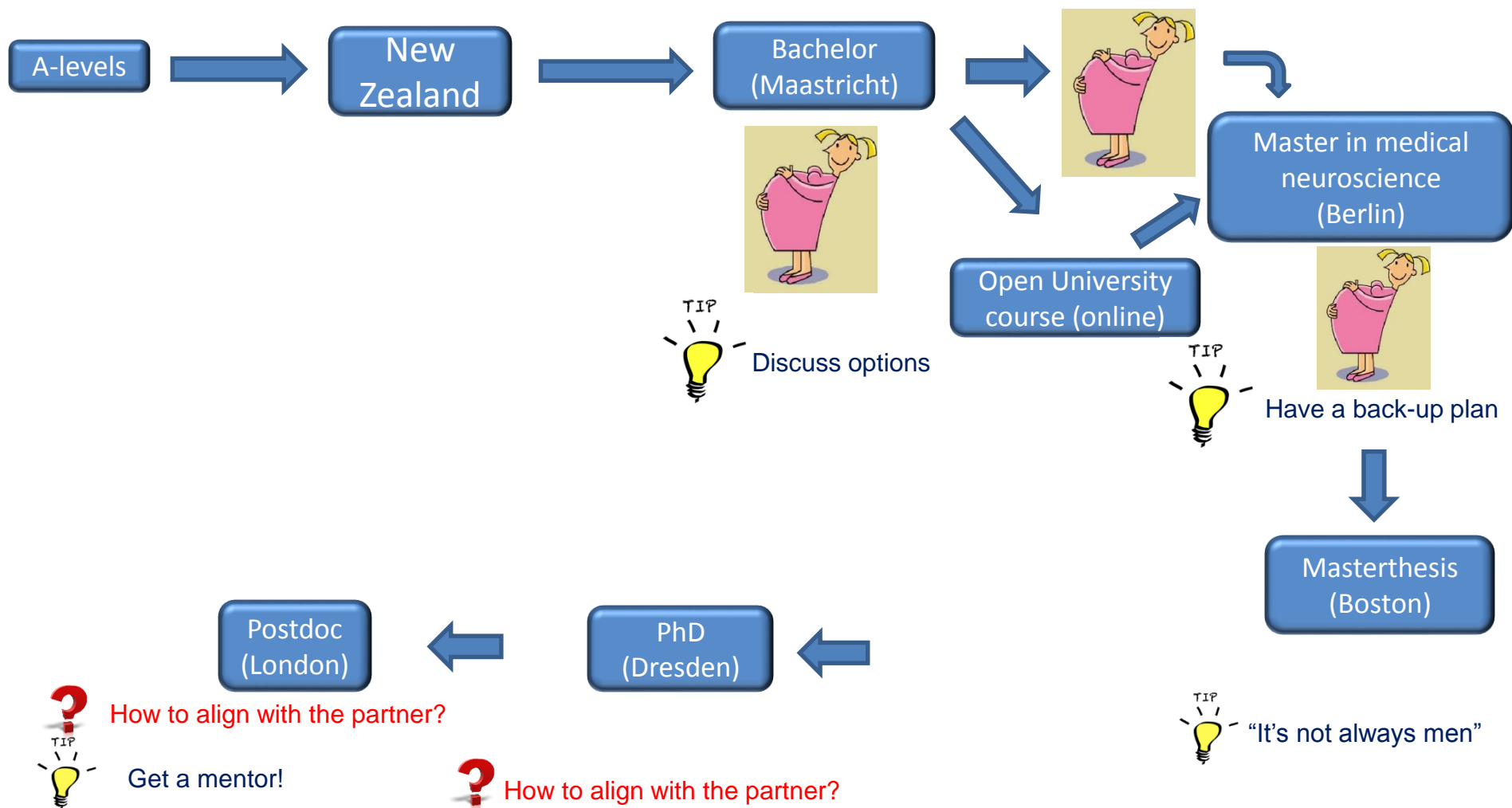
Walton et al., 2014

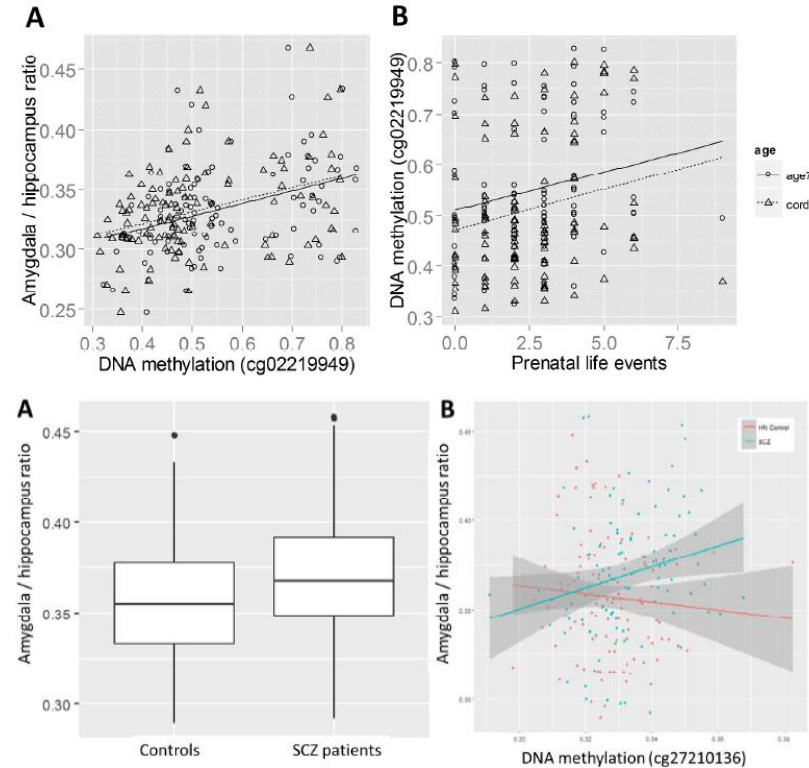
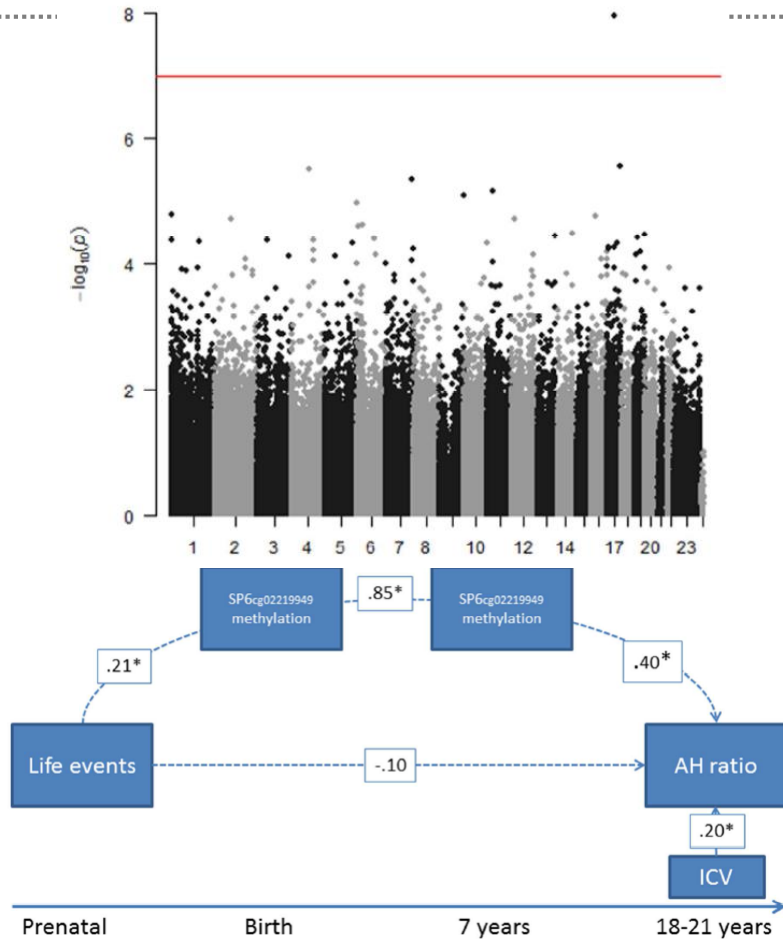




Hass et al., 2015

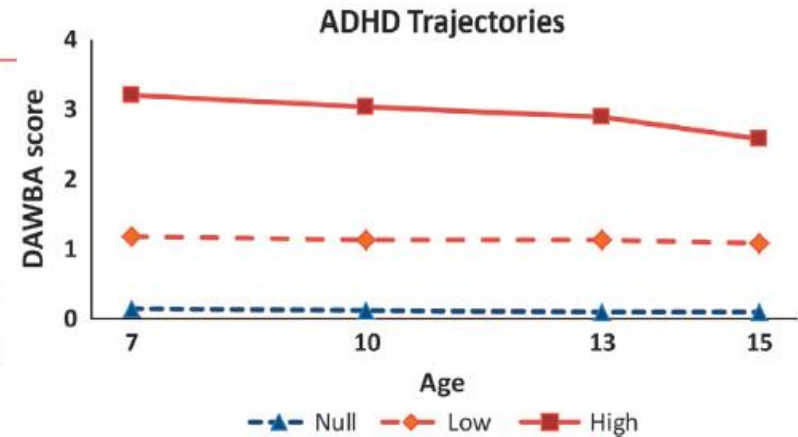
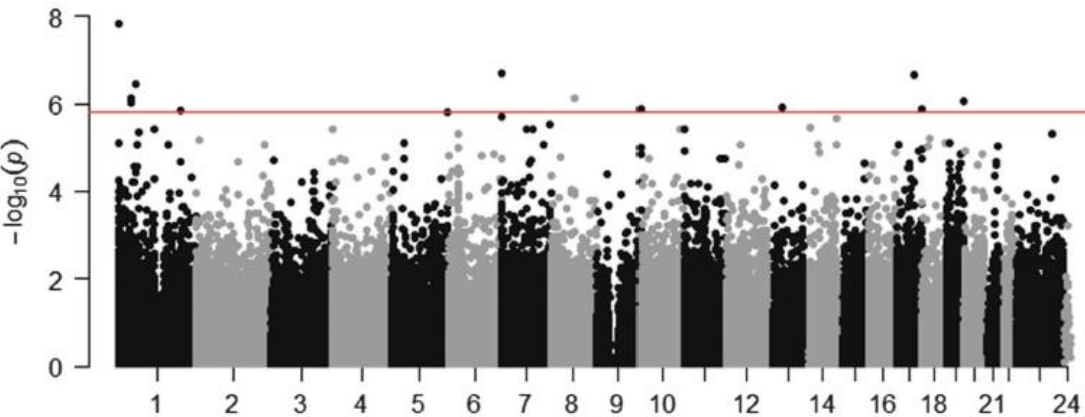
- => (dys)regulation of microRNA target genes by epigenetic mechanisms may confer additional risk for developing psychiatric symptoms





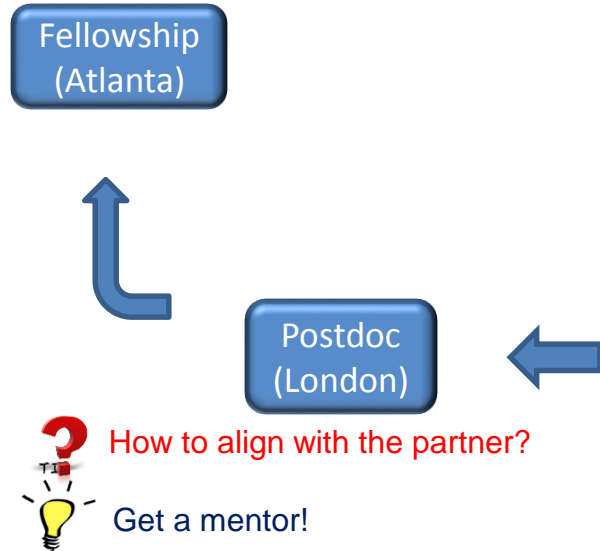
Walton et al., in press

- *SP6* methylation associated longitudinally with higher AH volume ratio

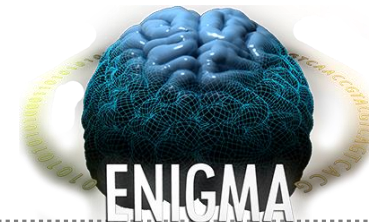


Walton et al., 2016

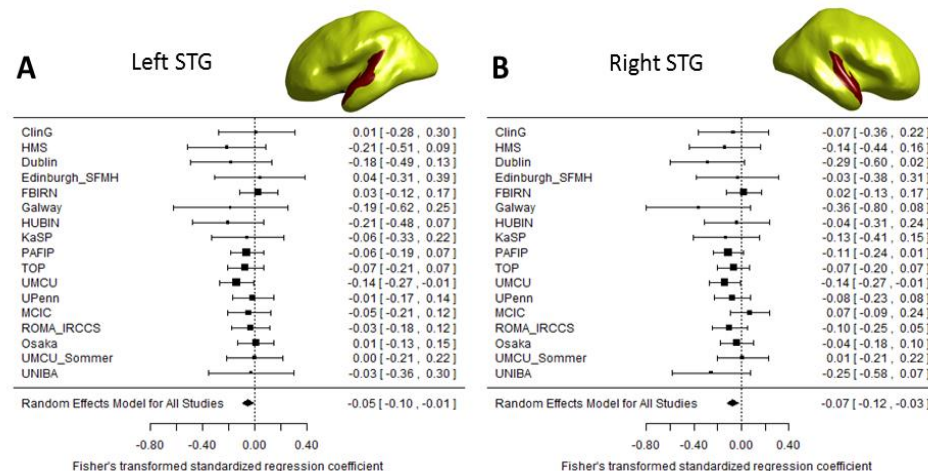
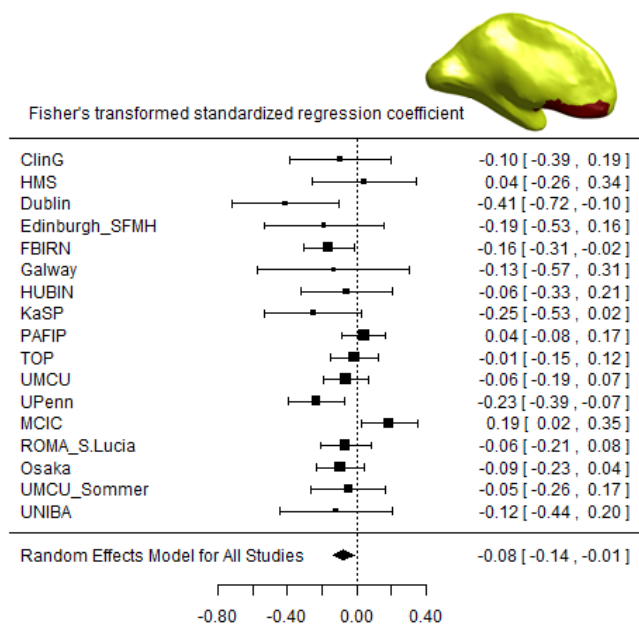
- DNA methylation at birth, but not at age 7, differentiated ADHD trajectories
- probes annotated to
  - SKI (involved in neural tube development)
  - ZNF544 (previously implicated in ADHD),
  - ST3GAL3 (linked to intellectual disability)
  - PEX2 (related to peroxisomal processes)



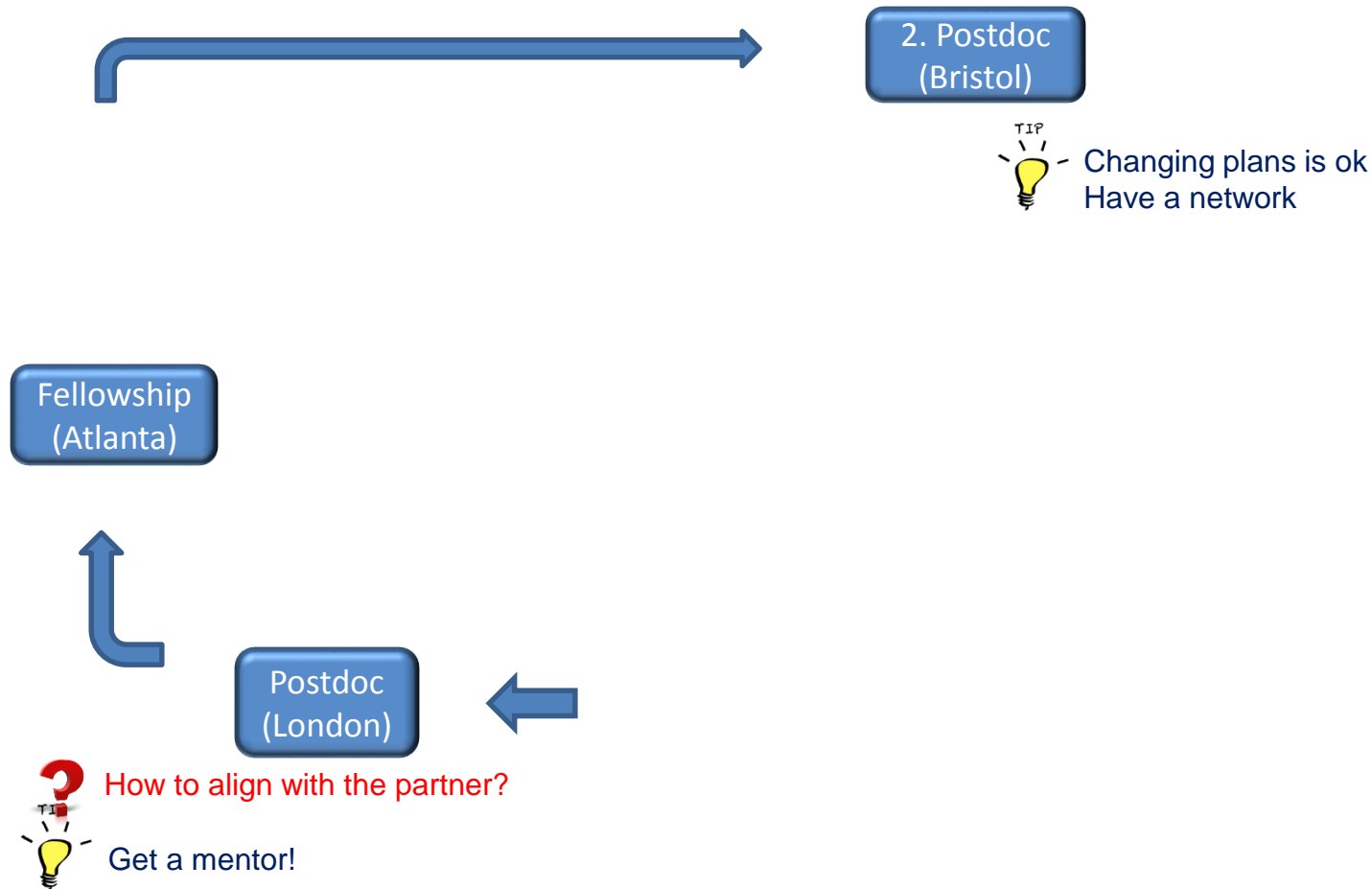
# Neural correlates of symptoms in SCZ



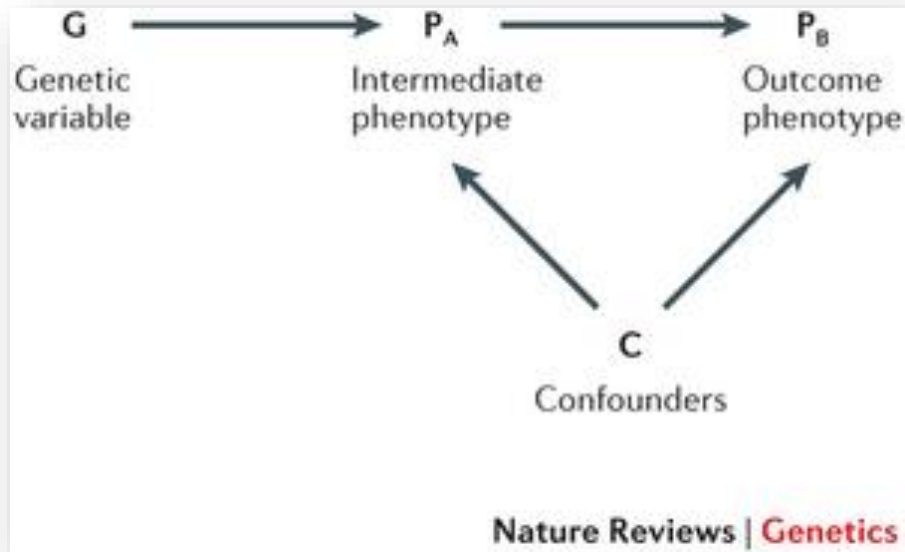
- Negative symptoms negatively associated with left, but not right mOFC thickness
- Positive symptoms were negatively related to STG thickness in both hemispheres



Walton et al., under review



## Towards causal associations!

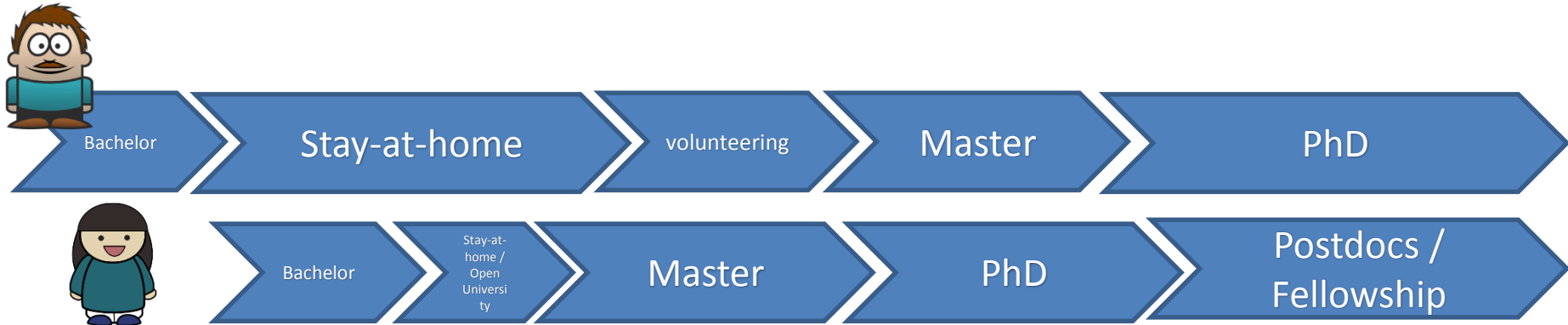


Solovieff et al., 2013



# What helped?

- An open mind (toward people, options and opportunities)
  - A supportive partner
  - A mentor
  - Economic support (government, funding, etc)
- 
- ...the shorter straw?





Thank you

