

Crowdsourcing Genome Wide Association Studies

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Overview

- 1 Introduction
 - Association studies?
- 2 Open GWAS
 - In company vaults
 - Out of vaults
- 3 Privacy & Implications
 - Some Implications
 - Consequences
- 4 Discussion
 - Outlook

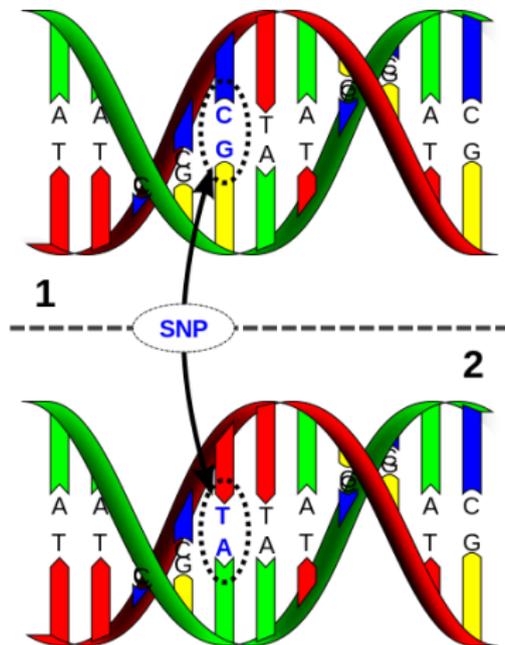
What are GWAS?

- Genome-wide Association Studies

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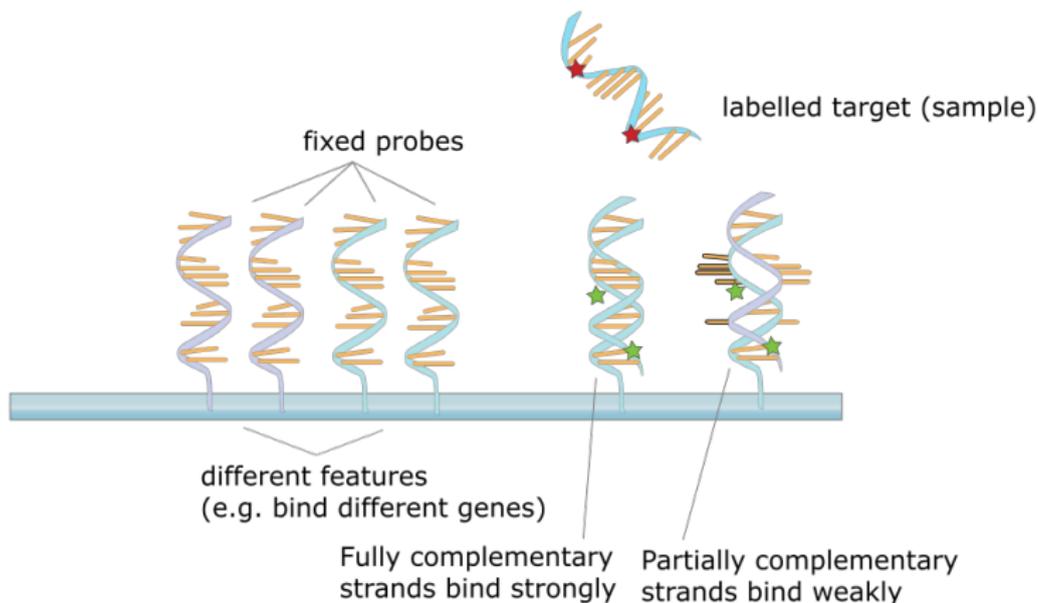
- Genome-wide Association Studies
- Link genetic variants (SNPs) to certain traits like eye or hair colour or to diseases like Diabetes, types of cancer

Single Nucleotide Polymorphism

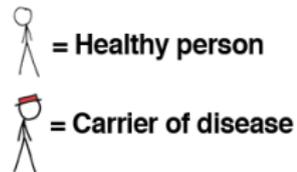
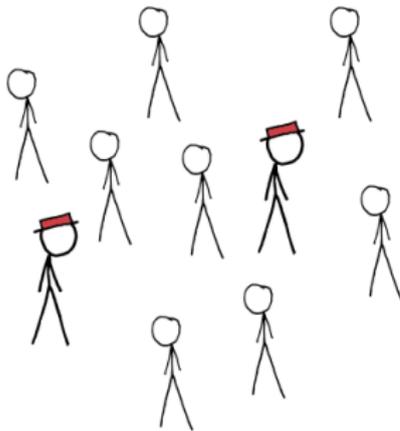


Source: <http://en.wikipedia.org/wiki/File:Dna-SNP.svg>

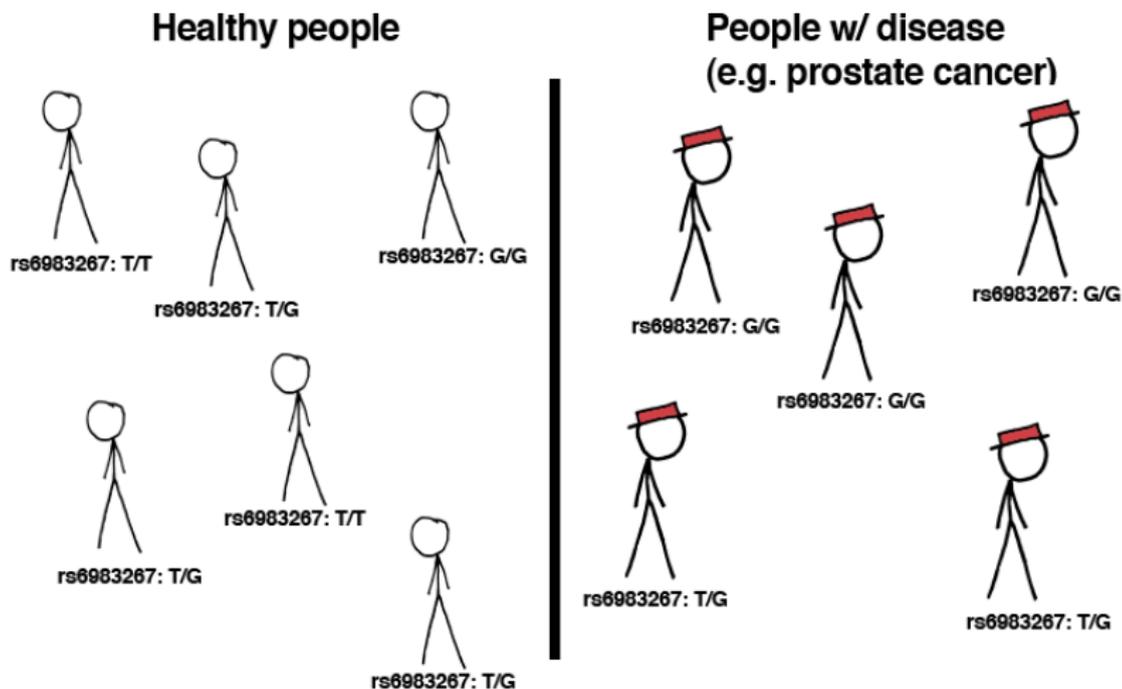
How to analyse SNPs?



How do GWAS work?

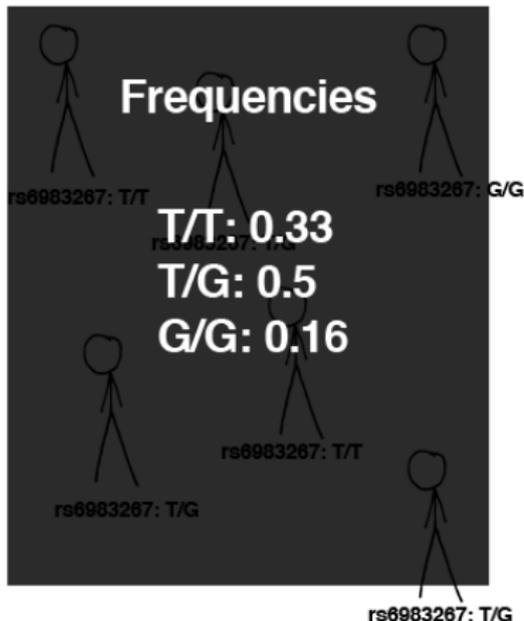


How do GWAS work?

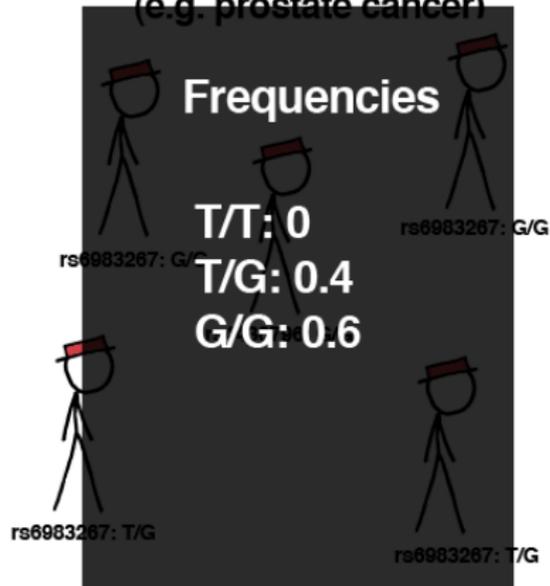


How do GWAS work?

Healthy people



People w/ disease (e.g. prostate cancer)



Some GWAS-examples

- Sladek *et al.* (2007) identified four gene locations linked to heightened type 2 diabetes risk

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- Kogan *et al.* (2011) linked rs53576 (G:G) to pro-social behaviour
- The Wellcome Trust Case Control Consortium (2007) linked 24 locations to 7 major diseases

Problems with GWAS



- Large enough sample size

Problems with GWAS



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- Correcting for multiple testing

Problems with GWAS



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- Correlation \neq Causation

Putting GWAS to use

- Direct-To-Consumer genetic testing
- Analyse about 1 million SNPs and provide summary of disease risks & ancestry
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- Providers: 23andMe, deCODEme, FamilyTree DNA, ...
- You get access to the raw data!

2_Shell

15					
16	rs4477212	1	72017	AA	
17	rs3894315	1	742429	AA	
18	rs3131972	1	742584	GG	
19	rs12124019	1	766499	AG	
20	rs11240777	1	788022	AG	
21	rs4661049	1	789078	CC	
22	rs4978383	1	828418	CC	
23	rs4475691	1	836671	CC	
24	rs7537756	1	844113	AA	
25	rs13382982	1	851871	GG	
26	rs1118852	1	863421	TT	
27	rs2272756	1	871896	GG	
28	rs3748597	1	878522	CC	
29	rs13283186	1	881888	GG	
30	rs20415373	1	883844	CC	
31	rs133881818	1	884436	AA	
32	rs6696281	1	892967	CC	
33	rs28391282	1	894828	GG	
34	rs2348932	1	908790	GG	
35	rs13282118	1	908241	TT	
36	rs6665888	1	914761	AA	
37	rs2341362	1	917172	CC	

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- 59 % of them share phenotypic information with 23andMe

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- Replication of older GWAS
- Finding new associations for Parkinsons disease

Data sharing

- People are already sharing the raw data of DTC tests

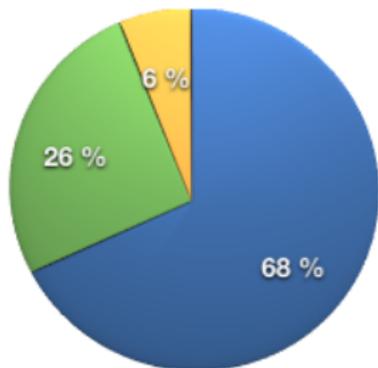
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- The *Personal Genome Project*: Open data, but closed participation

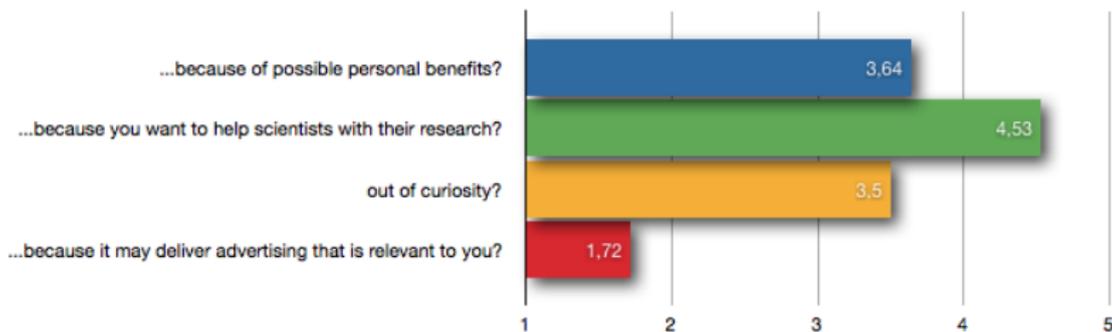
Willing to share?



- Would share
- Would share w/ company, but not public
- No Sharing

Willing to share?

Would you freely publish your genotyping results...



What can happen to your open data?

- Positive and negative consequences

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 - Possibly extremely bad consequences

What can happen to your open data?

- Positive and negative consequences
 - Possibly extremely bad consequences
- Up to you to decide whether you want to open your data

Positive consequences

- More knowledge about yourself

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- More knowledge about yourself
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- Great data-source for citizen scientists

Negative consequences

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- Knowledge isn't static: Future research could show new, negative (or positive) associations.
- Personal SNPs very similar to parents and relatives

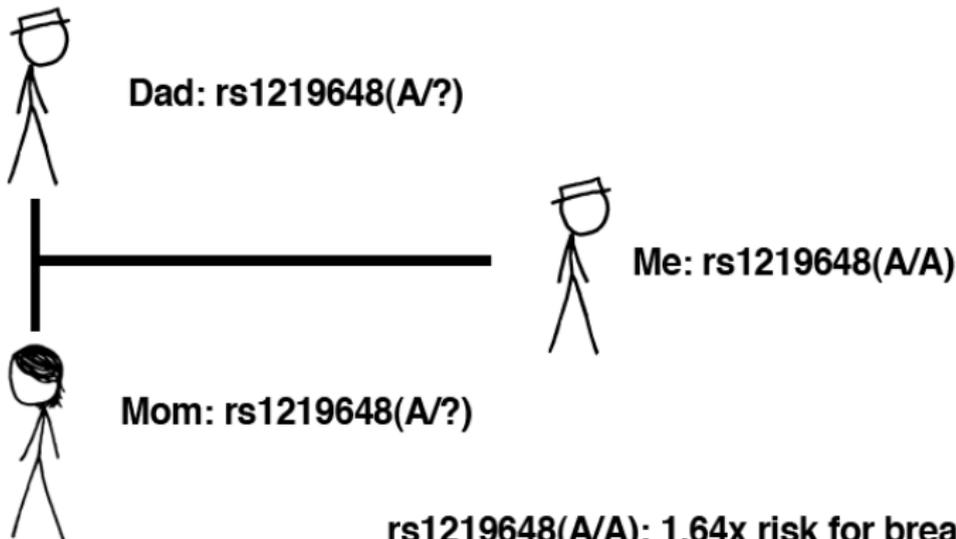
Somebody Else's Problem? A case study



Me: rs1219648(A/A)

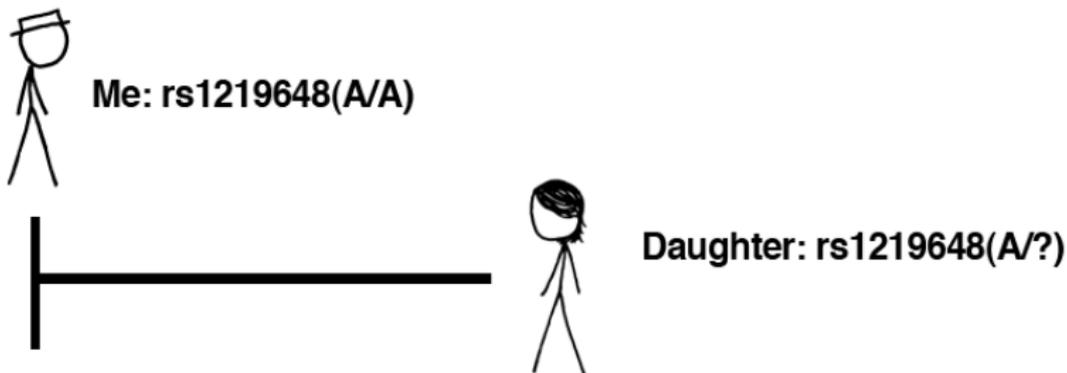
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Possible Solutions

- What about laws?

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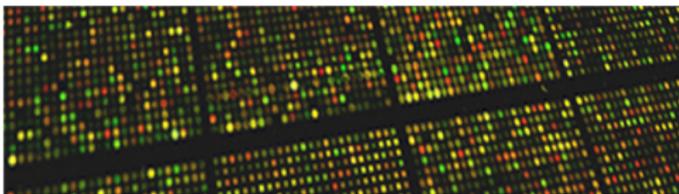
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- What about laws?
 - US: Genetic Information Nondiscrimination Act (GINA, 2008)
 - Germany: Gendiagnostikgesetz (GenDG, 2010)

For those who still want to share: Open GWAS

Welcome to *openSNP*



openSNP allows customers of direct-to-customer genetic tests to publish their test results, find others with similar genetic variations, learn more about their results, find the latest primary literature on their variations and help scientists to find new associations.

[Sign Up!](#)

[For Genotyping Users](#) [For Scientists](#) [FAQ](#)

Upload Your Genotyping File



Upload the genotyping raw-data you got from [23andMe](#) or [deCODEme](#) to the database of *openSNP* to make it available for everybody.

Share Your Phenotypes & Traits



Share as many phenotypes, characteristics and traits with other *openSNP* users and find others with similar characteristics. And maybe help scientists to discover new genetic associations.

Share your stories on variations & phenotypes



openSNP lets you share your stories on your genetic variations & phenotypes with others. Discover the stories of other users. Find others to exchange experiences about your variations.

Find literature on genetic variation



openSNP gets the latest open access journal articles on genetic variations via the [Public Library of Science](#). Additionally popular articles are indexed via the social reference manager [Mendeley](#). Summaries are provided by [SNPedia](#).

openSNP

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- We've created openSNP.org

openSNP

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- We've created openSNP.org
- open source repository for CC0-genotypings from 23andme, deCODEme and others

... continued

- Allows users to annotate with phenotypes (hair colour, nicotine dependence, SAT-scores...)

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- Everybody can download everything
- So far: 81 genotypings and 207 users

Conclusions

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- Chance to take science into our own hands

Future of openSNP

- We've won the PLoS/Mendeley Binary Battle

Future of openSNP

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- Got some funding to get more people (who are willing to share) genotyped (around 5000EUR)

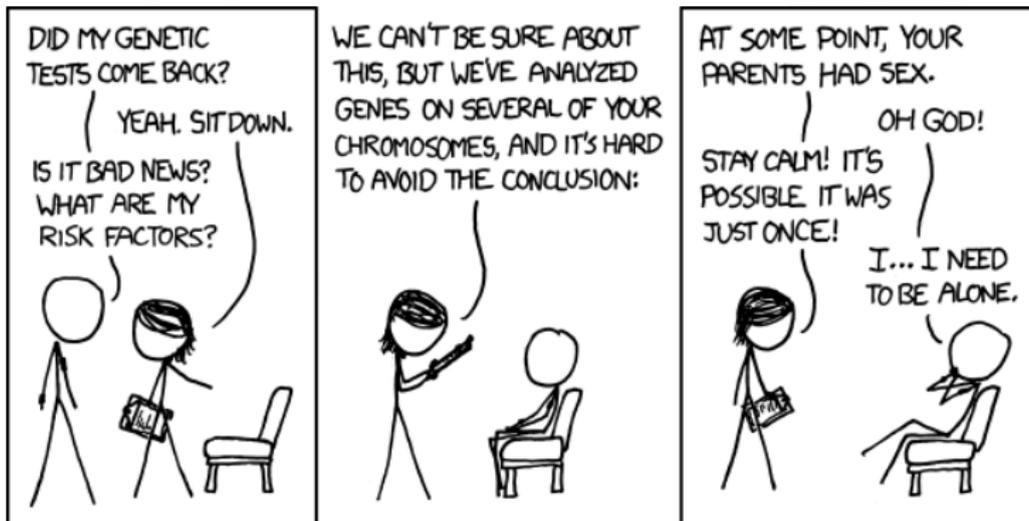
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- Constantly improving the project (and are happy if somebody wants to help)

The end



Thanks for listening. Any questions?
For further questions: @gedankenstuecke
or @PhilippBayer

References

- Do *et al.* (2011) Web-Based Genome-Wide Association Study Identifies Two Novel Loci and a Substantial Genetic Component for Parkinson's Disease. *PLoS Genetics* 7(6): e1002141. doi:10.1371/journal.pgen.1002141
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- The Wellcome Trust Case Control Consortium (2007): Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. *Nature* 447: 661-678.