

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

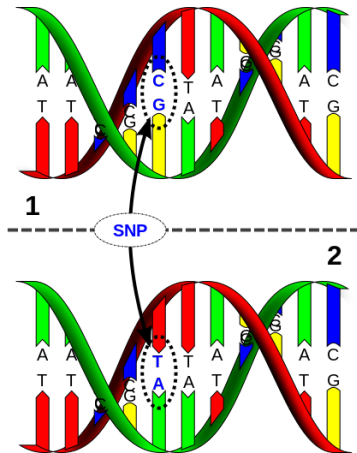
What are GWAS?

- Genome-wide Association Studies

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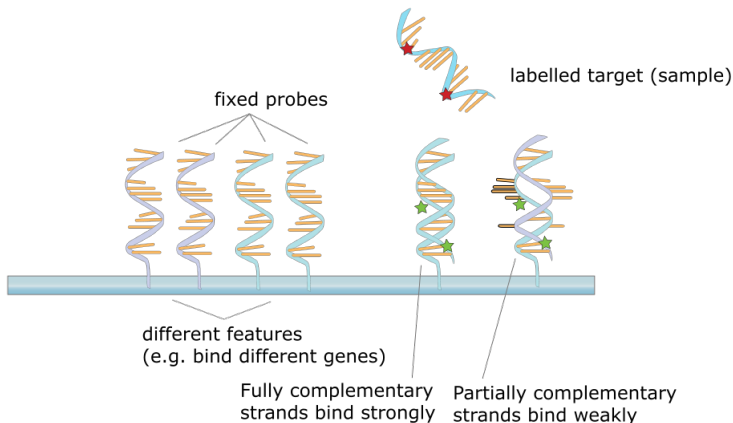
- Genome-wide Association Studies
- Link genetic variants (SNPs) to certain traits like eye or hair colour or to diseases like Diabetes, types of cancer

Single Nucleotide Polymorphism

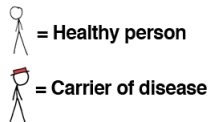
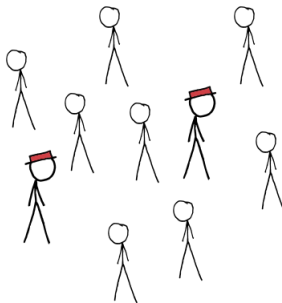


Source: <http://en.wikipedia.org/wiki/File:Dna-SNP.svg>

How to analyse SNPs?

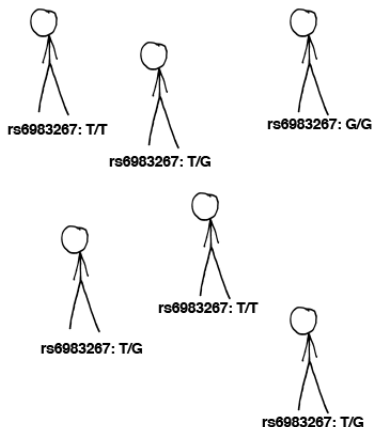


How do GWAS work?

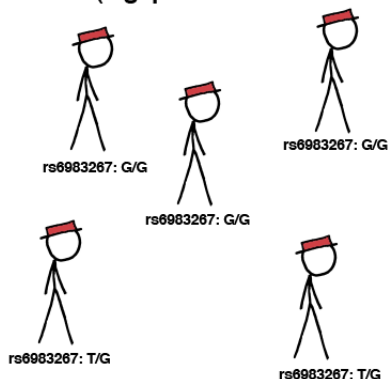


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Healthy people

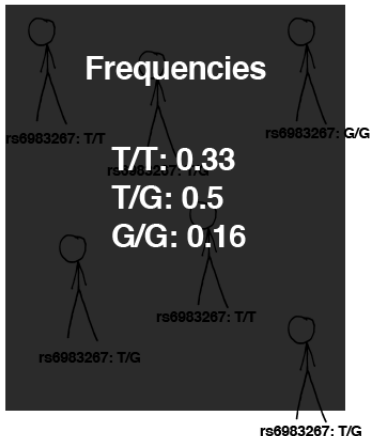


People w/ disease (e.g. prostate cancer)

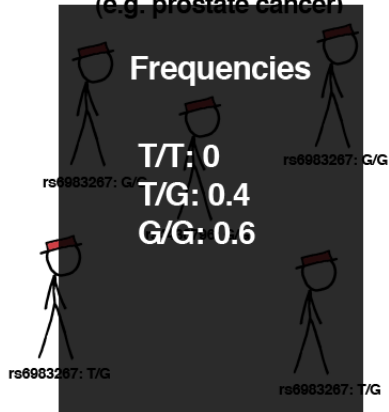


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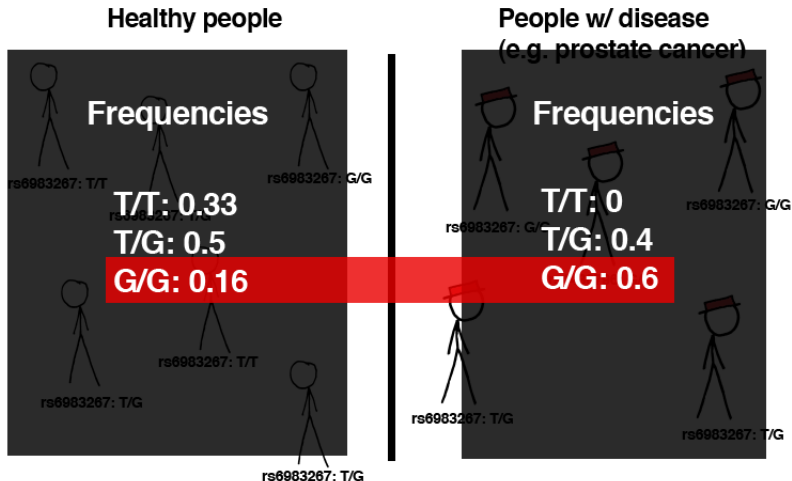
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Some GWAS-examples

- 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

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- Correlation \neq Causation

Putting GWAS to use

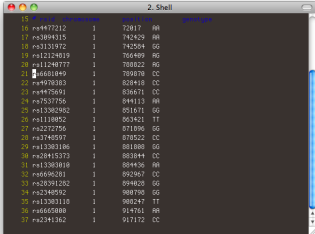
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- Analyse about 1 million SNPs and provide summary of disease risks & ancestry
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- Providers: 23andMe, deCODEme, FamilyTree DNA, ...
- You get access to the raw data!



```
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 rs4661849 1 789878 CC  
22 rs4978383 1 828418 CC  
23 rs4475691 1 836671 CC  
24 rs253756 1 841113 AA  
25 rs13362982 1 851671 GG  
26 rs1118852 1 863421 TT  
27 rs2272756 1 871096 GG  
28 rs3748597 1 878522 CC  
29 rs13281186 1 881888 GG  
30 rs28415373 1 883844 CC  
31 rs13383818 1 884436 AA  
32 rs6666281 1 892967 CC  
33 rs28391282 1 894820 GG  
34 rs2342592 1 908790 GG  
35 rs13282118 1 908247 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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- Finding new associations for Parkinsons disease

Data sharing

- People are already sharing the raw data of DTC tests

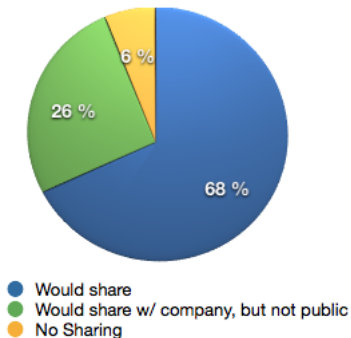
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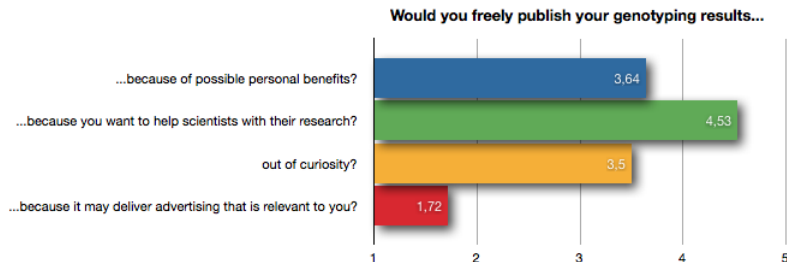
Data sharing

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- 1-5 % of 23andMe customers would be enough to perform simple GWAS
- The *Personal Genome Project*: Open data, but closed participation

Willing to share?



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What can happen to your open data?

- Positive and negative consequences

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- 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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- Cheap, open science

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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



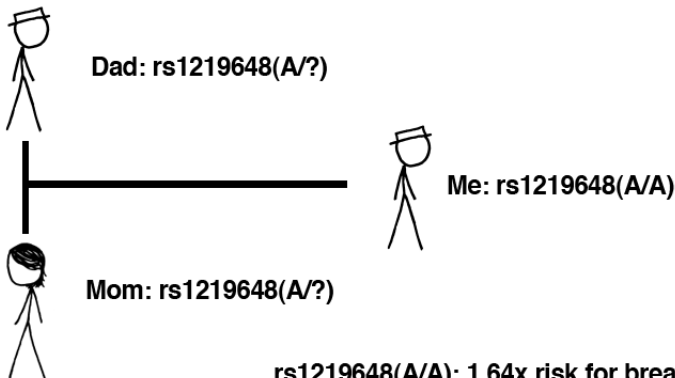
Me: rs1219648(A/A)

rs1219648(A/A): 1.64x risk for breast cancer

rs1219648(A/G): 1.20x risk for breast cancer

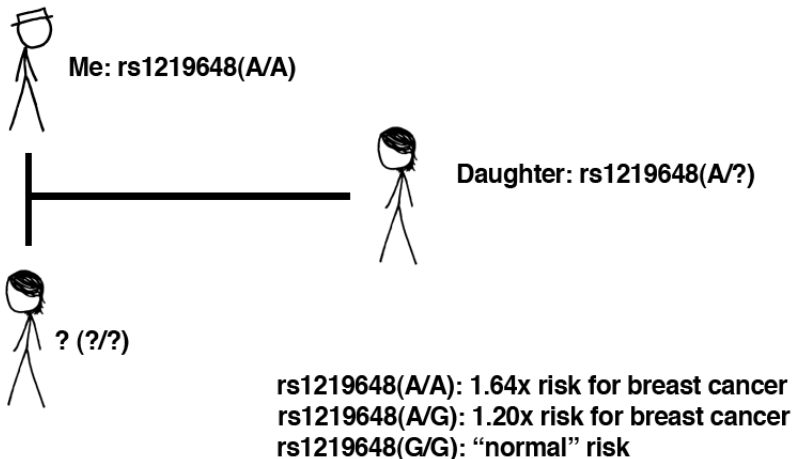
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Possible Solutions

- What about laws?

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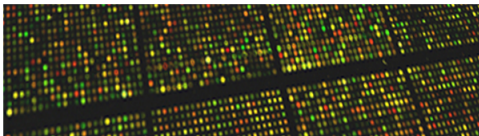
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Possible Solutions

- 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-consumer 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

- No central repository for open genotypings!

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- We've created openSNP.org

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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...)

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- So far: 78 genotypings and 188 users

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- It's in the hands of users to make or break the situation
- 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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- Trying got some funding to get more people (who are willing to share) genotyped

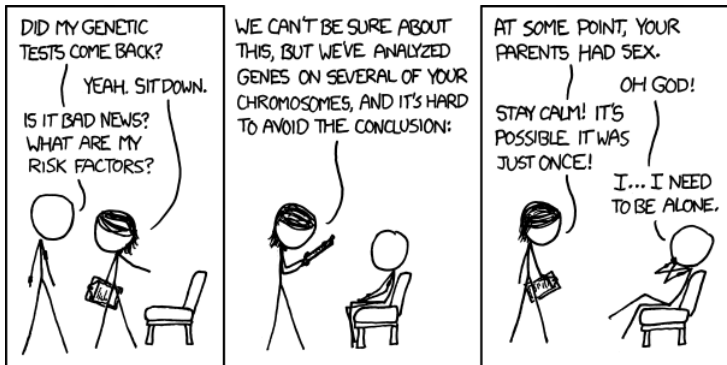
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- Constantly improving the project (and are happy if somebody wants to help)

The end



Thanks for listening. Any questions?

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
- Eriksson *et al.* (2010) Web-Based, Participant-Driven Studies Yield Novel Genetic Associations for Common Traits. *PLoS Genet* 6(6): e1000993. doi:10.1371/journal.pgen.1000993
- Kogan, *et al.* (2011): Thin-slicing study of the oxytocin receptor (OXTR) gene and the evaluation and expression of the prosocial disposition. *Proceedings of the National Academy of Sciences*
- Sladek *et al.* (2007): A genome-wide association study identifies novel risk loci for type 2 diabetes. *Nature* 445 (7130): 881-5.
- 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.