

GenomEUtwin

European Collaboration to identify genes underlying common diseases

www.genomeutwin.org

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Why genomEUtwin?

- There has been relatively little success in finding genes for complex disease or traits
- Most likely due to the expected small effect genes have on complex disease
- Large sample sizes will be necessary to find these genes

To identify genetic variants associated with disease; Pool data from twin cohorts in Denmark, Finland, Italy, Netherlands, Norway and Sweden (UK and Australia), potentially over 600 000 twin pairs

To verify their role; MORGAM cohort of 12 European countries, 187 000 participants

GenomEUtwin

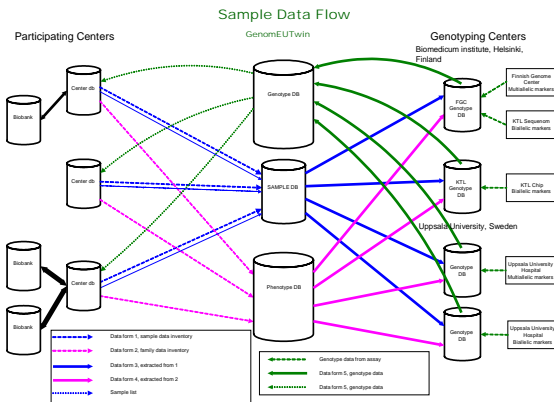
- Aims to benefit from the special advantages of Europe in population genetics
- Goal is to identify critical genetic and life-style risk factors for common diseases using European strengths in genetics, epidemiology and biocomputing

Intellectual core facilities

- DNA isolation and genotyping (Finland, Sweden)
- Epidemiological expertise (Denmark)
- Database expertise (Sweden)
- Statistical Core (the Netherlands)
- Ethical and legal expertise (Denmark)

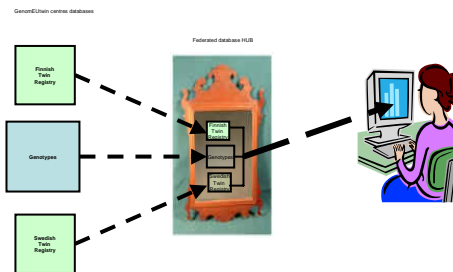
Developments

- Proof of principle succeeded in pooling data on height and weight
- Several genome-wide scans are currently performed on body composition, CVD risk factors and migraine
- This unique project of over 600 000 twin pairs may in future be able to detect small genetic effects influencing common diseases, which may not be detected in small-scaled family studies



A federated database in Europe for GenomEUtwin data

- Data remain in the original separate sources
- All operational data sources accessible with a single Query
- Query optimization on all data sources



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