The Importance Of Genetics On Mortality and Morbidity Risk
A Study Based On Half A Million Lives In The UK Biobank Cohort

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Lead Health Data Scientist

Stephen Courquin
VP, UK Head of Actuarial Research

Institute and Faculty of Actuaries Highlights of the Life Conference 2018 March 2019
Agenda

- Genetic Data and Insurance
- Genomic Medicine Today and in the Next 5 to 10 Years
- Genetic Risk to Disease and Polygenic Risk Scores
- RGA / King’s College London Research Collaboration
- Genetics and Risks of Anti-selection
- Key Messages
Genetic Data and Insurance
Genetics is a great case study for a potential future vision of risk selection.

If the Future of Medicine = Precision Medicine,

Does the Future of Risk Selection = Precision Underwriting?

Precision Underwriting brings a range of ethical, legal, competitive and social concerns.
Genetics has always elicited a varied set of views across stakeholders.

Increasing levels of interest in genetics and genomics from governments and regulators

- Council of Europe Recommendation: October 2016
- Canadian Genetic Non-discrimination Act: May 2017
- United States – Various Bills: 2017-2019
- Code Genetic Testing and Insurance: October 2018
- Australian Moratorium: July 2019
- England CMO Annual Report: Generation Genome: July 2017
Whole genome sequencing costs today

2003: $2.7 billion
2007: $2 million
2011: $100,000
2015: $1,000
2018: $199

Dante Labs Rare Disease Month: Dante Labs celebrates the Rare Disease Day offering “My Full DNA (Whole Genome Sequencing Test)” at a special price. To get more information about the “Rare Disease Month”, take a look at our FAQ.
Growing opportunities for genetic anti-selection

26 million
Consumer genetic tests sold since 2012

600,000
DNA variants measured by 23andMe

800+
Diseases tested for genetic susceptibility

No. 14
Genetic counsellors are the 14th fastest growing occupation according to US Bureau of Labour Statistics (2016 to 2026)

40 billion
Gigabytes of new genomic data generated a year by 2030
Genetic anti-selection risk: are these beliefs still valid?

1. Genetic risk information will not be widely available in the near future

2. Monogenic mutations that confer significantly higher risk of disease are rare therefore the cost imposed on insurers by any associated adverse selection is deemed small

3. Most common diseases are multifactorial, and the genetic contribution to these diseases is modest

4. Genetic test results will not deliver significant risk information that is not already available from traditional clinical/biometric measures used in underwriting

5. The genetic contribution to disease is adequately captured by family history
Genomic Medicine Today and in the Next 5 to 10 Years
Genomics medicine today

**Precision medicine**: pharmacogenetics, cancer treatments

- Prenatal and newborns **screening**
- Genome editing (CRISPR-Cas9)
- More accurate disease **prognosis**
- Accurate **diagnosis** of rare disease and detection of disease recurrence
- **Motivating** lifestyle modification
Genomic medicine in the next 5 to 10 years...

The personalisation journey

DNA diagnostics

Policy, System & Regulatory Alignment


Technology, Innovation & Knowledge Base

Genomic medicine in specific examples

2012

100,000 Genomes Project - use of WGS, panels & functional genomics for rare disease & cancer

2013-18

Genomic medicine embedded within specific pathways

Genomic medicine embedded as part of routine care - where appropriate

Clear role established for next-gen diagnostics

2018 - 2020

Data analytics and bioinformatics

Other functional diagnostics

Phenotypic characterisation

Patient generated data & self-reporting

Clinical Change & Operating Model

• Better prediction and prevention of disease

• A more precise diagnosis

• More targeted and personalised interventions

• A more participatory role for patients

Infrastructure change - informatics & commissioning

2020 and beyond
5 million genomes in 5 years – January 2019

The future of your health could soon be in the NHS’s hands

NHS to sell DNA tests to healthy people in push to find new treatments

Service will be free for patients with serious genetic conditions as health service in England aims to recruit 5 million volunteers

NHS to offer paid-for DNA tests if patients share data

NHS to sell patients genetic tests showing risk of killer diseases such as cancer and dementia

Sequencing will cost a few hundred pounds and patients will have to agree to DNA data being retained for research
‘Generation genome’: national programmes and spending

**United Kingdom**
Genomics England 2012-100,000 Genomes: rare disease, cancer £350M (USD$485M)
Scottish Genomes £5M (USD$8M)
Welsh Genomics for Precision Medicine £6.8M (USD$9M)
Northern Ireland Genomic Medicine Centre £3.3M (USD$4.8M)

**Switzerland**
Swiss Personalized Health Network 2017-2020 Infrastructure CHF68M (USD$99M)

**France**
Genomic Medicine Plan 2016-2025 Rare disease, cancer, diabetes €670M (USD$937M)

**Estonia**
Estonian Genome Project 2000 – Infrastructure and population-based cohort 2017: €5M for 100,000 individuals

**Netherlands**
RADICON-NL 2016-2025 Rare disease Health Research Infrastructure

**Finland**
National Genome Strategy 2015-2020 Infrastructure €50M (USD$59M)

**Denmark**
Genome Denmark 2012- DK 88M (USD$13.5M) FarGen 2011-2017 DK 10M (USD$1.6M) Infrastructure, population-based cohort, pathogen project

**Turkey**
Turkish Genome Project 2017-2023 Infrastructure, clinical and population-based cohorts

**Japan**
Japan Genomic Medicine Project Infrastructure, clinical and pop cohorts, drug discovery JPY10.2B (USD$90.05M)

**Qatar**
Qatar Genome 2015- Infrastructure, population cohort

**China**
Precision Medicine Initiative 100,000,000 genomes CNY60 billion (USD$9.2 billion)

Source: The American Journal of Human Genetics 2019 104, 13-20 DOI: (10.1016/j.ajhg.2018.11.014)
Genetic Risk to Disease and Polygenic Risk Scores (PRS)
Genetics 101: DNA, chromosomes and single nucleotide polymorphisms (SNPs)

DNA is composed of four ‘building blocks’ (nucleotides): adenine (A), cytosine (C), guanine (G) and thymine (T).

A single nucleotide polymorphism (SNP) describes variation in a single nucleotide position. E.g., here, a Thymine nucleotide exists instead of Cytosine, which is most commonly observed.
Genome-wide association studies (‘GWASes’)
Prevalence vs. penetrance of genetic variants

- **Highly unusual for common diseases**: Most variants identified by GWAS are common but have small genetic effects. I.e., a marginal contribution to disease susceptibility (‘low penetrance’).
**GWAS → Polygenic risk scores**

Polygenic risk scores (PRSs) add together the genetic risk from all SNPs associated with the disease.

\[
PRS = \beta_1 \cdot snp_1 + \beta_2 \cdot snp_2 + \cdots + \beta_n \cdot snp_n
\]

- **Cases** (people with disease)
- **Controls** (people without disease)

Compare DNA using DNA chip

Disease-specific SNPS

Non-disease SNPS

Increase ('relax') p-value
## Sample of PRS in literature

<table>
<thead>
<tr>
<th>Disorder</th>
<th>No. of Genetic Variants</th>
<th>Relative risk, comparing top 20% to bottom 20% PRS</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Coronary artery disease</td>
<td>50</td>
<td>2.0</td>
<td>Khera AV. et al. (2016), N Engl J Med.</td>
</tr>
<tr>
<td>Coronary artery disease</td>
<td>49,310</td>
<td>1.8 to 4.5</td>
<td>Abraham G. et al. (2016), Eur Heart J.</td>
</tr>
<tr>
<td>Type 2 diabetes</td>
<td>1000</td>
<td>3.5</td>
<td>Läll K. et al. (2017), Genet Med.</td>
</tr>
<tr>
<td>Ischemic stroke</td>
<td>10</td>
<td>1.2 to 2.0</td>
<td>Hachiya T. et al. (2017), Stroke</td>
</tr>
<tr>
<td>Breast cancer (East Asian ancestry)</td>
<td>44</td>
<td>2.9</td>
<td>Wen W. et al. (2016), Breast Cancer Res.</td>
</tr>
<tr>
<td>Prostate cancer</td>
<td>25</td>
<td>3.7 (25%)</td>
<td>Amin Al Olama A. et al. (2015), Cancer Epidemiol Biomarkers Prev.</td>
</tr>
<tr>
<td>Lung cancer</td>
<td>38</td>
<td>4.6 (25%)</td>
<td>Cheng Y. et al. (2016), Oncotarget</td>
</tr>
</tbody>
</table>
PRS for coronary heart disease increases predictive power, even after adjustment for clinical risk factors

- A study by Abraham and colleagues* tested the clinical utility of a PRS for coronary heart disease (CHD), in terms of lifetime CHD risk and relative to traditional clinical risk.
- PRS tested in independent cohorts (FINRISK and Framingham Heart Study [FHS]; combined n = 16,802 with 1,344 incident CHD events).
- The PRS was tested alongside the best clinical risk factors as well as family history. After controlling for these risk factors, the PRS still proved to be a very powerful differentiator of CHD risk.

How PRS could be adopted into clinical medicine – cancer screening

- Individuals with the highest 1% or 5% of PRS values could be offered:
  - Regular screening
  - Encouraged to participate in lifestyle modifications
  - Prescribed therapeutic interventions

- For example, in the UK, mammogram screening is initiated at age 47, based on a 10-year risk of breast cancer in the average woman, but:
  - Women in the top 5% of PRS-risk reach the average level at age 37
  - Women in the lowest 20% of PRS-risk will never reach the average level

PRRS make front page news – August 2018

THE TIMES

Genes put millions at triple risk of heart attack

£40 test would spot danger even with no symptoms

The Telegraph

Scientists hail DNA breakthrough that can detect if people are likely to have heart attacks

Finacial Times

Genetic screening set to identify common serious conditions

Aim is to give people a risk score from birth for illnesses such as heart disease and breast cancer

Clare Davenport and Clive Cookson AUGUST 14, 2018

A genetic test is set to identify heart disease, breast cancer even when there are no symptoms are evident.

Scientists hope to eventually offer a genetic test to all babies.

The “polygenic risk test” uses a person’s genome to look for small variations in multiple genes that increase susceptibility to disease.

Mail Online

$50 blood test could spot killer diseases from heart attacks to breast cancer BEFORE symptoms show:

Millions who are at risk due to their genes could be saved

- Harvard Medical School developed the test called ‘polygenic risk scoring’
- It measures a person’s risk of developing five life-threatening diseases based on their DNA
- The diseases they currently measure are: coronary artery disease, atrial fibrillation, type 2 diabetes, inflammatory bowel disease, and breast cancer
- It could be administered at birth to spot at risk people from the earliest age
Authors showed that common diseases can be predicted using PRSs for: coronary artery disease, type 2 diabetes, atrial fibrillation, breast cancer and inflammatory bowel disease.
RGA Research Collaboration with King’s College London

Prof. Cathryn Lewis
(Senior Lecturer)
Co-Principal Investigator

Dr Paul O’Reilly
(Senior Lecturer)
Co-Principal Investigator

Miss Jessye Maxwell
(PhD Student)
Project Research Assistant

Dr Beatrice Wu
(Postdoctoral Researcher)
Project Research Associate

Approved project: 23203
RGA Research Collaboration with KCL

- RGA-funded one year research project at KCL
- Desire to inform the debate around significance of (lack of) access to genetic information by insurers in non-compulsory insurance markets
- Collaborative agreement meets the principles set out in the UK Biobank Access Procedures, including commitment to publish all findings and results from the project so that they are available for other researchers to use for health-related research that is in the public interest
- Only approved King’s College London research staff have access to UK Biobank data
Why UK Biobank?

Breadth and Depth

Long-term follow up of multiple outcomes

Genotyping on all 500k participants

Data on UK Biobank participants
- Cognitive function and hearing tests
- Health outcome data
- Genotyping & imputation (~500,000)
- Web-based questionnaire data (~200,000)
- Physical activity monitor (100,000)
- Imaging (15,000+)
- Genetic data via the EGA (500,000)
- Environmental measures
- Urinary biomarkers
- Lifestyle, medical history, sociodemographic

‘Underwriting’ UKB participants and predicting disease incidence

UKB: c. ½ million individuals

‘Underwriting’ Process
- Prevalent disease in hospital records
- Self-reported illness at baseline verbal interview (with nurse)

‘Standard’ Risk (disease-free at baseline) c. 340k individuals

Non-Standard Risk (c. 160k individuals)

Prediction Model
- Phenotypic risk factors (age, gender, smoking, family history, BMI, BP, etc.)
- Genetics (PRS for disease)

### PRS to predict incidence of breast cancer (RGA-KCL study results)

<table>
<thead>
<tr>
<th>Percentile</th>
<th>Full cohort: Hazard ratio (95% CI)</th>
<th>Percentile</th>
<th>Standard cohort: Hazard ratio (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-1</td>
<td>0.39 (0.23 - 0.65)</td>
<td>0-1</td>
<td>0.44 (0.25 - 0.79)</td>
</tr>
<tr>
<td>1-5</td>
<td>0.6 (0.49 - 0.75)</td>
<td>1-5</td>
<td>0.68 (0.53 - 0.87)</td>
</tr>
<tr>
<td>5-10</td>
<td>0.63 (0.51 - 0.76)</td>
<td>5-10</td>
<td>0.66 (0.52 - 0.83)</td>
</tr>
<tr>
<td>10-20</td>
<td>0.67 (0.58 - 0.78)</td>
<td>10-20</td>
<td>0.69 (0.58 - 0.82)</td>
</tr>
<tr>
<td>20-40</td>
<td>0.88 (0.79 - 0.98)</td>
<td>20-40</td>
<td>0.9 (0.8 - 1.02)</td>
</tr>
<tr>
<td><strong>40-60</strong></td>
<td><strong>1</strong> (reference group)</td>
<td><strong>40-60</strong></td>
<td><strong>1</strong> (reference group)</td>
</tr>
<tr>
<td>60-80</td>
<td>1.22 (1.1 - 1.34)</td>
<td>60-80</td>
<td>1.25 (1.12 - 1.41)</td>
</tr>
<tr>
<td>80-90</td>
<td>1.5 (1.35 - 1.68)</td>
<td>80-90</td>
<td>1.58 (1.38 - 1.8)</td>
</tr>
<tr>
<td>90-95</td>
<td>1.73 (1.51 - 1.97)</td>
<td>90-95</td>
<td>1.74 (1.49 - 2.05)</td>
</tr>
<tr>
<td>95-99</td>
<td>2.02 (1.76 - 2.32)</td>
<td>95-99</td>
<td>2.04 (1.73 - 2.4)</td>
</tr>
<tr>
<td>99-100</td>
<td>2.47 (1.97 - 3.11)</td>
<td>99-100</td>
<td>2.71 (2.08 - 3.53)</td>
</tr>
</tbody>
</table>

**Total Participants:** 199,322  
**Number of breast cancers:** 3,947 (1.98%)

**Total Participants:** 143,898  
**Number of breast cancers:** 2,835 (1.97%)
### PRS to predict incidence of cardiovascular disease (RGA-KCL study results)

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<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0-1</td>
<td>0.56 (0.4 - 0.79)</td>
<td>0.51 (0.31 - 0.82)</td>
</tr>
<tr>
<td>1-5</td>
<td>0.49 (0.41 - 0.59)</td>
<td>0.43 (0.33 - 0.56)</td>
</tr>
<tr>
<td>5-10</td>
<td>0.71 (0.62 - 0.82)</td>
<td>0.7 (0.58 - 0.86)</td>
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<tr>
<td>10-20</td>
<td>0.73 (0.65 - 0.81)</td>
<td>0.75 (0.65 - 0.87)</td>
</tr>
<tr>
<td>20-40</td>
<td>0.82 (0.75 - 0.89)</td>
<td>0.86 (0.77 - 0.96)</td>
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<td>1.17 (1.09 - 1.27)</td>
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<td>95-99</td>
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<td>2.2 (1.9 - 2.54)</td>
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<tr>
<td>99-100</td>
<td>2.78 (2.35 - 3.29)</td>
<td>3.46 (2.79 - 4.29)</td>
</tr>
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</table>

Total Participants: 373,022  
Number of CAD events: 6,430 (1.72%)

Total Participants: 260,791  
Number of CAD events: 3,489 (1.34%)

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Genetics and Risks of Anti-selection
Research into anti-selection risk from genetics

- There have been several research papers.....
  - Alzheimer’s disease anti-selection (Zick et al., 2005)
  - Huntington’s disease anti-selection (Oster et al., 2009)
  - Work of GIRC / Angus MacDonald
  - CIA Genetic Testing (Mortality and Morbidity)
  - SOA reproduction of CIA work for US Markets
  - Australian paper, May 2017

- …suggesting a wide range of possible impacts

- Many modelling assumptions being made
  - Insurance buying behavior pre/post tests
  - Probability of disease and impact thereof
Research into anti-selection risk from genetics: assumptions

**Genetic Risk Assumptions**

- **Prevalence** of disease variants
- **Penetrance** of disease variants

Strengthen assumptions using UK Biobank results

**Insurance Assumptions**

- Testing Rate
- Seeking insurance etc.

Still great uncertainty and more research is needed
Predicting impact of PRSs is still early

- Many scientific, clinical, and social obstacles must still be overcome to bring PRSs into clinical practice
- Genetic loci associated with disease will continue to be found and could confer additional predictive power
- Correlations with other health and lifestyle factors could be more significant than high penetrance genes
- Correlations between PRS for different conditions
- Risk of developing a disease may be correlated with severity of disease
- Application of PRS to non-Caucasian populations

**Preventative or mitigating actions, such as:**
- Screening programs based on PRS may limit mortality impact
- Impact of preventative lifestyle actions unknown
- Pharmacogenomics, precision medicine etc.
## Potential for anti-selection – example in breast cancer

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Total Participants: 199,322  
Number of breast cancers: 3,947 (1.98%)

<table>
<thead>
<tr>
<th>Percentile</th>
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<tbody>
<tr>
<td>0-1</td>
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Total Participants: 143,898  
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Potential for anti-selection – example in breast cancer. Scenario 1:

<table>
<thead>
<tr>
<th>Percentile</th>
<th>% in general population</th>
<th>Hazard ratio for breast cancer</th>
<th>Probability of purchasing insurance *</th>
<th>% in new risk pool</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-1</td>
<td>1%</td>
<td>0.44</td>
<td>0.44x</td>
<td>0.4%</td>
</tr>
<tr>
<td>1-5</td>
<td>4%</td>
<td>0.68</td>
<td>0.68x</td>
<td>2.4%</td>
</tr>
<tr>
<td>5-10</td>
<td>5%</td>
<td>0.66</td>
<td>0.66x</td>
<td>3.0%</td>
</tr>
<tr>
<td>10-20</td>
<td>10%</td>
<td>0.69</td>
<td>0.69x</td>
<td>6.2%</td>
</tr>
<tr>
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<td>20%</td>
<td>0.9</td>
<td>0.9x</td>
<td>16.1%</td>
</tr>
<tr>
<td>40-60</td>
<td>20%</td>
<td>1</td>
<td>1x</td>
<td>17.9%</td>
</tr>
<tr>
<td>60-80</td>
<td>20%</td>
<td>1.25</td>
<td>1.25x</td>
<td>22.4%</td>
</tr>
<tr>
<td>80-90</td>
<td>10%</td>
<td>1.58</td>
<td>1.58x</td>
<td>14.1%</td>
</tr>
<tr>
<td>90-95</td>
<td>5%</td>
<td>1.74</td>
<td>1.74x</td>
<td>7.8%</td>
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<tr>
<td>95-99</td>
<td>4%</td>
<td>2.04</td>
<td>2.04x</td>
<td>7.3%</td>
</tr>
<tr>
<td>99-100</td>
<td>1%</td>
<td>2.71</td>
<td>2.71x</td>
<td>2.4%</td>
</tr>
</tbody>
</table>

- +12.6% increase in incidence
- Further +2.2% if include BRCA1/2 mutations (assuming 0.2% prevalence and 5x odds ratio)

### Potential for anti-selection – example in breast cancer. Scenario 2:

<table>
<thead>
<tr>
<th>Percentile</th>
<th>% in general population</th>
<th>Hazard ratio for breast cancer</th>
<th>Probability of purchasing insurance *</th>
<th>% in new risk pool</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-1</td>
<td>1%</td>
<td>0.44</td>
<td>0.73x</td>
<td>0.7%</td>
</tr>
<tr>
<td>1-5</td>
<td>4%</td>
<td>0.68</td>
<td>0.84x</td>
<td>3.2%</td>
</tr>
<tr>
<td>5-10</td>
<td>5%</td>
<td>0.66</td>
<td>0.83x</td>
<td>3.9%</td>
</tr>
<tr>
<td>10-20</td>
<td>10%</td>
<td>0.69</td>
<td>0.85x</td>
<td>8.0%</td>
</tr>
<tr>
<td>20-40</td>
<td>20%</td>
<td>0.9</td>
<td>0.96x</td>
<td>17.9%</td>
</tr>
<tr>
<td>40-60</td>
<td>20%</td>
<td>1</td>
<td>1x</td>
<td>18.9%</td>
</tr>
<tr>
<td>60-80</td>
<td>20%</td>
<td>1.25</td>
<td>1.13x</td>
<td>21.3%</td>
</tr>
<tr>
<td>80-90</td>
<td>10%</td>
<td>1.58</td>
<td>1.29x</td>
<td>12.2%</td>
</tr>
<tr>
<td>90-95</td>
<td>5%</td>
<td>1.74</td>
<td>1.37x</td>
<td>6.5%</td>
</tr>
<tr>
<td>95-99</td>
<td>4%</td>
<td>2.04</td>
<td>1.53x</td>
<td>5.7%</td>
</tr>
<tr>
<td>99-100</td>
<td>1%</td>
<td>2.71</td>
<td>1.87x</td>
<td>1.8%</td>
</tr>
</tbody>
</table>

- +6.6% increase in incidence
- Further +1.2% if include BRCA1/2 mutations (assuming 0.2% prevalence and 5x odds ratio)

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### Potential for anti-selection – example in breast cancer. Scenario 3:

<table>
<thead>
<tr>
<th>Percentile</th>
<th>% in general population</th>
<th>Hazard ratio for breast cancer</th>
<th>Probability of purchasing insurance</th>
<th>% in new risk pool</th>
</tr>
</thead>
<tbody>
<tr>
<td>0-1</td>
<td>1%</td>
<td>0.44</td>
<td>1x</td>
<td>0.9%</td>
</tr>
<tr>
<td>1-5</td>
<td>4%</td>
<td>0.68</td>
<td>1x</td>
<td>3.6%</td>
</tr>
<tr>
<td>5-10</td>
<td>5%</td>
<td>0.66</td>
<td>1x</td>
<td>4.5%</td>
</tr>
<tr>
<td>10-20</td>
<td>10%</td>
<td>0.69</td>
<td>1x</td>
<td>9.1%</td>
</tr>
<tr>
<td>20-40</td>
<td>20%</td>
<td>0.9</td>
<td>1x</td>
<td>18.2%</td>
</tr>
<tr>
<td>40-60</td>
<td>20%</td>
<td>1</td>
<td>1x</td>
<td>18.2%</td>
</tr>
<tr>
<td>60-80</td>
<td>20%</td>
<td>1.25</td>
<td>1.13x</td>
<td>20.4%</td>
</tr>
<tr>
<td>80-90</td>
<td>10%</td>
<td>1.58</td>
<td>1.29x</td>
<td>11.7%</td>
</tr>
<tr>
<td>90-95</td>
<td>5%</td>
<td>1.74</td>
<td>1.37x</td>
<td>6.2%</td>
</tr>
<tr>
<td>95-99</td>
<td>4%</td>
<td>2.04</td>
<td>1.53x</td>
<td>5.5%</td>
</tr>
<tr>
<td>99-100</td>
<td>1%</td>
<td>2.71</td>
<td>1.86x</td>
<td>1.7%</td>
</tr>
</tbody>
</table>

- +5.0% increase in incidence
- Further +1.1% if include BRCA1/2 mutations (assuming 0.2% prevalence and 5x odds ratio)

Key Messages
Genetic anti-selection risk: are these beliefs still valid?

1. Genetic risk information will not be widely available in the near future

2. Monogenic mutations that confer significantly higher risk of disease are rare therefore the cost imposed on insurers by any associated adverse selection is deemed small, while genetic risk information remains not widely available

3. Most common diseases are multifactorial, and the genetic contribution to these diseases is modest, much greater than previously thought

4. Genetic test results will not deliver significant risk information that is not already available from traditional clinical measures used in underwriting

5. The genetic contribution to disease is adequately captured by family history
Closing Remarks

- Polygenic risk scores increase our concerns about anti-selection risk from genetic information asymmetry. It is a classic emerging risk for our industry.

- Advances in genomic medicine will undoubtedly improve disease diagnosis and ultimately disease prognosis which will drive improvements in life expectancy and healthy life expectancy.

- Genetic data is one example of data that has the potential to enable “Precision Underwriting”. There are a range of social, ethical, regulatory and competitive issues that need to be addressed before that happens.
Thank you for your attention

Any Questions?