

Coevolution of sociality and human life-history in humans

Influence of culture and behaviours on the **evolution of senescence:**
selection of susceptibility alleles to late-onset diseases

Are old ages useless with respect to selection? A reconsideration of the
common variants/common diseases hypothesis

Pavard, Coste et al. *In prep.*

Introduction

Nineties – “*genetic map of old age diseases*”

On the HapMap web site two years ago

“*to a common disease (such as diabetes, cancer, stroke, heart disease, depression, and asthma) is associated common genetic variants*”

Genetic diseases after menopause ► No selection ► Only genetic drift ►
Lower number of genetic variants but at higher frequency (**Common variants**) ► high prevalence of the disease (**Common disease**)

ABCA1	MACULAR DEGENERATION...	DSP	DESMOPLAKIN	PLN	CARDIOMYOPATHY, DILATED, 1P
ABCC9	CARDIOMYOPATHY, DILATED, 1O	DSP	ARRHYTHMOGENIC DYSPLASIA...	POLG	PROGRESSIVE OPHTHALMOPLÉGIA...
APOB	HYPERCHOLESTEROLEMIA...	DSP	DENTINOGENESIS IMPERFECTA...	POLG	PROGRESSIVE OPHTHALMOPLÉGIA...
APP	OCCIPITAL CALCIFICATIONS...	DSP	DEAFNESS...	POLG	ENCEPHALOPATHY SYNDROME...
APP	CEREBRAL HEMORRHAGE...	DYSF	MIYOSHI MYOPATHY	POLG	ATAXIC NEUROPATHY...
C1QTNF5	RETINAL DEGENERATION	DYSF	MYOPATHY...	POLH	XERODERMA PIGMENTOSUM ...
CFH	MACULAR DEGENERATION	EFEMP1	RETINAL DYSTROPHY...	PPARG	LIPODYSTROPHY...
CHMP2B	FRONTOTEMPORAL DEMENTIA	ELN	CUTIS LAXA	PRKAG2	WOLFF-PARKINSON...
COL8A2	CORNEAL DYSTROPHY	ERCC4	XERODERMA PIGMENTOSUM...	PRNP	CREUTZFELDT-JAKOB DISEASE
ENO3	ENOLASE 3 DEFICIENCY	EYA4	CARDIOMYOPATHY, DILATED, 1J	PRNP	GERSTMANN-STRAUSSLER DISEASE
FGA	FIBRINOGEN	FBLN5	CUTIS LAXA	PRNP	FATAL FAMILIAL INSOMNIA
FLNC	FILAMINOPATHY	FGA	AMYLOIDOSIS...	PRNP	HUNTINGTON DISEASE-LIKE 1
GBE1	POLYGLUCOSAN BODY DISEASE	FLCN	BIRT-HOGG-DUBE SYNDROME	PRNP	SPONGIFORM ENCEPHALOPATHY...
GRN	FRONTOTEMPORAL DEMENTIA	FOXL2	PREMATURE OVARIAN FAILURE 3	PRSS1	PANCREATITIS, HEREDITARY
HTRA2	PARKINSON DISEASE 13	FSHR	OVARIAN HYPERSTIMULATION	PSEN1	PICK DISEASE OF BRAIN
ITM2B	DEMENTIA, FAMILIAL BRITISH	FTL	BASAL GANGLIA DISEASEpre-40	PSEN1	ALZHEIMER DISEASE...
LRRK2	PARKINSON DISEASE 8	GF11	NEUTROPENIA, NONIMMUNE...	PTEN	COWDEN DISEASE
MAPT	FRONTOTEMPORAL DEMENTIA	GLB1	GANGLIOSIDOSIS, GENERALIZED...	PTEN	MENINGIOMA, FAMILIAL
MAPT	SUPRANUCLEAR PALSY...	GNE	INCLUSION BODY MYOPATHY 2...	PYGM	GLYCOGEN STORAGE DISEASE V
MLH1	MUIR-TORRE SYNDROME	GNE	NONAKA MYOPATHY	RAB7	CHARCOT-MARIE-TOOTH DISEASE...
MPZ	CHARCOT-MARIE-TOOTH ...	GUCA1A	CONE DYSTROPHY 3	RLBP1	FUNDUS ALBIPUNCTATUS
PLEKHG4	SPINOCEREBELLAR ATAXIA	HCRT	NARCOLEPSY 1	RS1	RETINOSCHISIS 1, X-LINKED, JUVENILE
PMP22	GULLAIN-BARRE SYNDROME...	HMBS	PORPHYRIA, ACUTE INTERMITTENT	SCN5A	BRUGADA SYNDROME
PRNP	DEMENTIA, LEWY BODY	HRG	HISTIDINE-RICH GLYCOPROTEIN	SCNN1B	LIDDLE SYNDROME
PSEN2	ALZHEIMER DISEASE, FAMILIAL...	HRPT2	HYPERPARATHYROIDISM 1	SCNN1G	LIDDLE SYNDROME
RDS	VITELLIFORM MACULAR DYSTROPHY...	HRPT2	HYPERPARATHYROIDISM 2	SERPINA1	PROTEASE INHIBITOR 1
RNASEL	PROSTATE CANCER, HEREDITARY, 1	HSPB1	CHARCOT-MARIE-TOOTH DISEASE...	SERPIND1	HEPARIN COFACTOR II
SNCA	DEMENTIA, LEWY BODY	HSPB1	NEUROPATHY, DISTAL HEREDITARY...	SERPINF2	PLASMIN INHIBITOR DEFICIENCY
SNCA	PARKINSON DISEASE, FAMILIAL...	HSPB8	CHARCOT-MARIE-TOOTH DISEASE...	SERPING1	ANGIOEDEMA, HEREDITARY
SNCA	PARKINSON DISEASE 4...	ITM2B	DEMENTIA, FAMILIAL DANISH	SERPINI1	ENCEPHALOPATHY, FAMILIAL
SNCB	DEMENTIA, LEWY BODY	KCN2E	ATRIAL FIBRILLATION, FAMILIAL, 1	SGCD	CARDIOMYOPATHY, DILATED, 1L
TGFB1	CORNEAL DYSTROPHY...	KCNQ1	ATRIAL FIBRILLATION, FAMILIAL, 1	SLC16A1	ERYTHROCYTE LACTATE...
TGFBR2	COLORRECTAL CANCER...	KRT17	STEATOCYSTOMA MULTIPLEX	SLC25A4	PROGRESSIVE OPHTHALMOPLÉGIA...
TNFRSF11A	PAGET DISEASE OF BONE	KRT5	DOWLING-DEGOS DISEASE	SMN1	SPINAL MUSCULAR ATROPHY, TYPE IV
TNN3	TROPONIN I, CARDIAC...	LCAT	FISH-EYE DISEASE	SPAST	SPASTIC PARAPLEGIA
TTID	MYOTILINOPATHY	LCAT	LECITHIN DEFICIENCY	SPG7	SPASTIC PARAPLEGIA 7...
VMD2	VITELLIFORM MACULAR DYSTROPHY...	LMNA	CARDIOMYOPATHY, DILATED, 1A	SPINK1	PANCREATITIS, HEREDITARY
ACTC	CARDIOMYOPATHY, DILATED, 1R	LMNA	MUSCULAR DYSTROPHY...	SPTLC1	NEUROPATHY...
ACTC	CARDIOMYOPATHY, DILATED, 1A	LMNA	EMERY-DREIFUSS MUSCULAR DYSTROPHY	TCF1	HEPATIC ADENOMAS, FAMILIAL
ALPL	HYPOPHOSPHATASIA, ADULT TYPE	LMNA	CHARCOT-MARIE-TOOTH DISEASE...	TCF2	MATURITY-ONSET DIABETES...
ALS4	AMYOTROPHIC SCLEROSIS 4...	LMNA	CARDIOMYOPATHY, DILATED...	TGFB1	CORNEAL DYSTROPHY...
ANKH	CHONDROCALCINOSIS 2	LMNA	LIPOATROPHY WITH DIABETES...	TGFBR2	MARFAN SYNDROME, TYPE II
APC	ADENOMATOUS POLYPOSIS, COLON	MAPT	PICK DISEASE OF BRAIN	TNNT2	CARDIOMYOPATHY...
APOA1	AMYLOIDOSIS, FAMILIAL VISCERAL	MAPT	PARKINSON-DEMENTIA SYNDROME	TP53	BREAST CANCER, FAMILIAL
APOB	APOLIPOPROTEIN B	MEN1	MULTIPLE ENDOCRINE NEOPLASIA...	TP53	LI-FRAUMENI SYNDROME 1
APOE	SEA-BLUE HISTIOCYTE DISEASE	MEN1	HYPERPARATHYROIDISM 1	TSC1	LYMPHANGIOLEIOMYOMATOSIS
ARHGEF10	SLOWED NERVE CONDUCTION...	MFN2	CHARCOT-MARIE-TOOTH DISEASE...	TSC2	LYMPHANGIOLEIOMYOMATOSIS
ATP2A1	BRODY MYOPATHY	MLH1	COLORRECTAL CANCER...	TSHR	HYPOTHYROIDISM...
ATP2C1	BENIGN CHRONIC PEMPHIGUS	MPZ	CHARCOT-MARIE-TOOTH DISEASE...	TSHR	HYPERTHYROIDISM...
BMPR2	PULMONARY HYPERTENSION...	MPZ	CHARCOT-MARIE-TOOTH DISEASE...	TTID	MUSCULAR DYSTROPHY...
BRCA2	BREAST CANCER, FAMILIAL	MSH2	COLORRECTAL CANCER...	TTN	TIBIAL MUSCULAR DYSTROPHY
BRIP1	BREAST CANCER, FAMILIAL	MSH2	MUIR-TORRE SYNDROME	TTN	HEREDITARY MYOPTHY...
CDK73	PARATHYROID CARCINOMA	MYH9	SEBASTIAN SYNDROME	TTN	MUSCULAR DYSTROPHY...
CDKN2A	MELANOMA-PANCREATIC CANCER	NAGA	KANZAKI DISEASE	TTR	AMYLOIDOSIS VII
CFTR	PANCREATITIS, HEREDITARY	NEUROD1	MATURITY-ONSET DIABETES ...	TTR	TRANSTHYRETIN
CHK2	LI-FRAUMENI SYNDROME 2	NF1	NEUROFIBROMATOSIS...	VAPB	SPINAL MUSCULAR ATROPHY...
CLCN2	EPILEPSY WITH GRAND MAL SEIZURES	NOTCH3	CEREBRAL ARTERIOPATHY...	VAPB	AMYOTROPHIC LATERAL SCLEROSIS
COCH	MENIERE DISEASE	NR3C1	GLUCOCORTICOID RECEPTOR	VHL	VON HIPPEL-LINDAU SYNDROME
COCH	DEAFNESS	PARK7	PARKINSON DISEASE...	VPS13A	CHOREOACANTHOCYTOSIS
COL2A1	AVASCULAR NECROSIS	PAX2	PAPILLORENAL SYNDROME	VXS1	CORNEAL DYSTROPHY...
CPT2	CARNITINE PALMITOYLTRANSFERASE...	PEX7	REFSUM DISEASE	WFS1	DEAFNESS...
CRYAB	ALPHA-B CRYSTALLINOPATHY	PFKM	GLYCOGEN STORAGE DISEASE VII	BRCA1	BREAST CANCER, FAMILIAL
CSR3P	CARDIOMYOPATHY, DILATED, 1M	PGAM2	PHOSPHOGLYCERATE MUTASE...	GSN	AMYLOIDOSIS V
CST3	AMYLOIDOSIS VI	PHKA1	MUSCLE GLYCOGENOSIS	HGD	ALKAPTONURIA
CYP11B2	IgA NEPHROPATHY	PHYH	REFSUM DISEASE	LYZ	AMYLOIDOSIS, FAMILIAL VISCERAL
DCTN1	LOWER MOTOR NEURON DISEASE...	PINK1	PARKINSON DISEASE 6...	MUTYH	COLORRECTAL POLYPOSIS...
DMD	CARDIOMYOPATHY, DILATED...	PLAT	PLASMINOGEN ACTIVATOR...	OPTN	GLAUCOMA...
TYROBP	PRESENILE DEMENTIA ...	PLG	PLASMINOGEN...	SOD1	AMYOTROPHIC...
				TNN3	CARDIOMYOPATHY...

20 years later

Blekhman (2008) – 205 couple gene - late onset diseases from OMIM

1 gene ► different diseases

1 diseases ► different genes

« most alleles involved in genetic diseases including familial forms of cancer, coronary artery diseases and Alzheimer dementia, are recent and rare. » Wright A et al. (2003)

Ex. BRCA1 - Breast Cancer Information Core (BIC): More than 1000 alleles recorded

3/4 of mutations at very low frequency (often in only one family)

Introduction

SCIENTIST AT WORK | DAVID B. GOLDSTEIN

A Dissenting Voice as the Genome Is Sifted to Fight Disease

By NICHOLAS WADE
Published: September 15, 2008

The principal rationale for the \$3 billion spent to decode the human genome was that it would enable the discovery of the variant genes that predispose people to common diseases like [cancer](#) and [Alzheimer's](#). A major expectation was that these variants had not been eliminated by natural selection because they harm people only later in life after their reproductive years are over, and hence that they would be common.

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Ken Cedeno for The New York Times
GENE THINKER David Goldstein has not shied from unpopular positions.

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This idea, called the common disease/common variant hypothesis, drove major developments in biology over the last five years. Washington financed the HapMap, a catalog of common genetic variation in the human population. Companies like Affymetrix and Illumina developed powerful gene chips for scanning the human genome. Medical statisticians designed the genomewide association study, a robust methodology for discovering true disease genes and sidestepping the many false positives that have plagued the field.

But David B. Goldstein of [Duke University](#), a leading young population geneticist known partly for his research into the genetic roots of Jewish ancestry, says the effort to nail down the [genetics](#) of most common diseases is not working. "There is absolutely no question," he said, "that for the whole hope of personalized medicine, the news has been just about as bleak as it could be."

« The **common disease/common variant** idea is largely **wrong** [...] **natural selection** has been far **more efficient** than many researchers expected »

J. Goldstein, Septembre 16, 2008

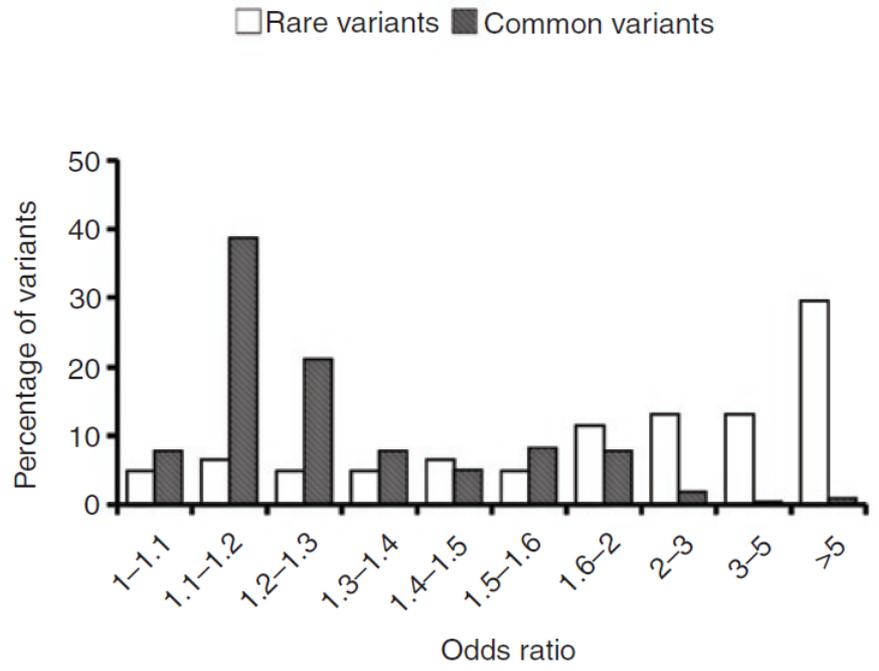


Figure 2 Distribution of odds ratios for common and rare variants. Odds ratios were obtained from the literature (**Supplementary Note**). We included 61 rare variants and 217 common variants in this analysis.

Bodmer and Bonilla (*Nature genetics*, 2008)

Introduction

Problem for population geneticists:

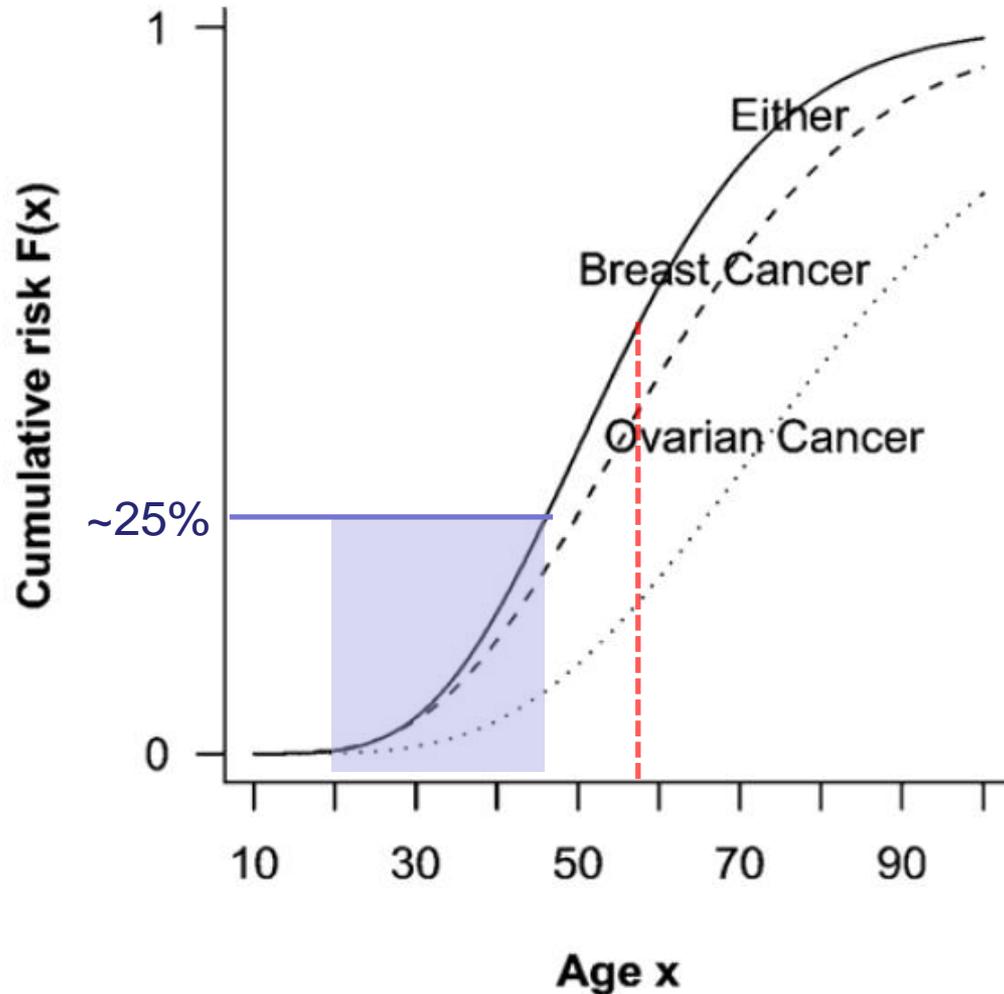
Multigenic diseases + Complex molecular pathway + Weak selection

▶ Selection tests from genetic data failed

What can then predict demographers?

Introduction

1. Variance in disease onset



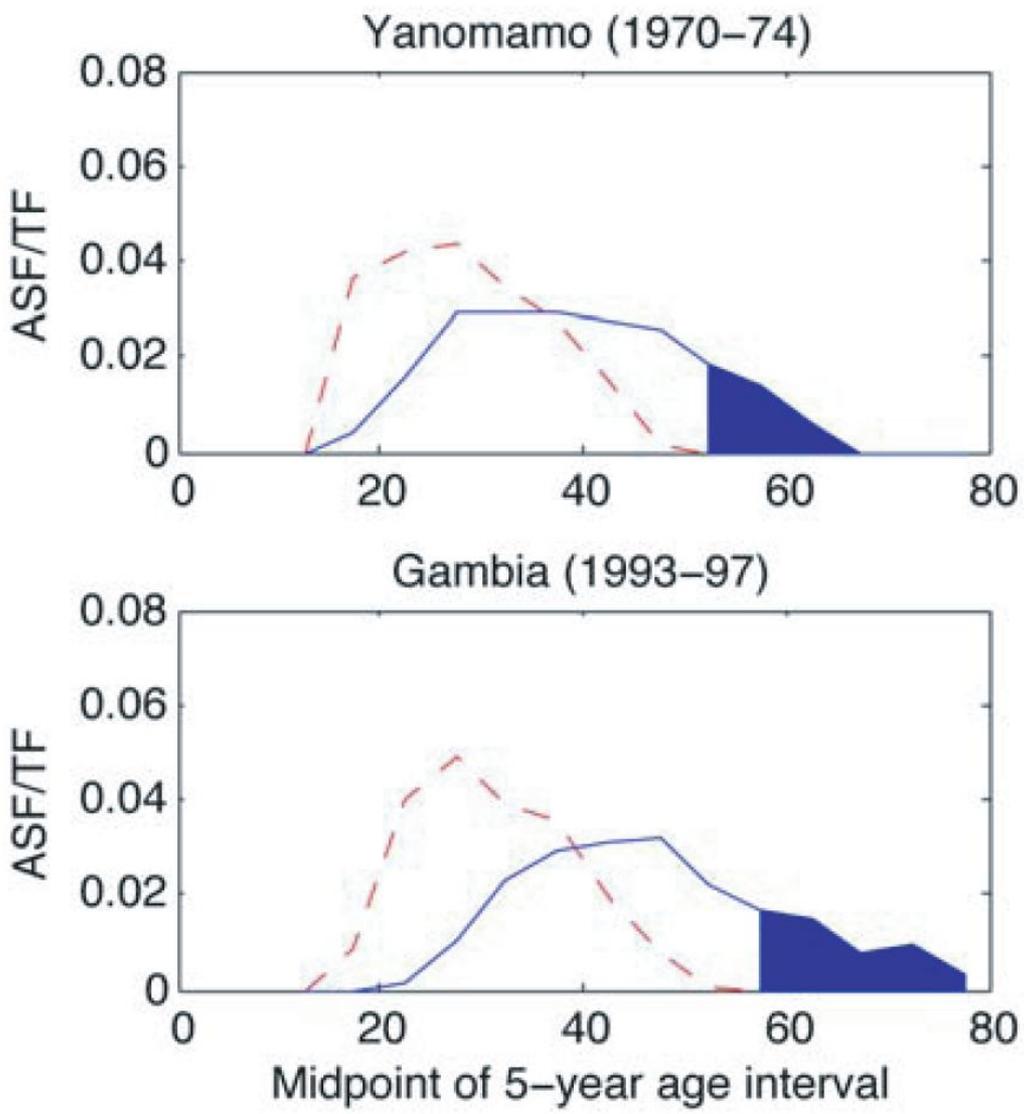
Diseases may occur *before* menopause even when the mean age at onset is *after* menopause

Ex. BRCA1

Pavard and Metcalf (2007)

Introduction

2. Males reproduction until old ages



Men (in blue) reproduce until old ages with younger women (in red).

Because of later age at marriage, remarriage and polygamy,

Tuljapurkar et al. (2007)

Introduction

3. Parental and grandparental care



This woman's age is 41...

Mothers, Fathers and Grandmothers may care for their immature children long after menopause

Introduction

3. Parental and grandparental care

Who keeps children alive?
Sear and Mace (2008)

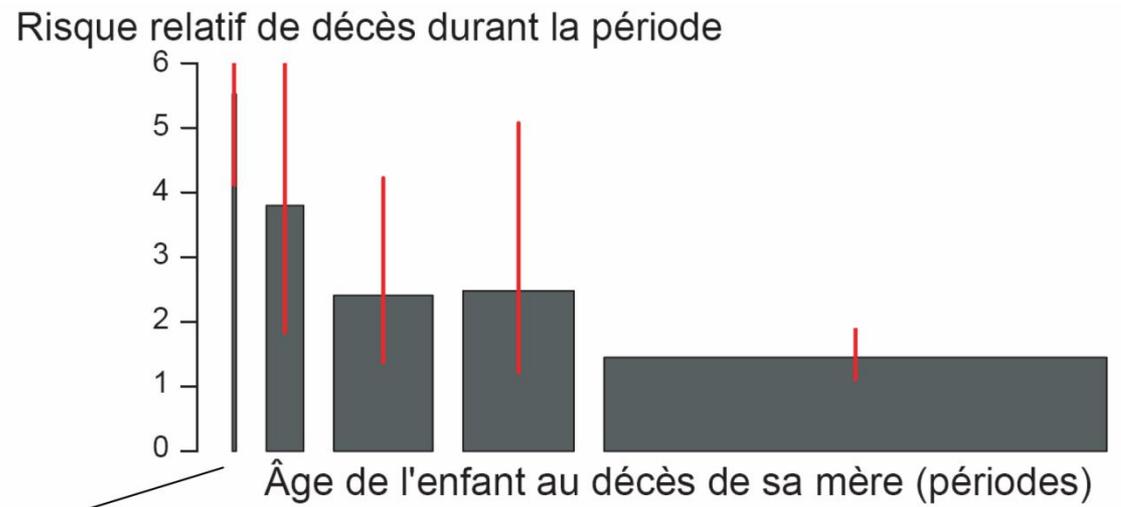
Motherless children have a
higher risk of death than children
whose mother are alive

Population	Authors	Effect of mothers	Age of children studied
Nepal (Sarlahi) 1994–97	Katz et al. (2003)	+	0–24 weeks
Caribbean (St. Barthélemy) 1878–1976	Brittain (1992)	+	0–1 yr
Gambia (four villages) 1950–74	Sear et al. (2000, 2002)	+	0–5 yrs
Kenya (Kipsigis) 1945–90	Borgerhoff Mulder, (2007)	+	0–5 yrs
Burkina Faso (Nouna) 1992–99	Becher et al. (2004)	+	0–5 yrs
Sub-Saharan Africa ^c 1980s–2000	Zaba et al. (2005)	+	0–5 yrs
Canada (Quebec) 1680–1750	Beise (2005)	+	0–5 yrs
Poland (Bejsce) 1737–1968	Tymicki (2006)	+	0–5 yrs
Guinea–Bissau 1990–98	Masmas et al. (2004)	+	0–8 yrs
Paraguay (Ache) 1890–1971	Hill and Hurtado (1996)	+	0–9 yrs
Netherlands (Woerden) 1850–1930	Beekink et al. (1999, 2002)	+	0–12 yrs
Italy (Tuscany) 1819–59	Breschi and Manfredini (2002)	+	0–12 yrs
Canada (Quebec) 1625–1759	Pavard et al. (2005)	+	0–15 yrs
Sweden (Sundsvall) 1800–1895	Andersson et al. (1996)	+	0–15 yrs
Japan (Central) 1671–1871	Sorenson Jamison et al. (2002)	+	1–16 yrs
China (North East) 1774–1873	Campbell and Lee (1996, 2002)	+	~1–15 yrs

Introduction

3. Parental and grandparental care

Pavard et al. (2005)
Données du Québec ancien
N=9840



Néonatal



Postnéonatal



Nourrisson



Petite enfance



Enfance et adolescence



Methods – *Presentation of the model*

Coefficient of selection of susceptibility allele:

For a large and realistic **parameter space for disease onset** (mean and variance)

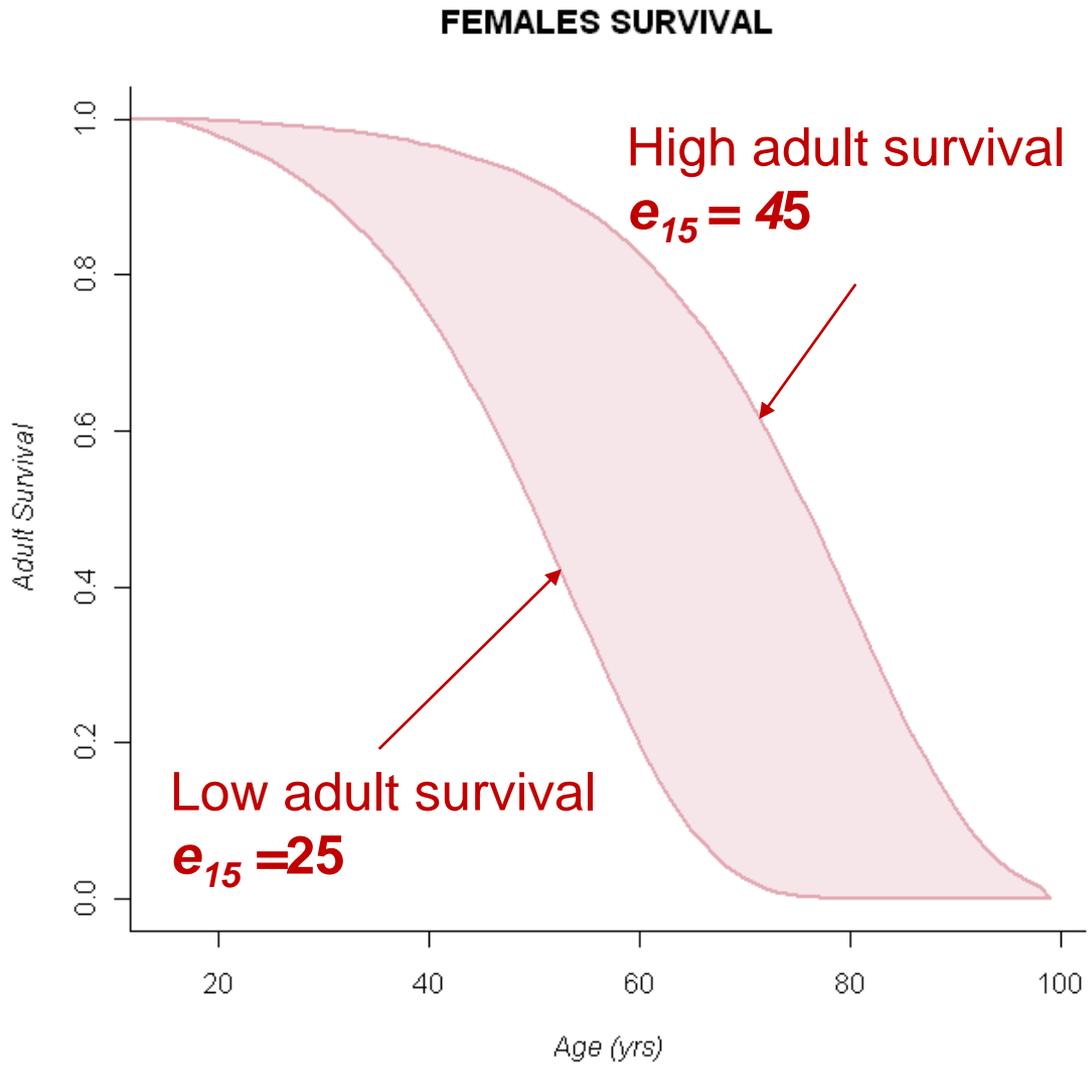
In a two-sex model were **men can reproduce at old ages**

Where child survival depends on **maternal, paternal and grandmaternal care**

▶ Selective value of non-carriers (*population survival*) and carriers (*population survival * disease survival*)

Methods – Survival of carriers and non-carriers

Non Carriers adult survival



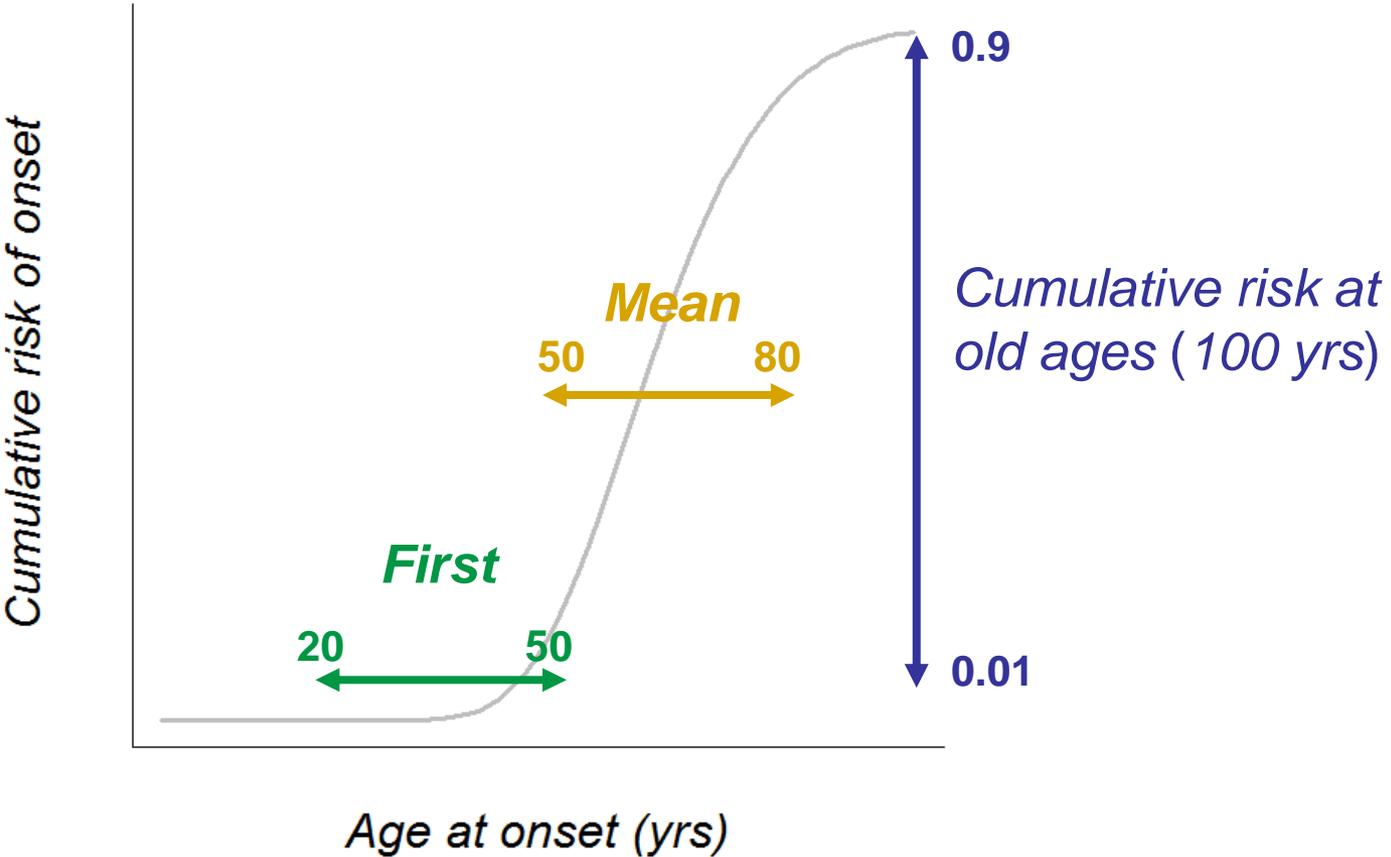
Gompertz

$$L^f(x) = \exp\left[\frac{\rho a}{b}\left(e^{-b^\dagger x} - 1\right)\right]$$



Methods – *Survival of carriers and non-carriers*

Carriers' morbidity (*Gamma*)

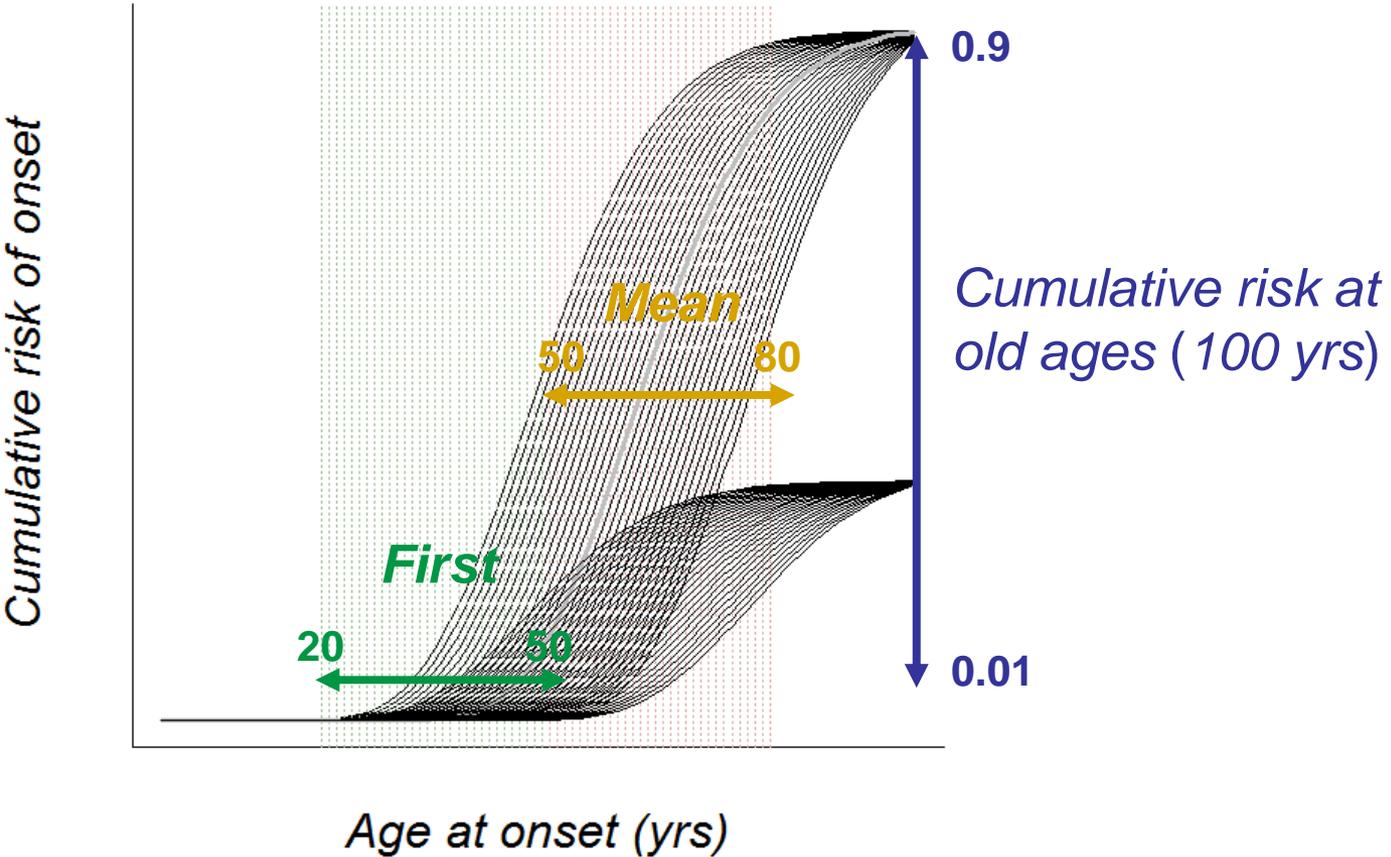


Except for BRCA1 and Huntington, **distribution of age at onset is rare**

For most diseases: familial cases study

Methods – *Survival of carriers and non-carriers*

Carriers' morbidity (*Gamma*)

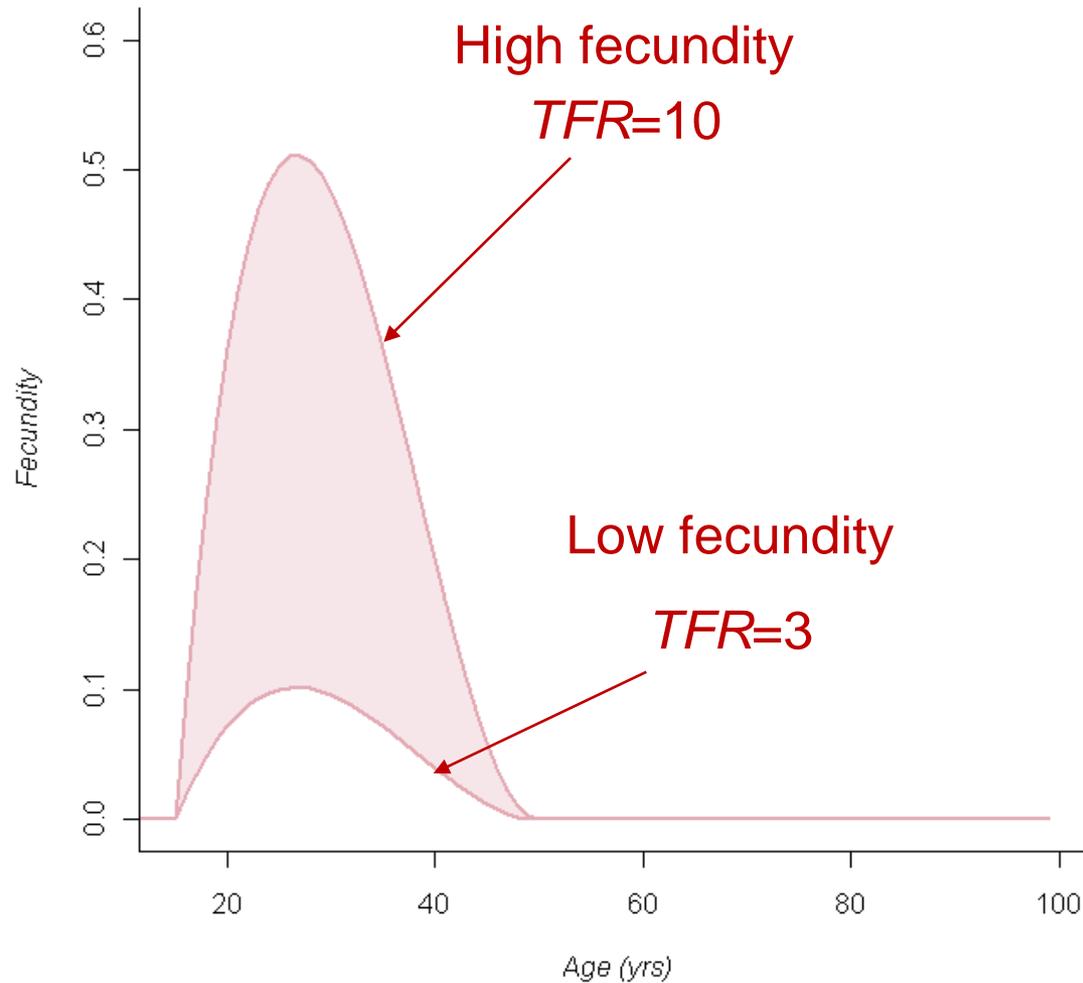


Except for BRCA1 and Huntington, **distribution of age at onset is rare**

For most diseases: familial cases study

Methods – Fecundity (Brass Polynomial)

FECUNDITY FEMALES



Brass Polynomial

$$f^f(x) = c(x - \alpha)(\beta - x)^2$$

for $\alpha \leq x \leq \beta$

$$\alpha = 15$$

$$\beta = 50$$

c scales up and down

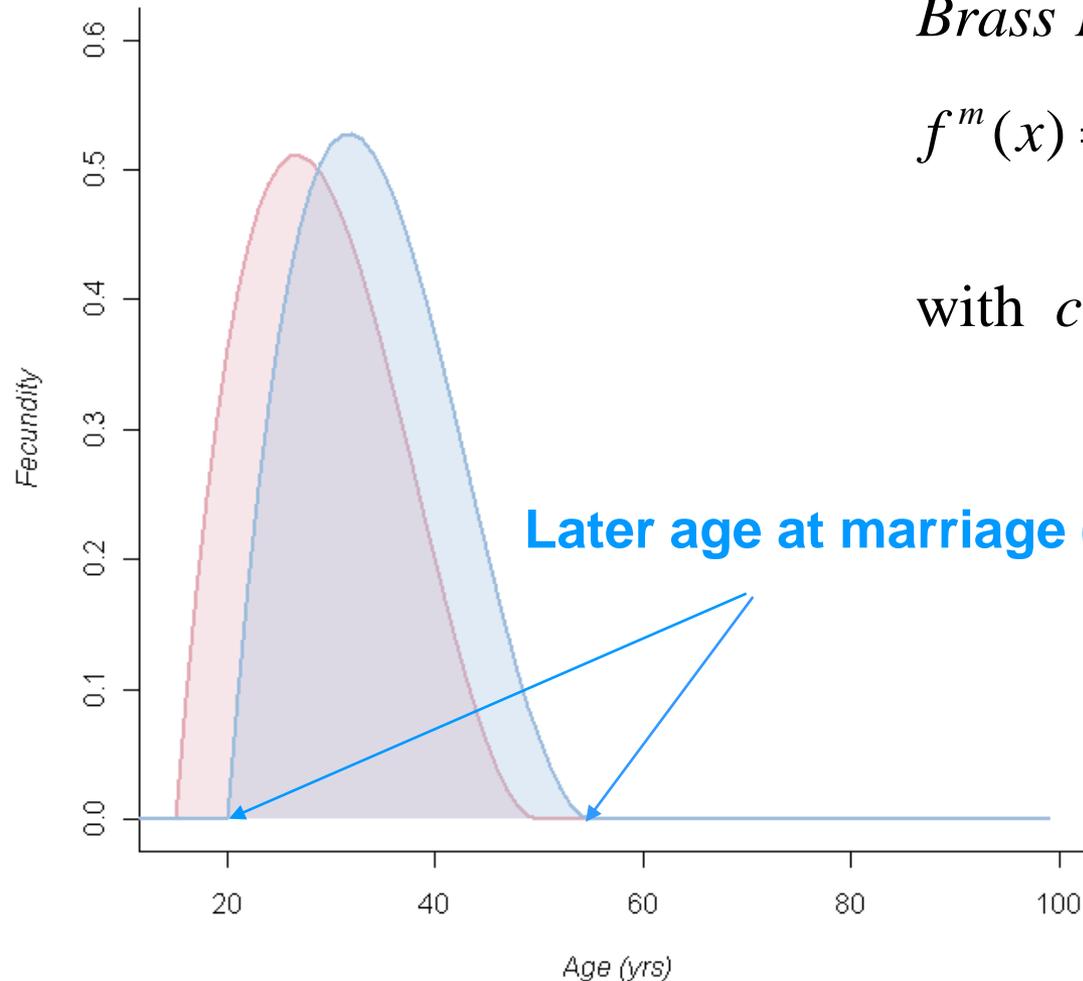
Methods – Fecundity (Brass Polynomial)

FECUNDITY MALES

Brass Polynomial

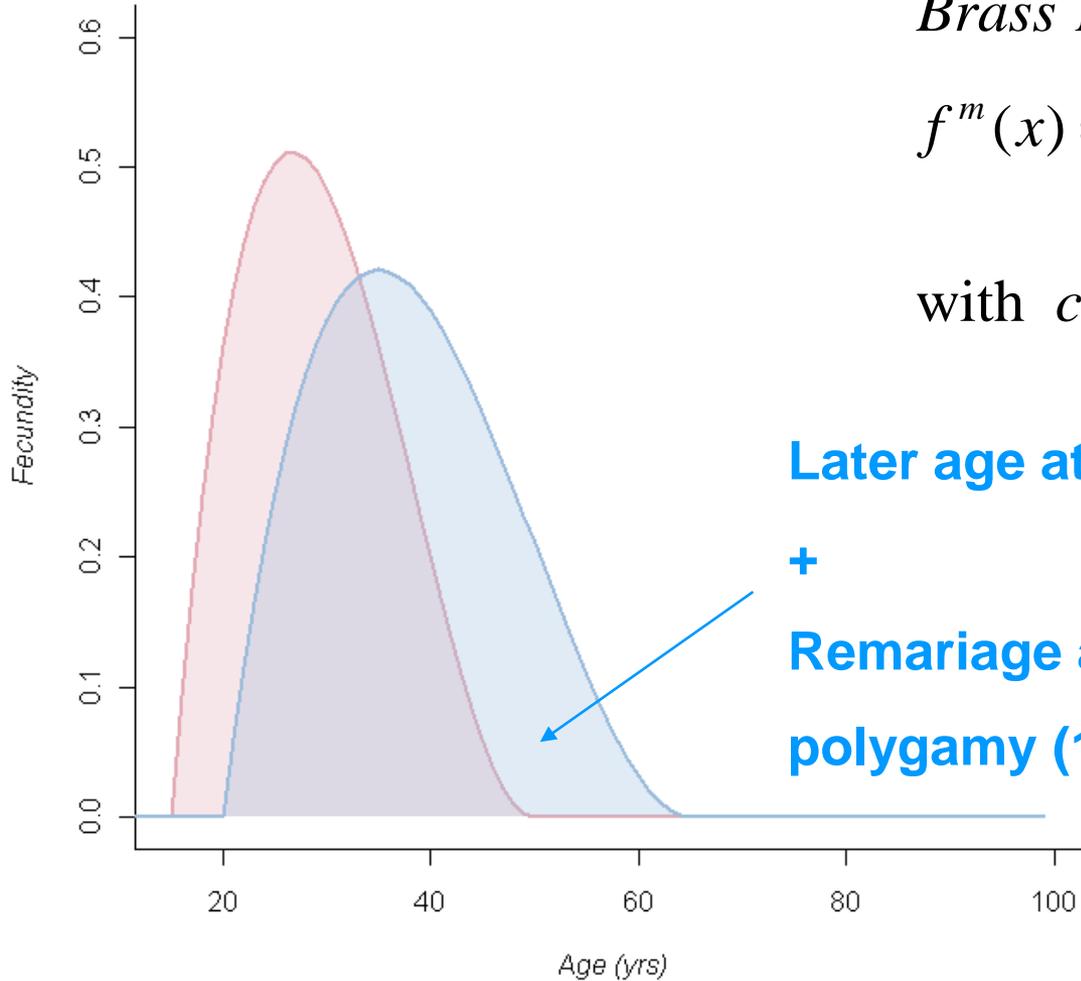
$$f^m(x) = c^m (x - \alpha^m) (\beta^m - x)^2$$

$$\text{with } c^{\dagger} = \frac{\int_x L^f(x) f^f(x) dx}{\int_x L^m(x) (x - \alpha^m) (\beta^m - x)^2 dx}$$



Methods – Fecundity (Brass Polynomial)

FECUNDITY MALES



Brass Polynomial

$$f^m(x) = c^m (x - \alpha^m) (\beta^m - x)^2$$

$$\text{with } c^{\dagger} = \frac{\int_x L^f(x) f^f(x) dx}{\int_x L^m(x) (x - \alpha^m) (\beta^m - x)^2 dx}$$

Later age at marriage (5 yrs)

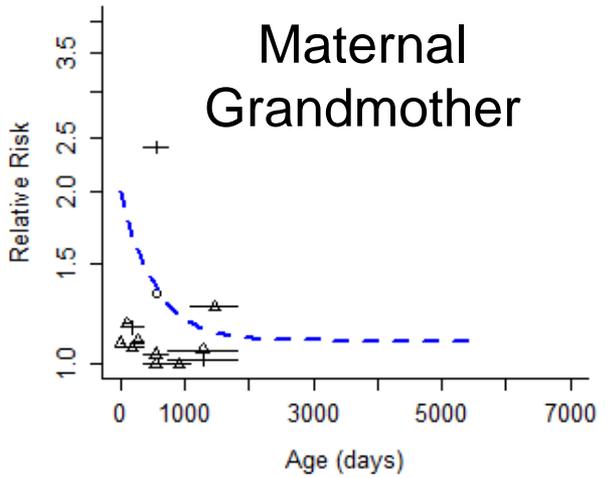
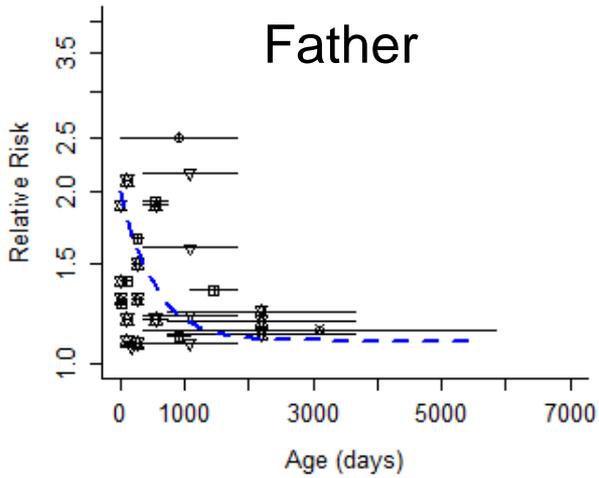
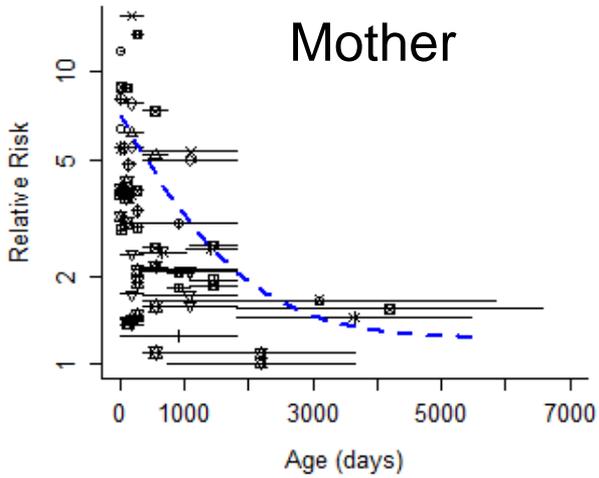
+

Remarriage after divorce or wife's death ;

polygamy (10 yrs)

Methods – Maternal, Paternal and Grandmaternal care

Relative Risk of death of Orphans (from mother, father and maternal grandmother) **compared to non-orphans**



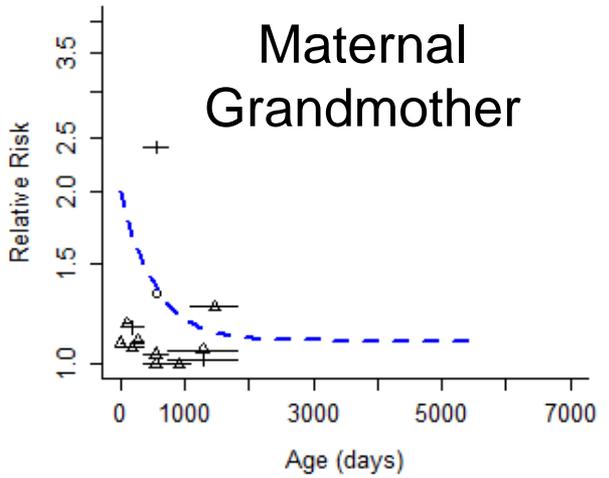
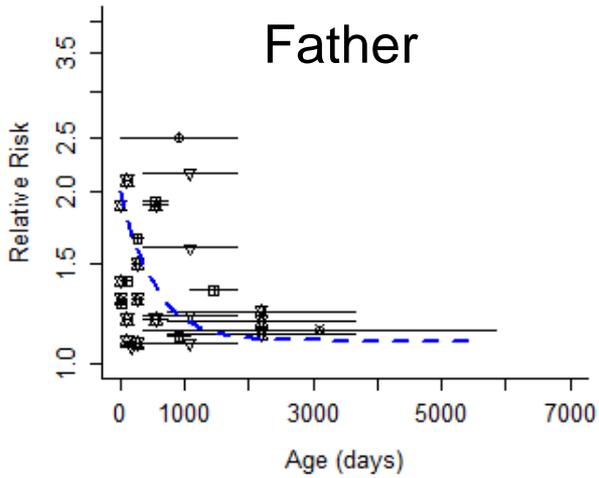
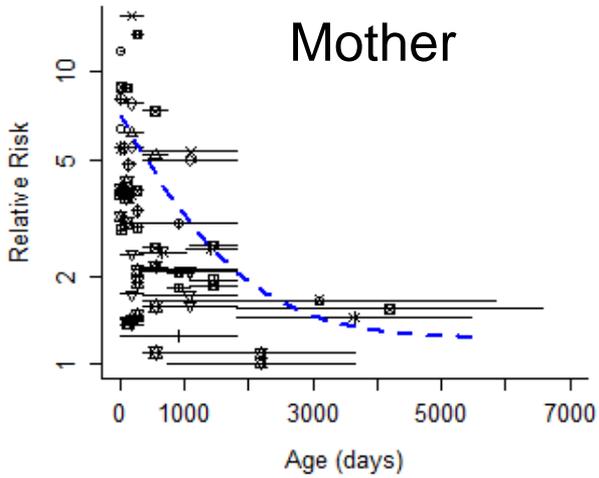
- ◊ Katz et al. (2003)
- △ Sear and Mace (2009)
- + Bergerhoff Mulder (2007)
- × Becher et al. (2004)
- ◇ Zaba et al. (2003)
- ▽ Tymiocki (2009)
- Masmas et al. (2004)
- * Pavard et al. (2005)
- ✕ Jamison et al. (2002)
- ◆ Koenig et al. (1988)
- ♣ Bishai et al. (2003)
- ✱ Reher and González-Quiñones (2003)
- Belse (2005)

- ◊ Tymiocki (2009)
- △ Jamison et al. (2002)
- + Gilson and Mace (2005)
- × Campbell and Lee (1996, 2002)
- ◇ Belse (2005)

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- + Sear and Mace (2009)
- × Sear et al. (2000)
- ◇ Belse (2005)

Methods – Maternal, Paternal and Grandmaternal care

Relative Risk of death of Orphans (from mother, father and maternal grandmother) compared to non-orphans



$$S^\alpha(y_1)$$

y_1 age at mother's death

$$S^\alpha(y_3)$$

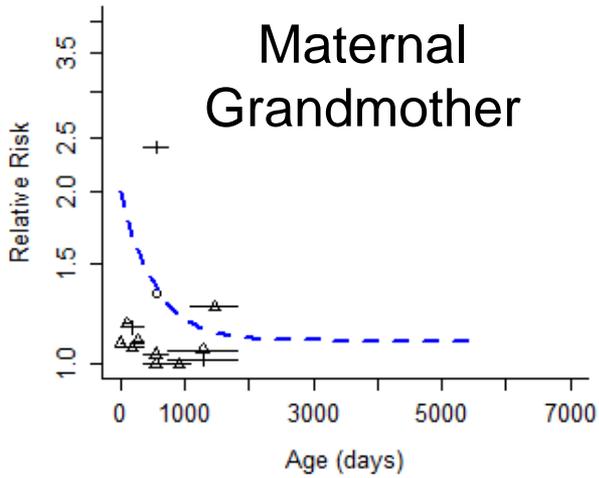
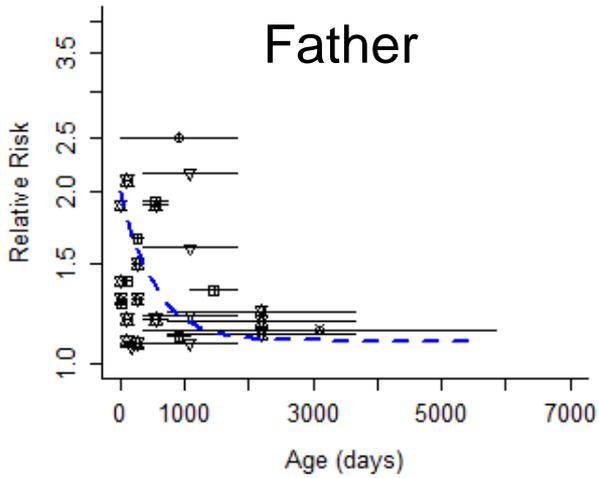
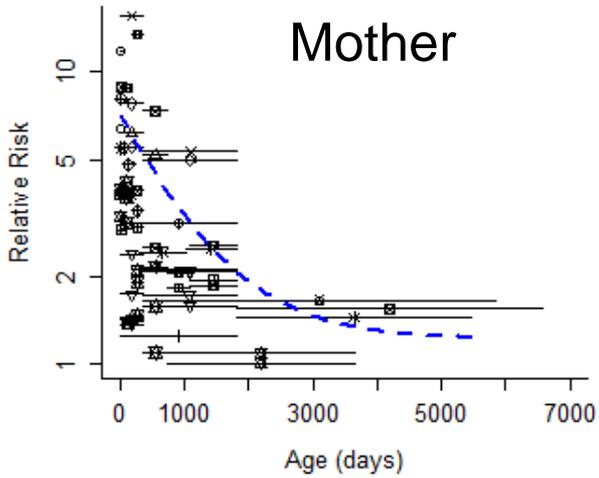
y_3 age at father's death

$$S^\alpha(y_2)$$

y_2 age at GM's death

Methods – Maternal, Paternal and Grandmaternal care

Relative Risk of death of Orphans (from mother, father and maternal grandmother) compared to non-orphans



$$S^\alpha(y_1)$$

y_1 age at mother's death

$$S^\alpha(y_3)$$

y_3 age at father's death

$$S^\alpha(y_2)$$

y_2 age at GM's death

$$S^\alpha(y_1, y_2, y_3)$$

Methods – *Calculation of the reproductive value*

The Euler-Lotka equation is:

$$1 = \int_0^{\omega} (\lambda^f)^{-x_1} l^f(x_1) f^f(x_1) dx_1$$

Replacing $L^f(x_1) = l^f(x_1) / \overline{S^\alpha}$

$$1 = \overline{S^\alpha} \int_{\alpha}^{\omega} (\lambda^f)^{-x_1} L^f(x_1) f^f(x_1) dx_1$$

Pavard (2007) showed that this is equivalent to:

$$1 = \int_{\alpha}^{\omega} (\lambda^f)^{-x_1} L^f(x_1) f^f(x_1) S^\alpha(x_1) dx_1$$

With $S^\alpha(x_1)$ being the child survival until maturity as a function of the mother's age at its birth

Methods – *Calculation of the reproductive value*

What we want is expressing $S^\alpha(x_1)$ as a function of $S^\alpha(y_1, y_2, y_3)$

To do this, we are looking for the probabilities for a child born to a mother at age x_1 to lose its mother, its maternal grandmother and its father at ages y_1 , y_2 and y_3 respectively.

$$S^\alpha(x_1) = \iiint p(y_1 | x_1) p(y_2 | x_1) p(y_3 | x_1) S^\alpha(y_1, y_2, y_3) dy_1 dy_2 dy_3$$

Methods – *Calculation of the reproductive value*

Probability for a child to loose its mother at age y_1

$$p(y_1 | x_1) = \frac{L^f(x_1 + y_1)}{L^f(x_1)} h(x_1 + y_1)$$

Over all possible age y_1

$$\int_{y_1} p(y_1 | x_1) dy_1 = \int_0^{\omega - x_1} \left(L^f(x_1 + y_1) / L^f(x_1) \right) h(x_1 + y_1) dy_1$$

Methods – Calculation of the reproductive value

Probability for a child to lose its maternal grandmother at age y_2

$$p(y_2 | x_1) = \int_{\alpha^f}^{\beta^f} p(x_2 | x_1) p(y_2 | x_1, x_2) dx_2$$

With

$$p(x_2 | x_1) = p(x_2) = (\lambda^f)^{-x_2} L^f(x_2) f^f(x_2) \overline{S}^\alpha$$

And

$$p(y_2 | x_1, x_2) = \frac{L^f(x_2 + x_1 + y_1)}{L^f(x_2)} h(x_2 + x_1 + y_1)$$

Over all possible age y_2

$$\int_{y_2} p(y_2 | x_1) dy_2 = \int_{-x_1}^{\omega - x_1} \int_{\alpha^f}^{\beta^f} p(x_2) p(y_2 | x_1, x_2) dx_2 dy_2$$

Methods – *Calculation of the reproductive value*

Probability for a child to loose its father at age y_3

Assuming that fathers are always of the same age or older than the mother without further matrimonial structuring (structuring matrimony would indeed imply extending the model for incorporating widowing and divorced probability, remarriage probability and polygamy).

$$p(y_3 | x_1) = \int_{x_1}^{\beta^m} p(x_3 | x_1) p(y_3 | x_3) dx_3$$

With

$$p(x_3 | x_1) = \frac{(\lambda^m)^{-x_3} L^m(x_3) f^m(x_3)}{\int_{x_1}^{\beta^m} (\lambda^m)^{-x_3} L^m(x_3) f^m(x_3) dx_3}$$

Methods – *Calculation of the reproductive value*

Probability for a child to loose its father at age y_3

And
$$p(y_3 | x_3) = \frac{L(x_3 + y_3)}{L(x_3)} h(x_3 + y_3)$$

Over all possible age y_3

$$\int_{y_3} p(y_3 | x_1) dy_3 = \int_0^{\omega - x_1} \int_{x_1}^{\beta^m} p(x_3 | x_1) p(y_3 | x_3) dx_3 dy_3$$

Methods – *Calculation of the reproductive value*

- Input parameters are

$$L^f, L^m, F^f, F^m, S^\alpha(y_1, y_2, y_3)$$

- Euler-Lotka has 2 unknown parameters λ^f, λ^m

- But $\log \lambda \approx \frac{\log R_0}{T}$ is true at the third decimal in humans when the age unit is the year, therefore: $\log(\lambda^m) = \log(\lambda^f)(T^f / T^m)$

- We can then solve

$$1 = \int_{\alpha}^{\omega} (\lambda^f)^{-x_1} L^f(x_1) f^f(x_1) S^\alpha(x_1) dx_1$$

- And find the corresponding distribution $S^\alpha(x_1)$

Methods – *Calculation of the reproductive value*

Reproductive value of non carriers females

$$W^{NC} = \int_0^{\omega} L^f(x_1) f^f(x_1) S^{\alpha}(x_1) dx_1$$

(We can demonstrate that this holds when derivation are done for males)

W^C : similar equation + **Morbidity**

- ▶ Genetic compartment (Autosome, X-Chr, Y-Chr, Mt-Chr)
- ▶ Segregation coefficient (kin selection)
- ▶ Dominance
- ▶ Sex-specific pathology (male, female, both sex)

Methods – *Calculation of the reproductive value*

Here: **Autosomal, Dominant mutation, disease in both sex**

$$W^C = \frac{1}{2} W \left[\text{men}^C, \text{wife}^{NC}, \text{wife's mother}^{NC} \right] +$$

$$\frac{1}{2} \frac{1}{2} W \left[\text{women}^C, \text{husband}^{NC}, \text{mother}^{NC} \right] +$$

$$\frac{1}{2} \frac{1}{2} W \left[\text{women}^C, \text{husband}^{NC}, \text{mother}^C \right]$$

- ▶ First population genetics model incorporating maternal, grandmaternal and paternal care
- ▶ First compact model over only one generation

Methods – *Estimation of selection*

Assuming ...

- An allele of susceptibility at very **low frequency**
- The disease is **lethal** (not benign as corneal dystrophy leading to night blindness)
- Death occurs at **age at onset** (not slowly degenerative disease)
- **Independence** between risk of onset and other causes of death within the population
- **No pleiotropic effect** of the alleles (eg. Smith et al. 2011 for BRCA1)
- Epidemiology of the disease was **identical in the past** (which is likely not the case in the cases of cancers, see Eaton et al. 1994)

Methods – *Estimation of selection*

Selection Coefficient

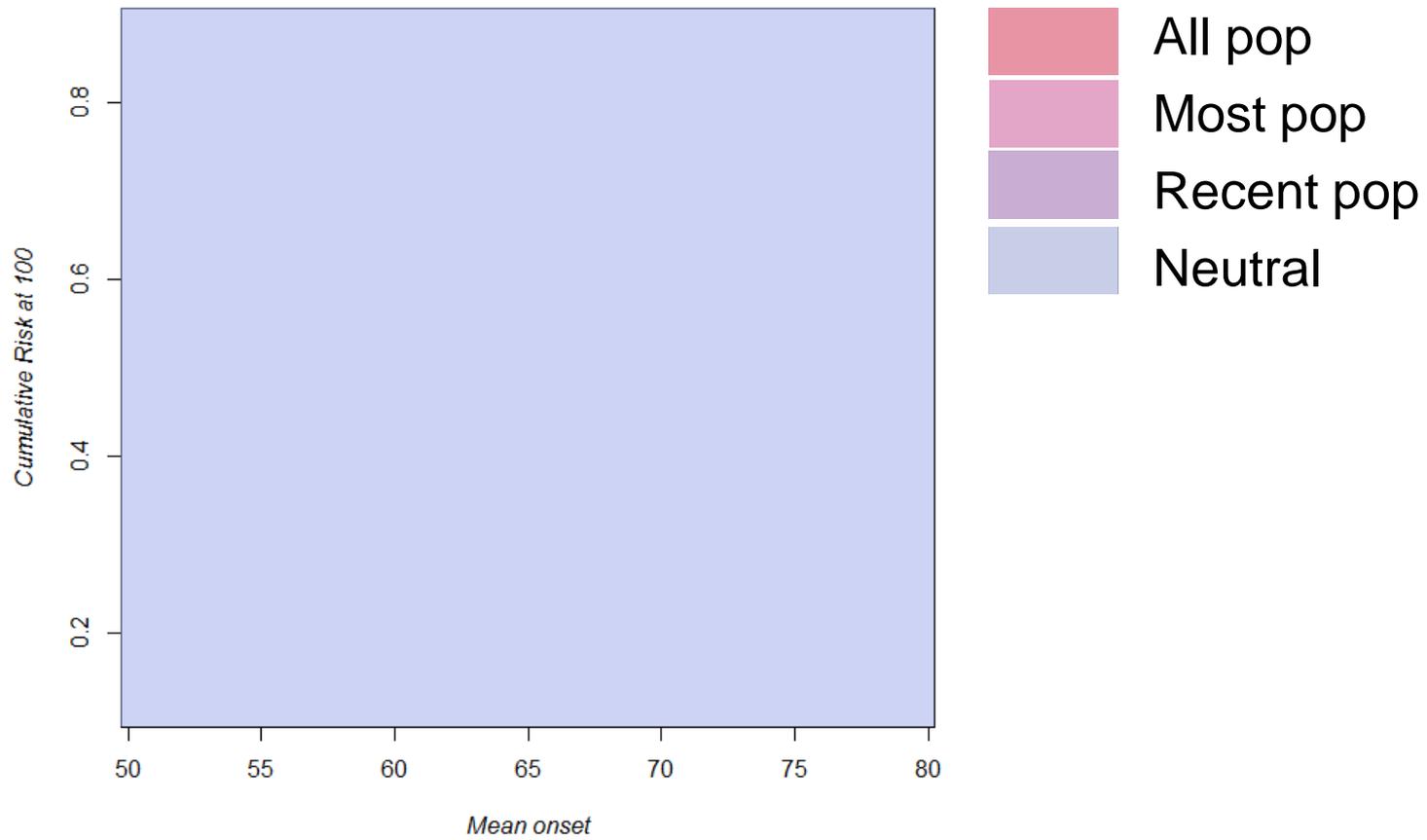
$$s = 1 - \frac{W^C}{W^{NC}}$$

Minimum effective size for which selection overcomes genetic drift

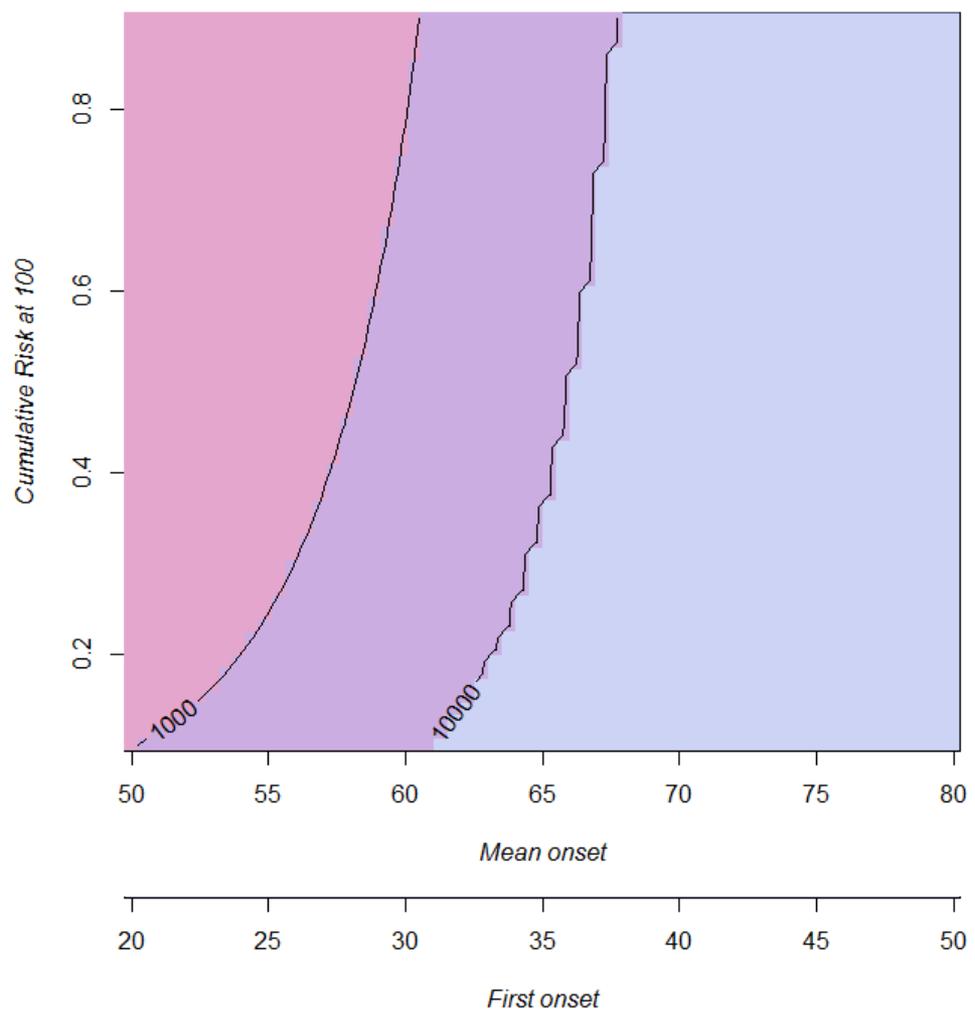
$$Ne_{\min} = \frac{10}{2s} \quad \text{Kimura (1973)}$$

	$Ne_{\min} < 100$	Negative selection all human pop
	$100 < Ne_{\min} < 1000$	Negative selection most human pop
	$1000 < Ne_{\min} < 10\,000$	Negative selection only in recent human pop
	$Ne_{\min} > 10\,000$	Neutral

Results



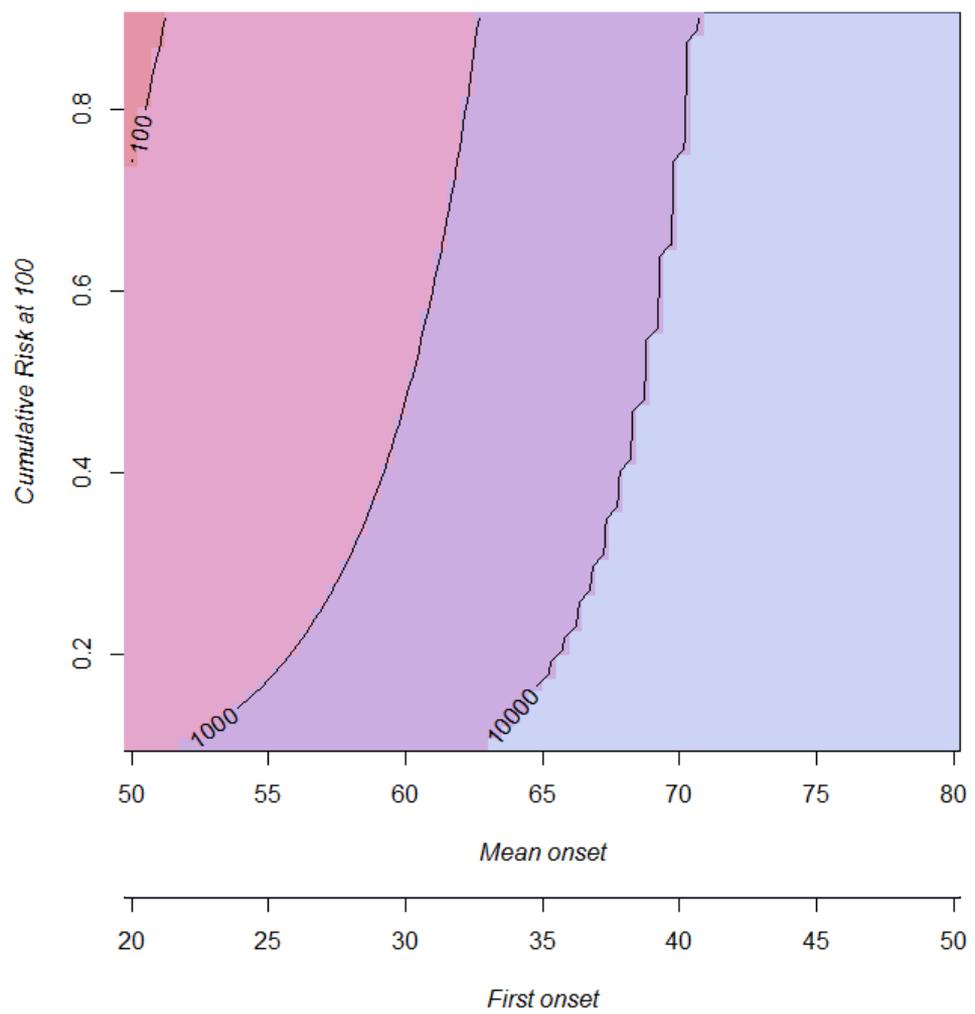
Results



- All pop
- Most pop
- Recent pop
- Neutral

Variance in age at onset

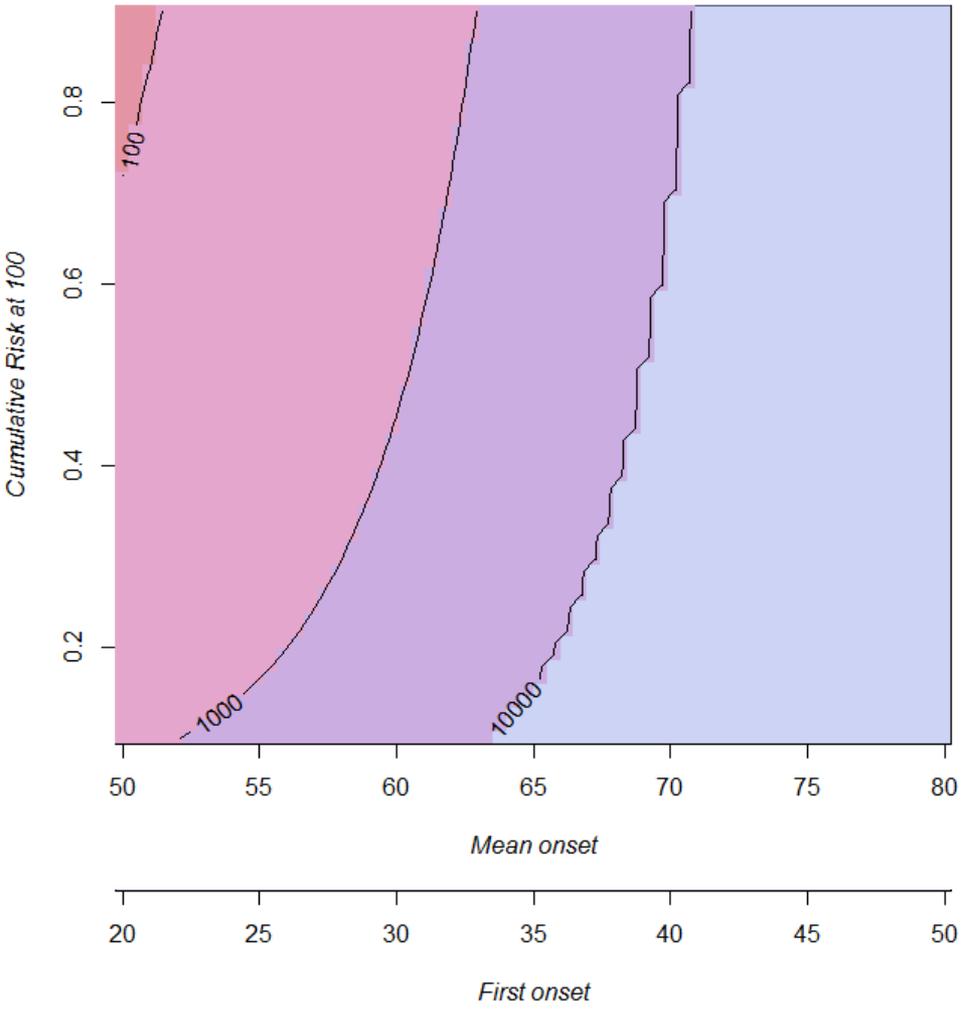
Results



- All pop
- Most pop
- Recent pop
- Neutral

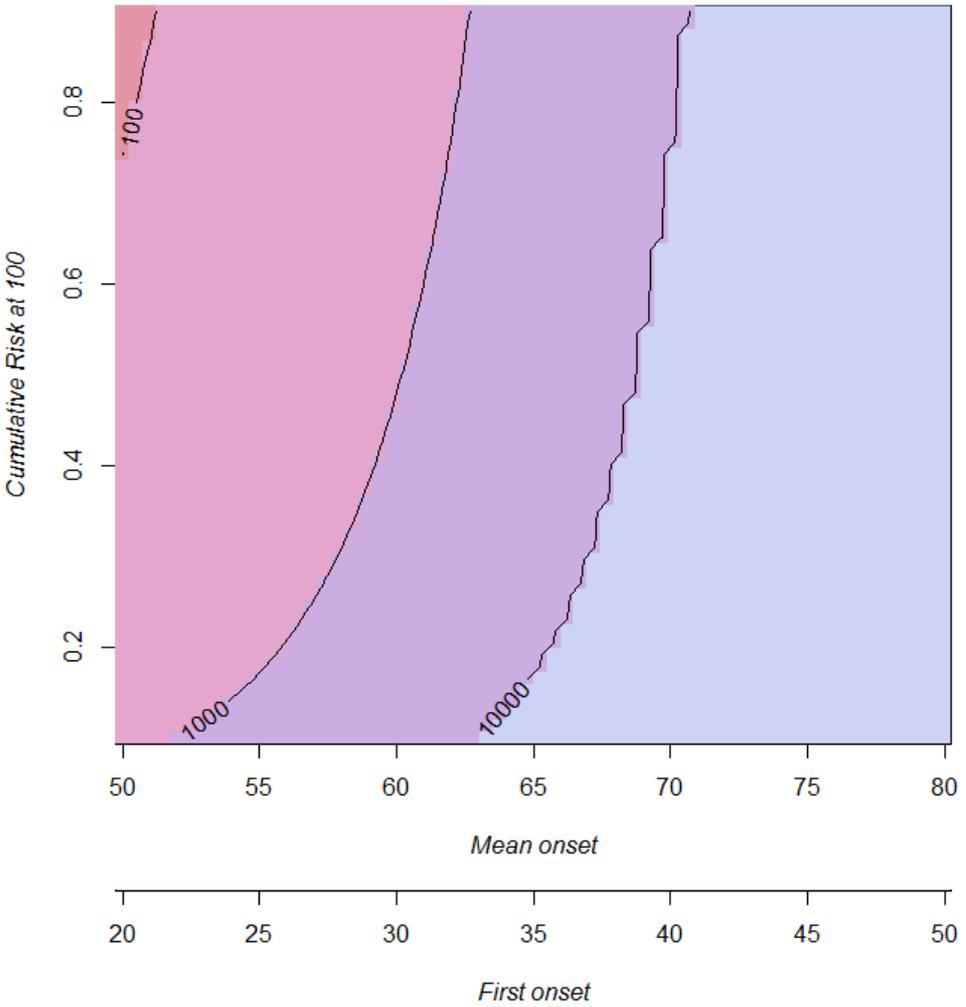
Variance in age at onset
Maternal care

Results



- All pop
 - Most pop
 - Recent pop
 - Neutral
- Variance in age at onset
- Maternal care
- Paternal care

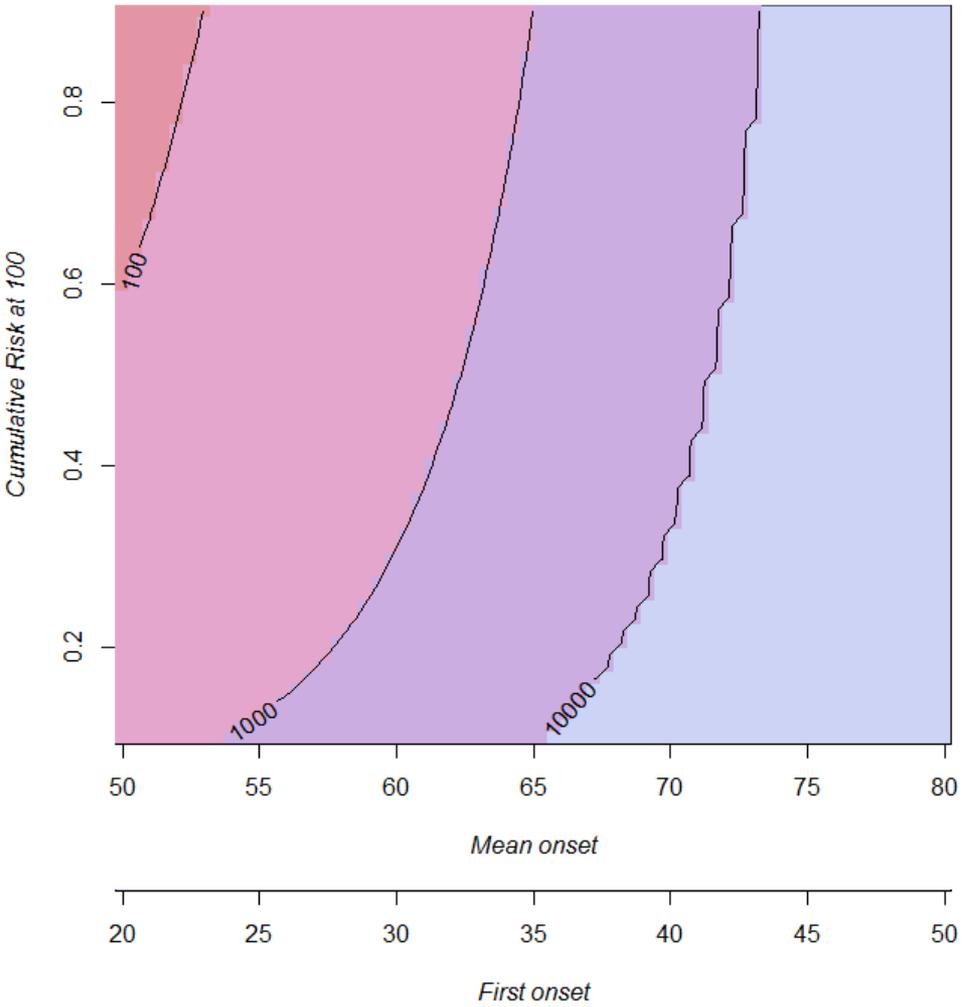
Results



- All pop
- Most pop
- Recent pop
- Neutral

Variance in age at onset
Maternal care
~~Paternal care~~

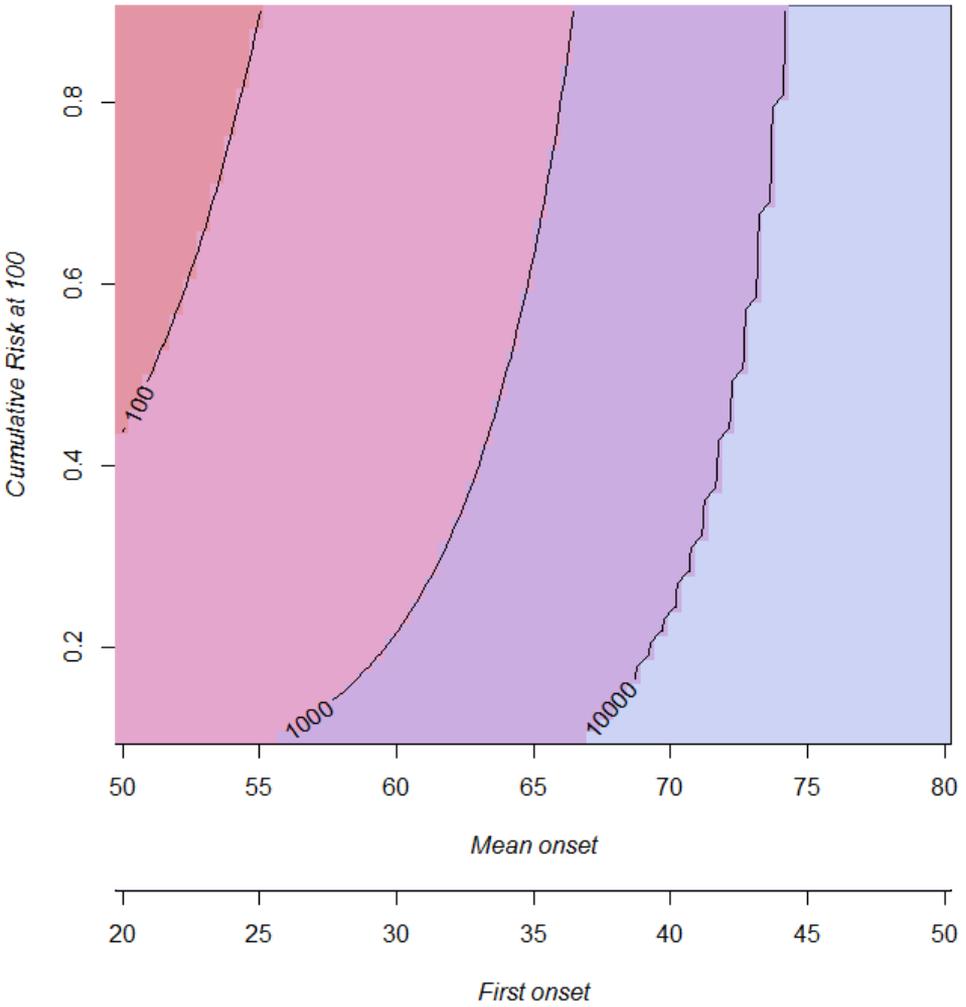
Results



- All pop
- Most pop
- Recent pop
- Neutral

- Variance in age at onset
- Maternal care
- ~~Paternal care~~
- Grandmaternal care

Results



- All pop
- Most pop
- Recent pop
- Neutral

Variance in age at onset

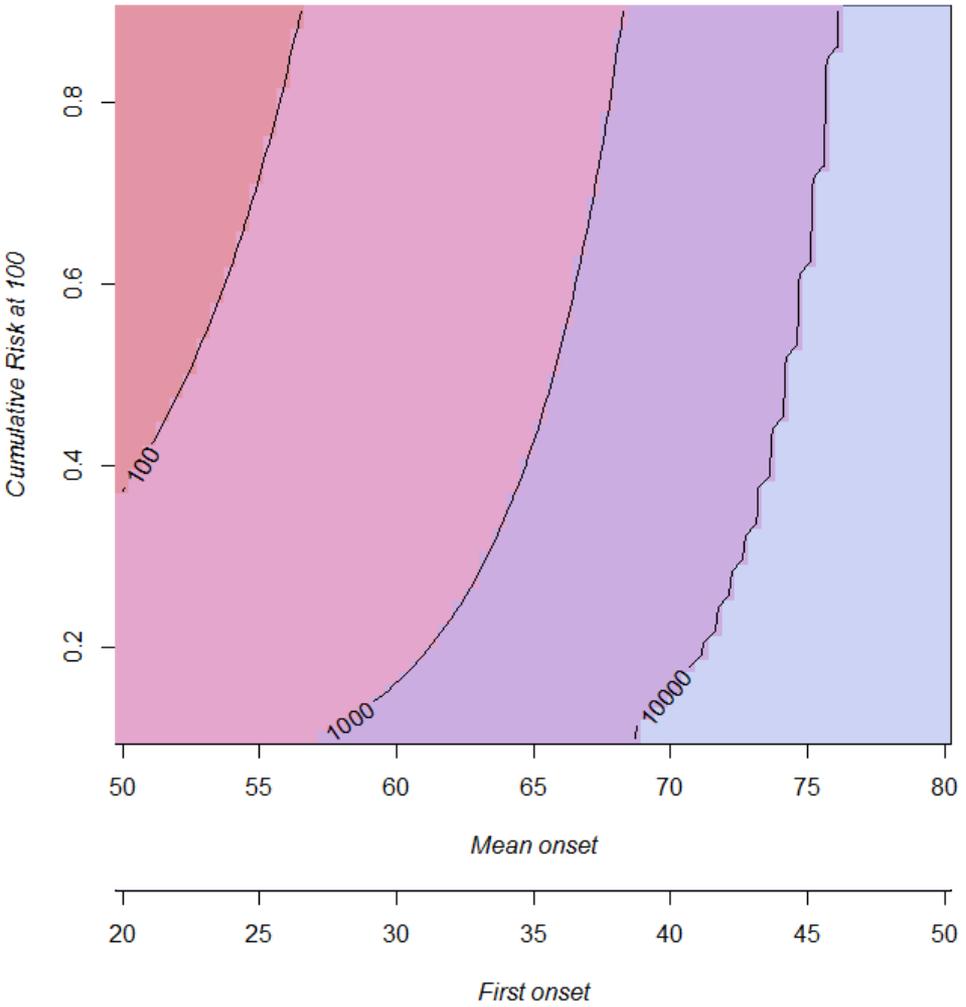
Maternal care

~~Paternal care~~

Grandmaternal care

Later age at first birth of men

Results



- All pop
- Most pop
- Recent pop
- Neutral

Variance in age at onset

Maternal care

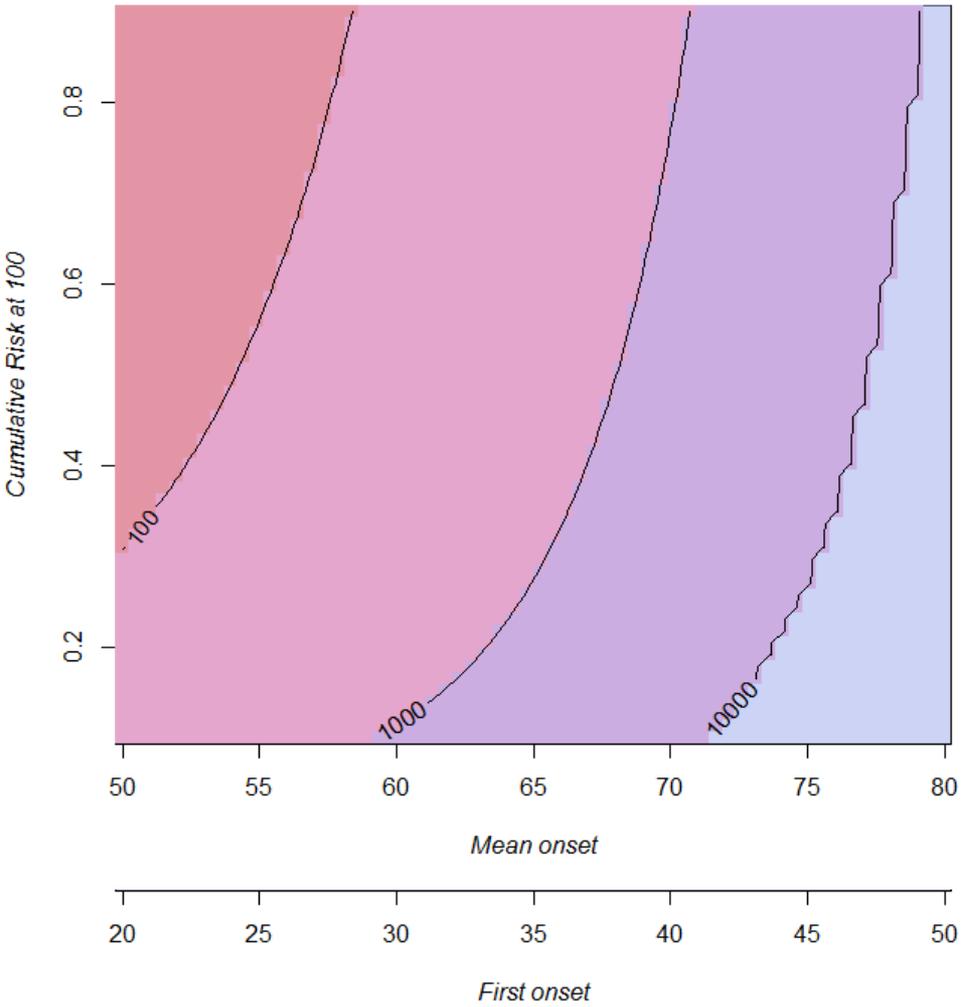
~~Paternal care~~

Grandmaternal care

Later age at first birth of men

Remarriage/polygamy

Results



- All pop
- Most pop
- Recent pop
- Neutral

Variance in age at onset

Maternal care

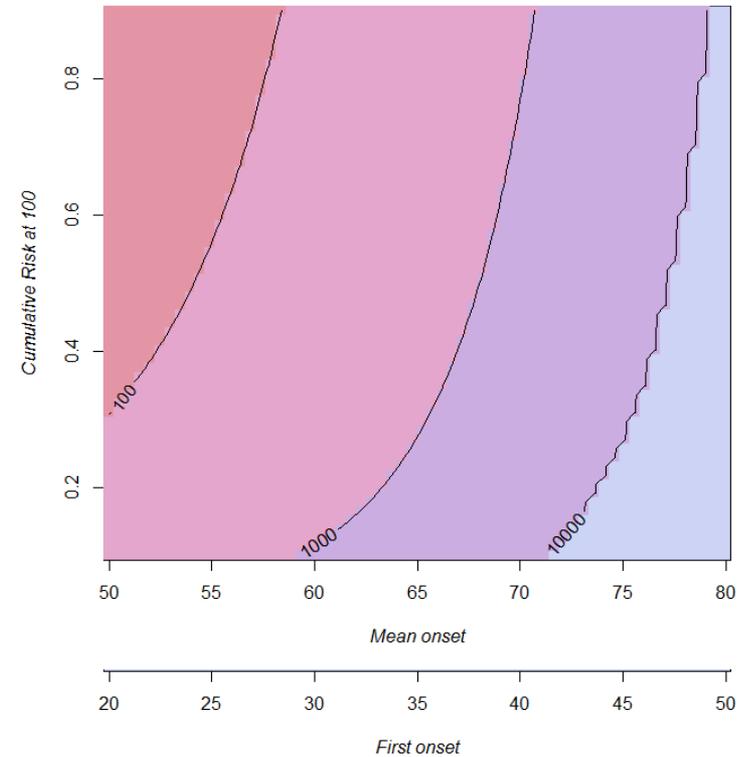
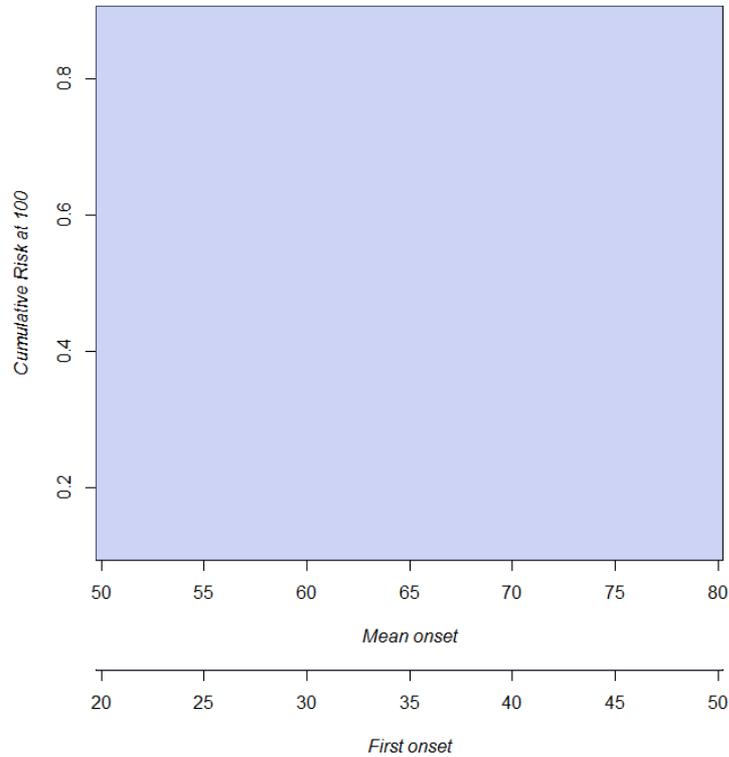
Paternal care

Grandmaternal care

Later age at first birth of men

Remarriage/polygamy

Conclusion

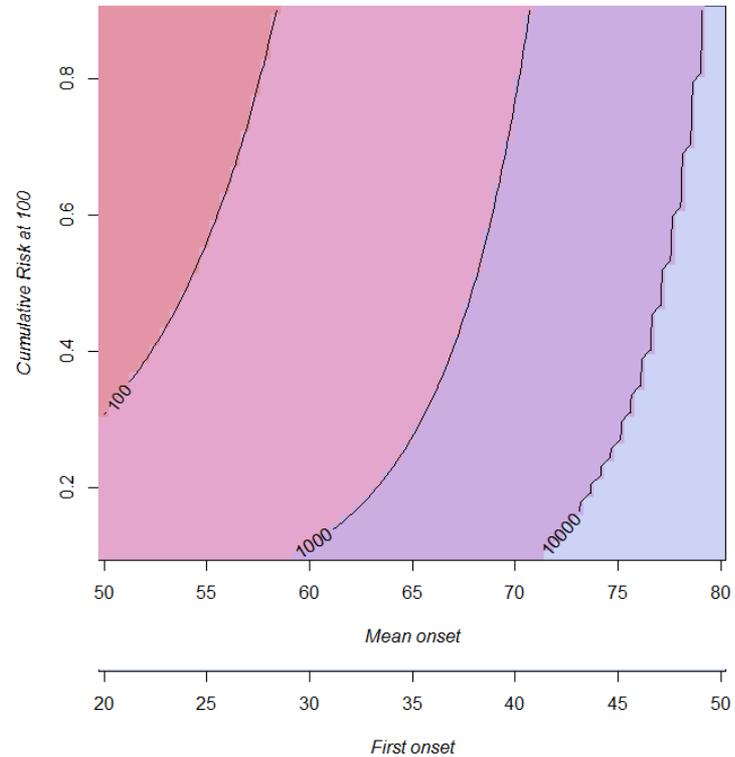
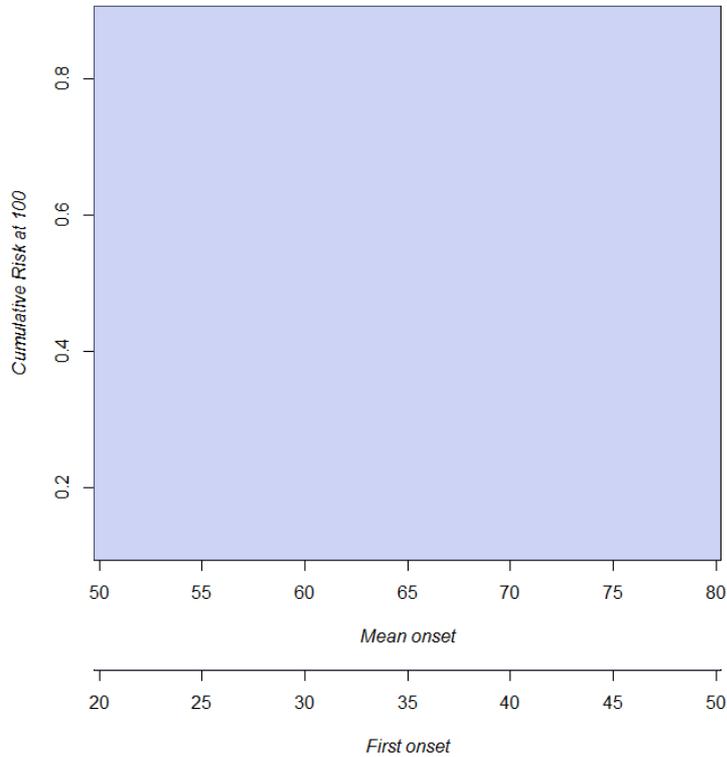


Negative selection at old ages is possible

➤ Physiopathology ► Epidemiologie

➤ Social - behavioural (care, matrimonial system) ► Demography

Conclusion



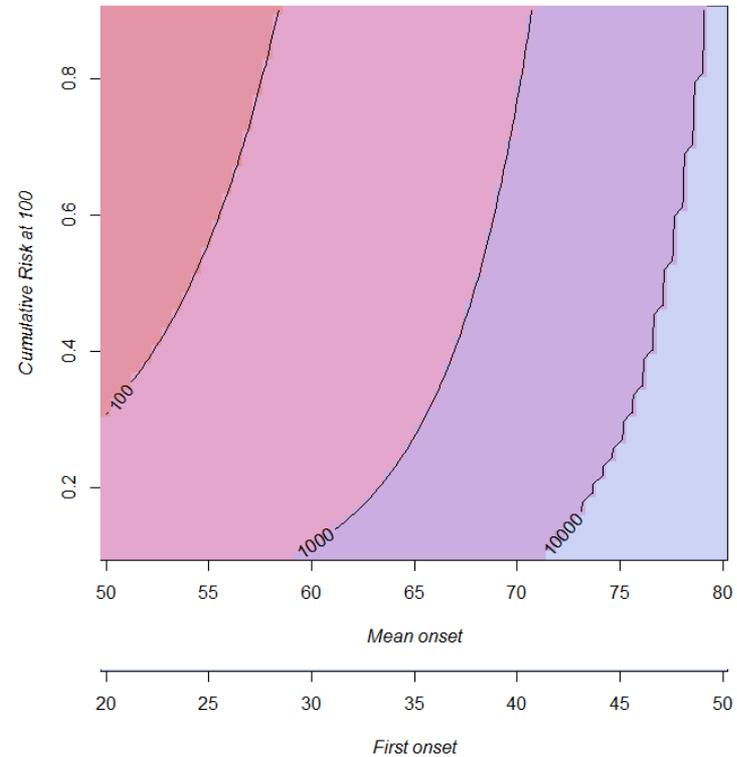
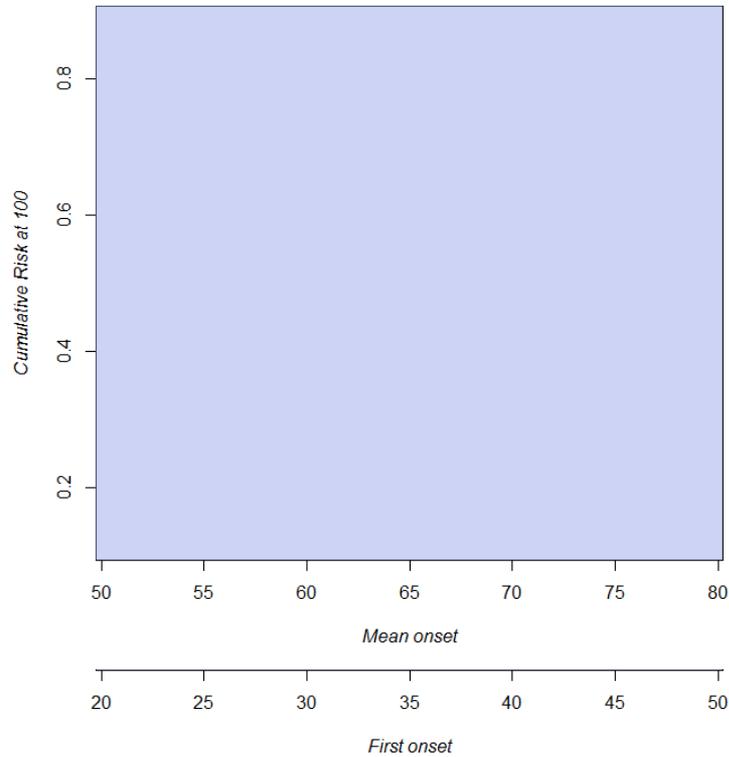
Negative selection at old ages is possible

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➤ Social - behavioural (care, matrimonial system) ► Demography

These factors are not independent: age at onset and care, matrimony and paternal care

Conclusion



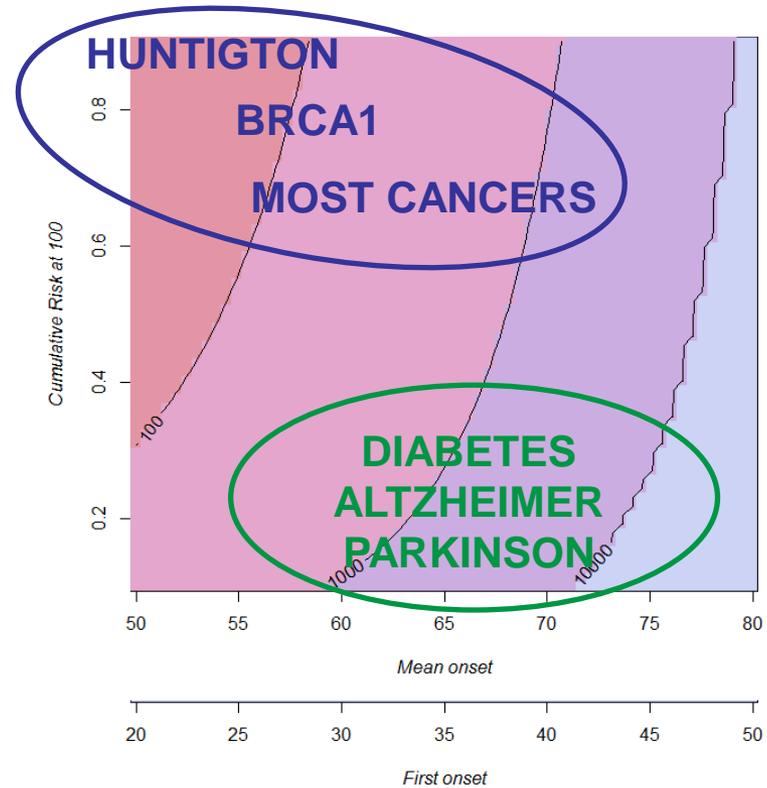
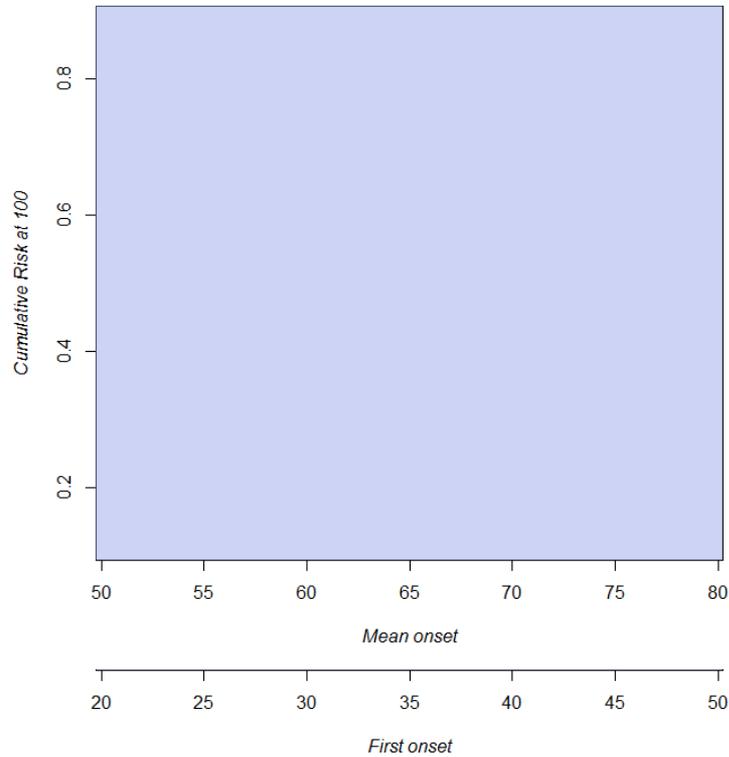
Negative selection at old ages is possible

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Purge of deleterious mutations even at old ages (eg 40-70 yrs old)

Conclusion



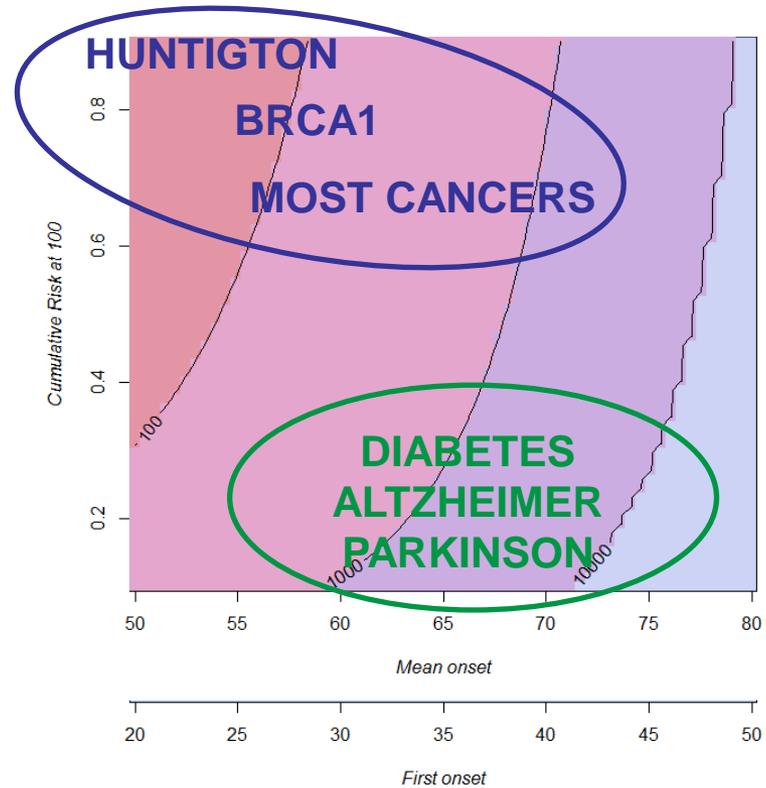
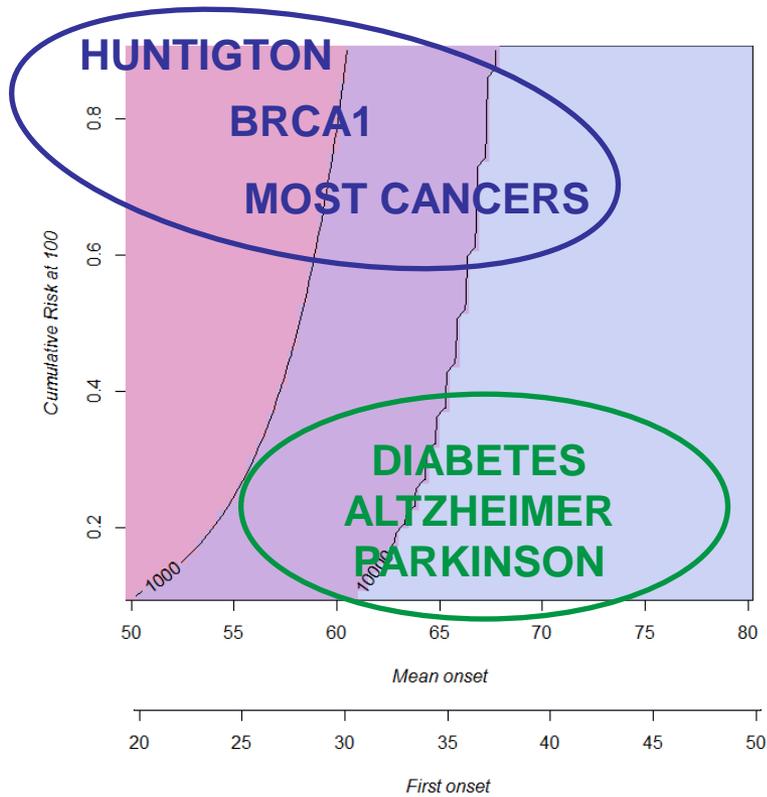
Negative selection at old ages is possible

➤ Physiopathology ► Epidemiologie

➤ Social - behavioural (care, matrimonial system) ► Demography

Possible predictions for couples gene-disease

Conclusion



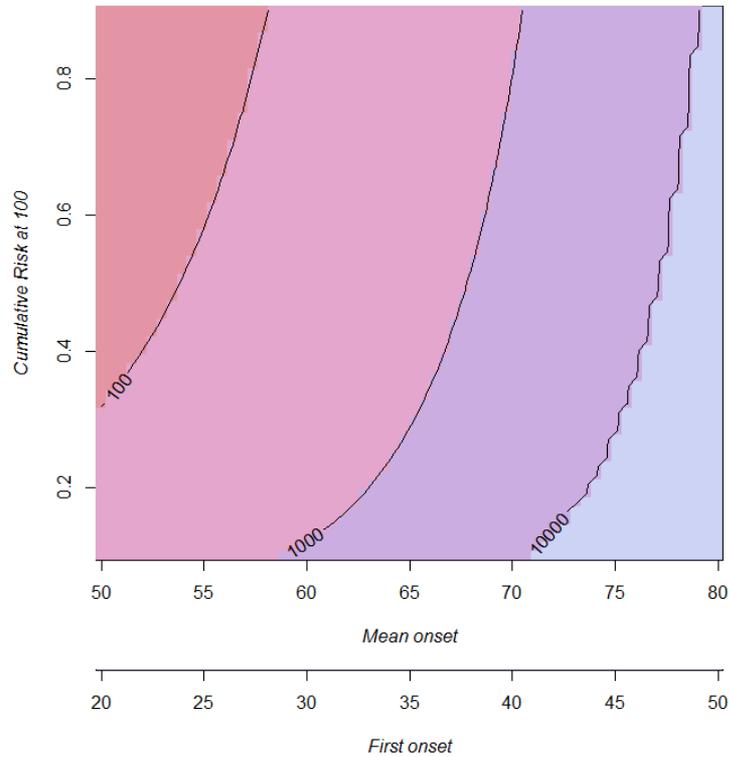
Negative selection at old ages is possible

➤ Physiopathology ► Epidemiologie

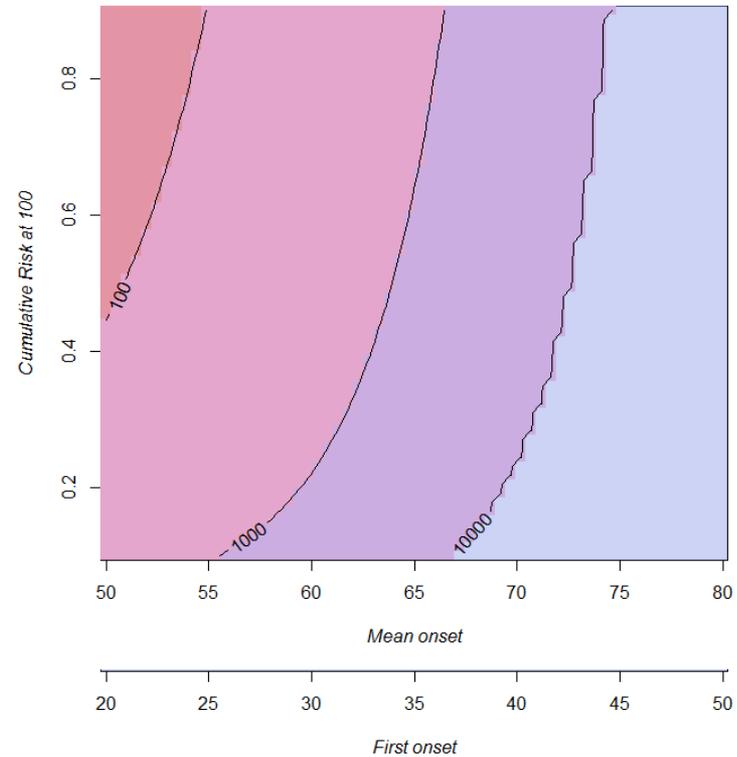
➤ Social - behavioural (care, matrimonial system) ► Demography

Differences are expected between population due to culture

Conclusion



High survival, High fertility



Low survival, Low fertility

But no large influence of **demographic regimes**

- ▶ a change in 20 yrs in e_{15} is pushing back the selection gradient of only ~3 yrs in mean onset

Conclusion

Effect of care on child survival but...

- Effect of paternal and maternal care of adult children survival and repro
- Effect of sibling care and/or competition

Population dynamics is the key. Going beyond stable environment:

$$\mathbf{n}_{t+1} = \mathbf{A}\mathbf{n}_t$$

$$\mathbf{n}_{t+1} = \mathbf{A}(t)\mathbf{n}_t$$

$$\mathbf{n}_{t+1} = \mathbf{A}(\mathbf{n}(t))\mathbf{n}_t$$

$$\mathbf{n}_{t+1} = \mathbf{A}(k)\mathbf{n}_t$$

$$\mathbf{n}_{t+1} = \mathbf{A}(\mathbf{w}, \mathbf{K})\mathbf{n}_t$$

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