Re-analyses of historical series of variety trials: lessons from the past and opportunities for the future

Genetic change over time

Breakdown in disease resistance

GEI and climate change

Genomic selection

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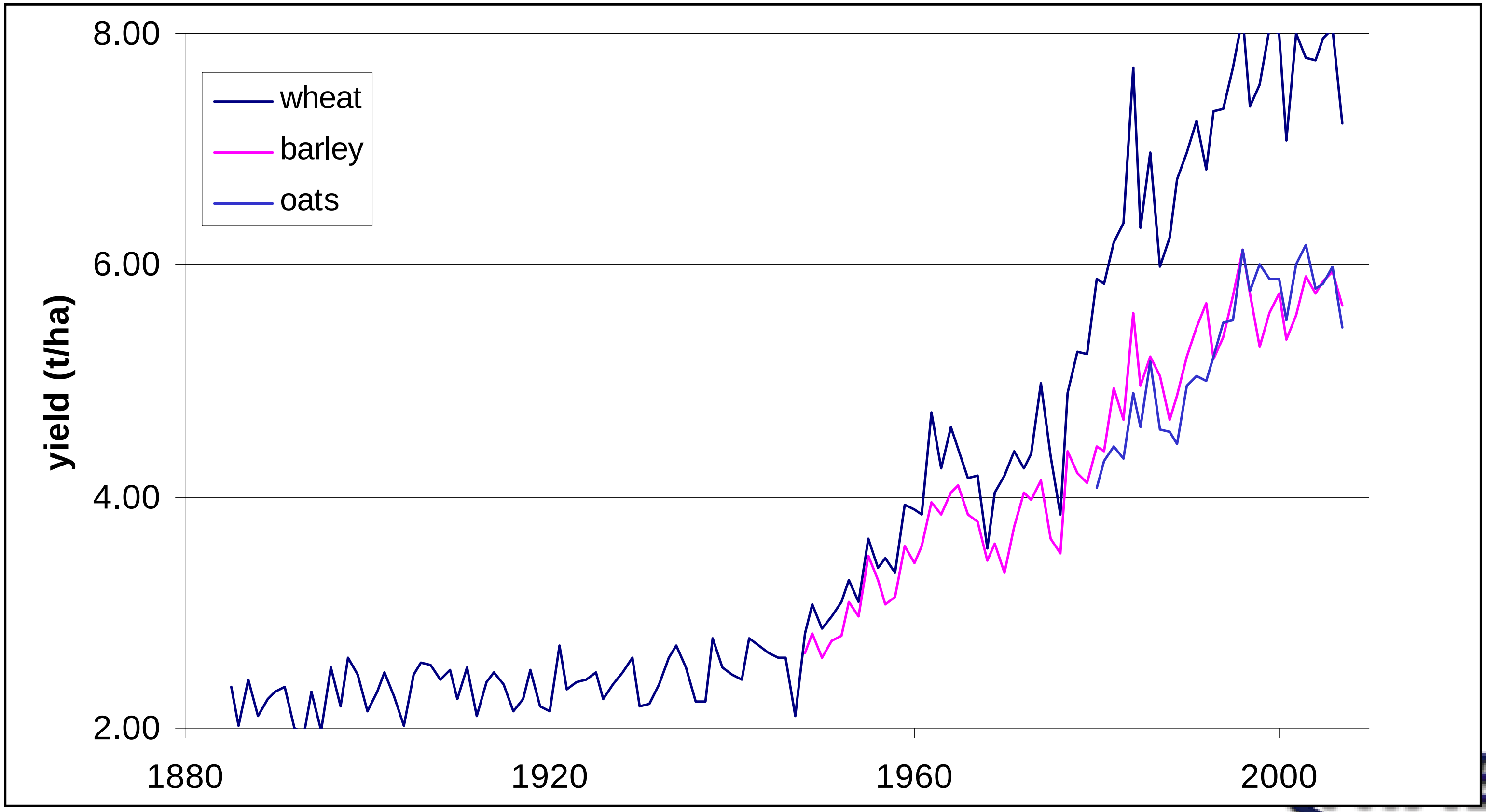
DEFRA statistics on national yields

Yields have increased ~3 fold in WW since 1948 as a result of improved varieties and agronomy.



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Re-analyses from 1948-2007

What proportion of yield increase is genetic?

Winter wheat

Spring barley

Winter barley

Oil seed rape

Forage Maize

Sugar beet

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Data are extensive

Total data points	52 909
No. varieties	308
No. years	60
minimum years per variety	3
Average life time	5.8
Trials	3 590
Trials x varieties missing data	95%

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Statistical analysis kept simple:

Fixed vars + years

Random vars.years + years.trials + vars.trials.years

No data for replicates within trials

No weighting of trials

No chronology (years fitted as a factor not as a covariate)

No linking of trials over years or analysis by region

Cannot simply treat varieties or years as random:

trends

relationships

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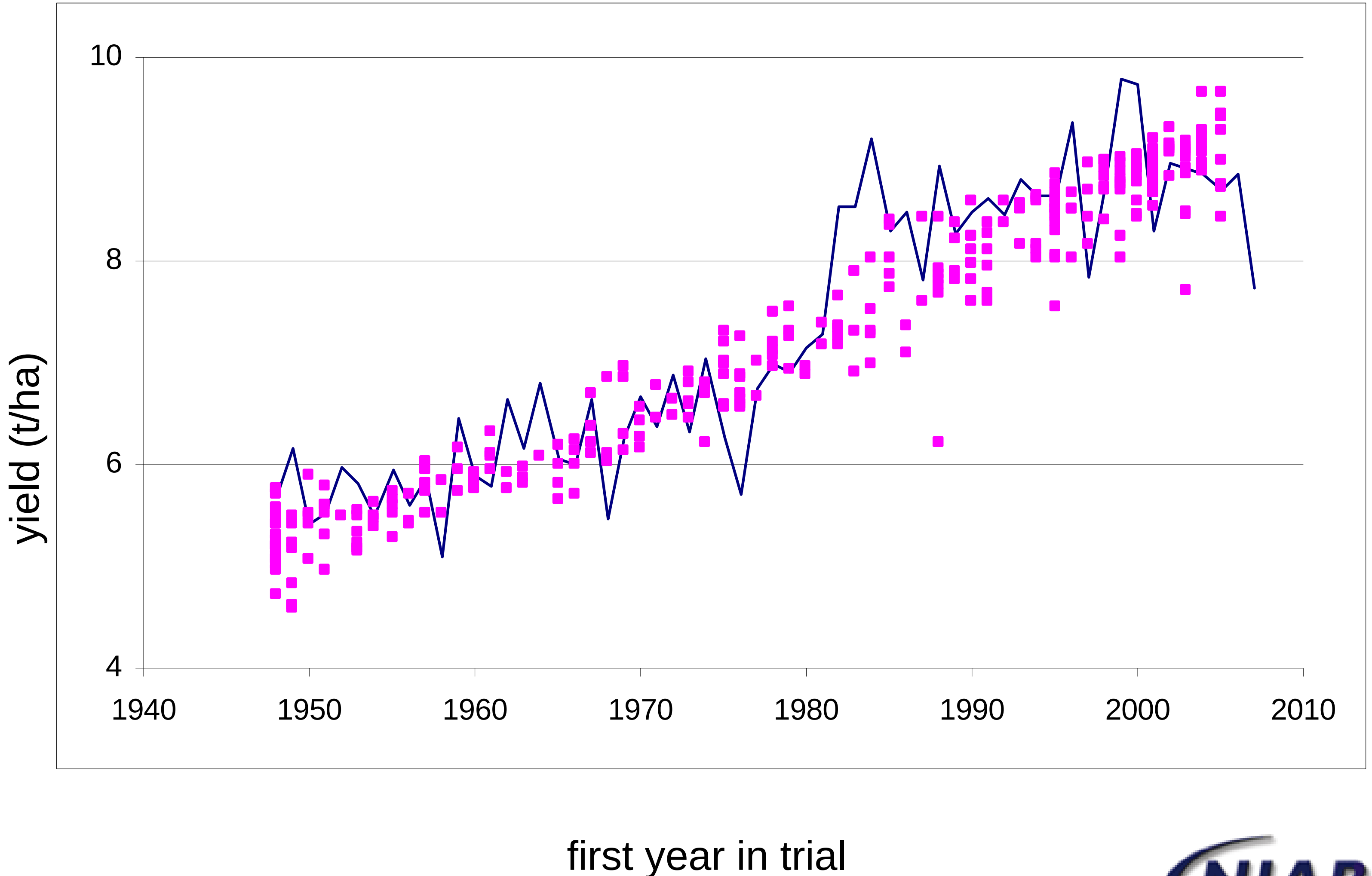
winter wheat



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Linear trends in yield

	G	E
1948 - 2007	0.071	0.069
1948 - 1981	0.061	0.041
1982 - 2007	0.074	0.010

Improvements in both agronomy and genetics brought about big improvements in yield for ~ 30 years from 1948.

However, for the last 25 years, yields have increased primarily from plant breeding alone.

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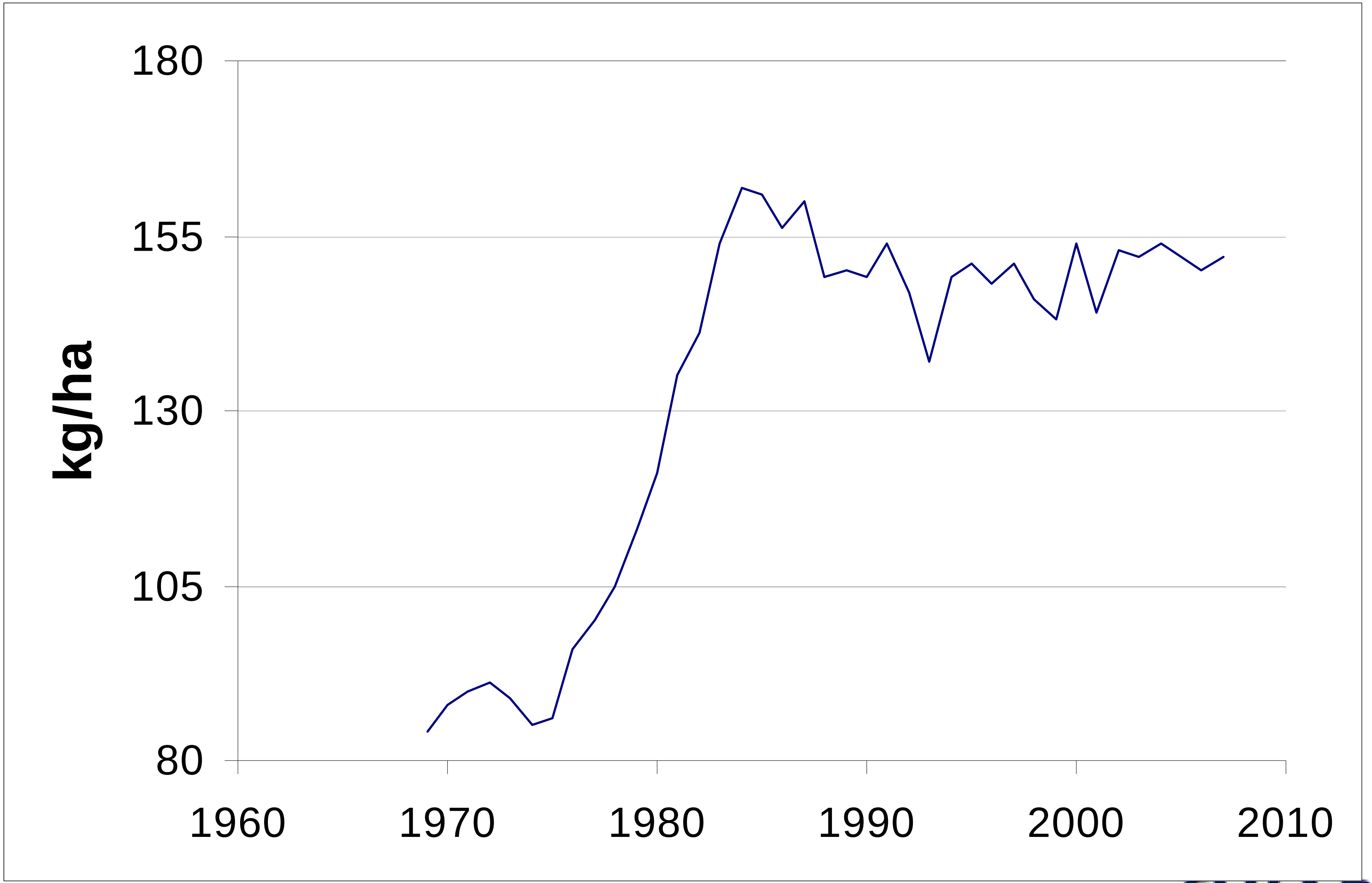
N use for tillage crops: England & Wales



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treated and untreated trials

Since 1982 trials have been conducted as two series:

Treated:	fungicide treated.
Untreated:	no fungicide.

Series analysed separately and results compared

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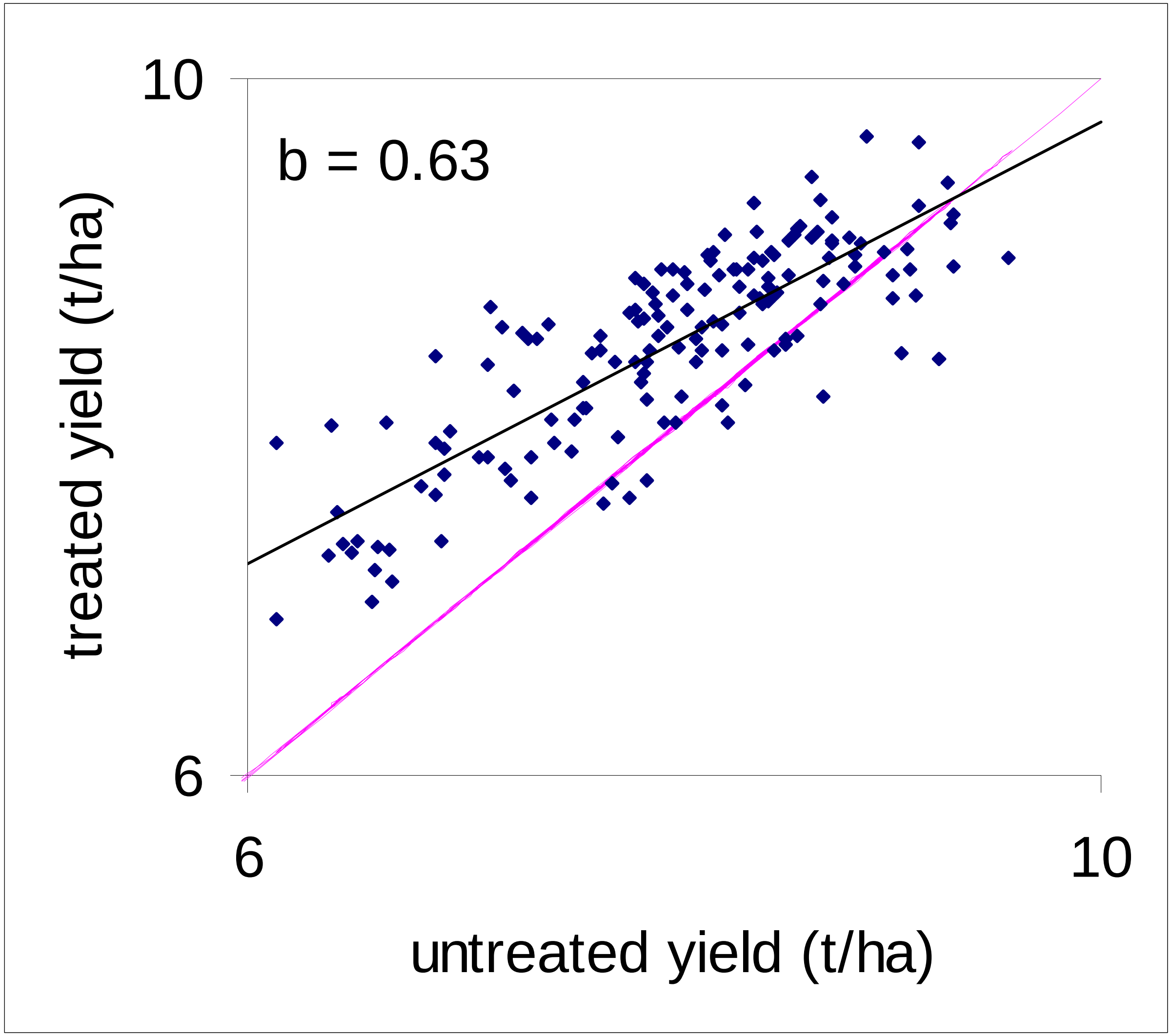
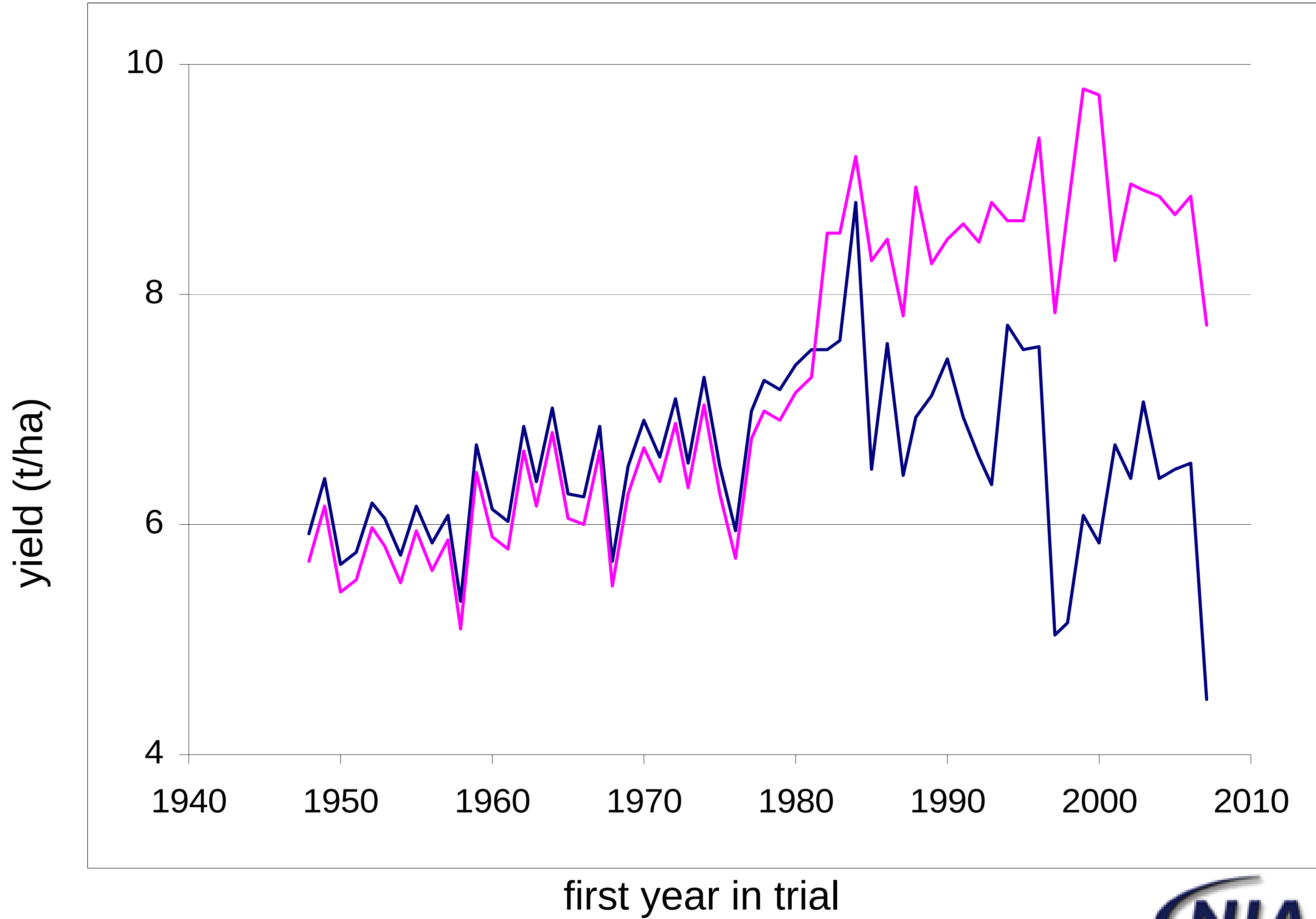
Genetic effects correlate between the two series:

(analysis 1982-2007 only)



but year effects diverge



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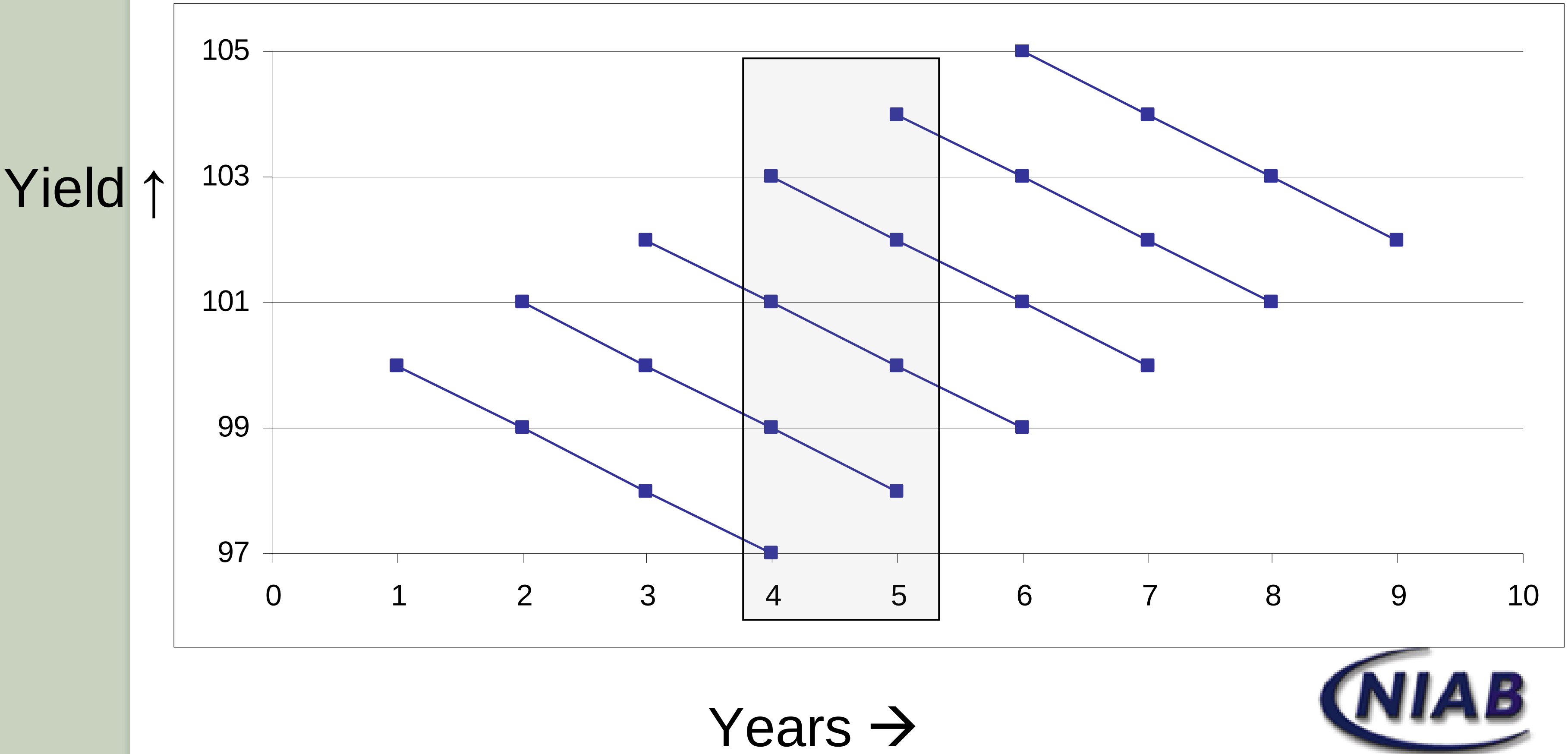
Can the apparent decline in the environment in untreated trials be explained by breakdown of disease resistance?

Simple model:
no years effect
yields increase while resistance breaks down.



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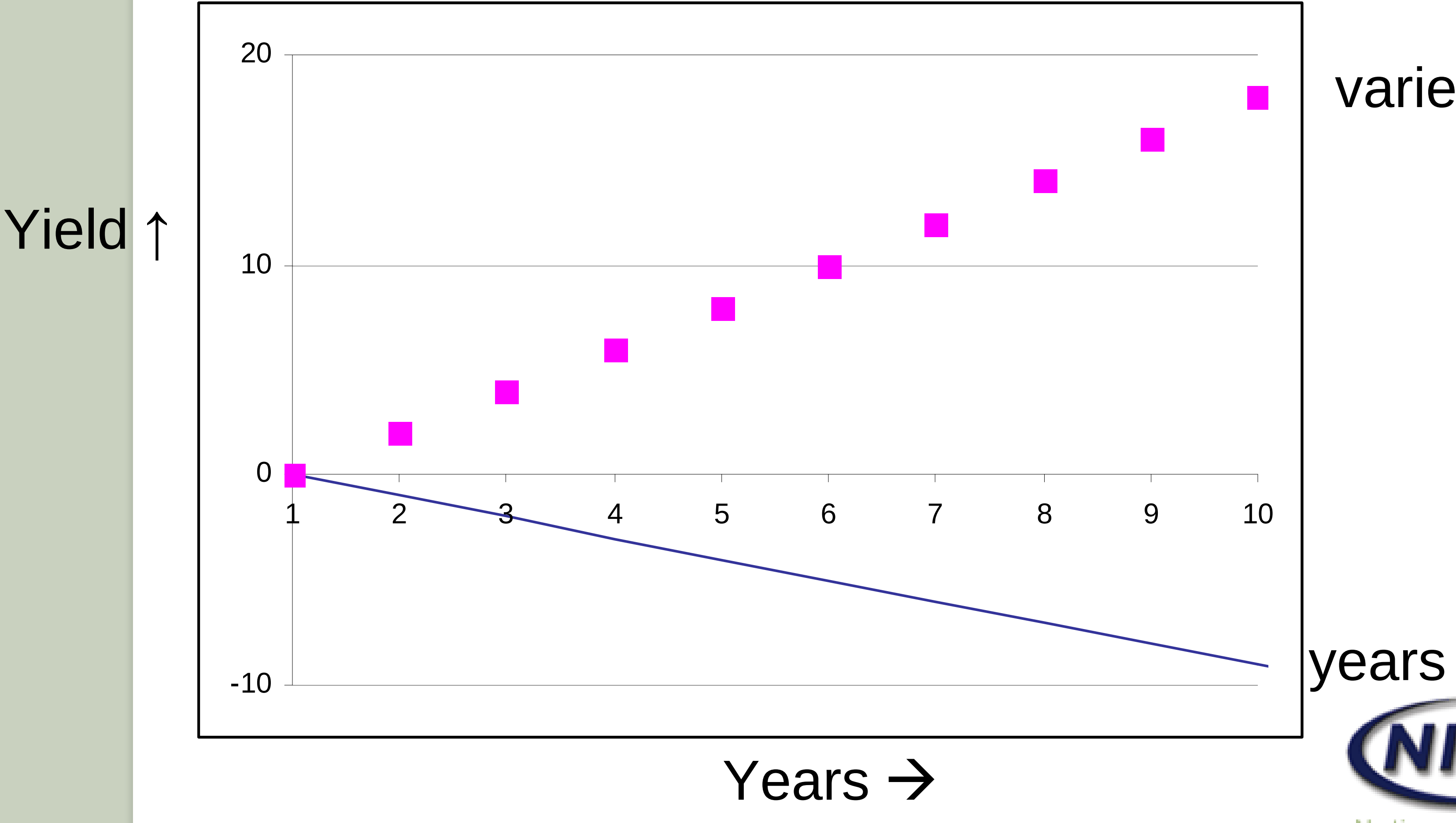
Estimated effects

Variety effect is overestimated but compensated by a progressive decline in the year effect.



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A matched set of T & U winter wheat trials.

748 paired trial locations (T and U)

Analyse differences in variety means at each paired site.

Common environment effects (inc. year) should cancel.

Estimate the effect of “trial year" on the difference.

Is there a progressive increase?

Fixed	varieties + trial year
Random	varieties.trial year + sites + error

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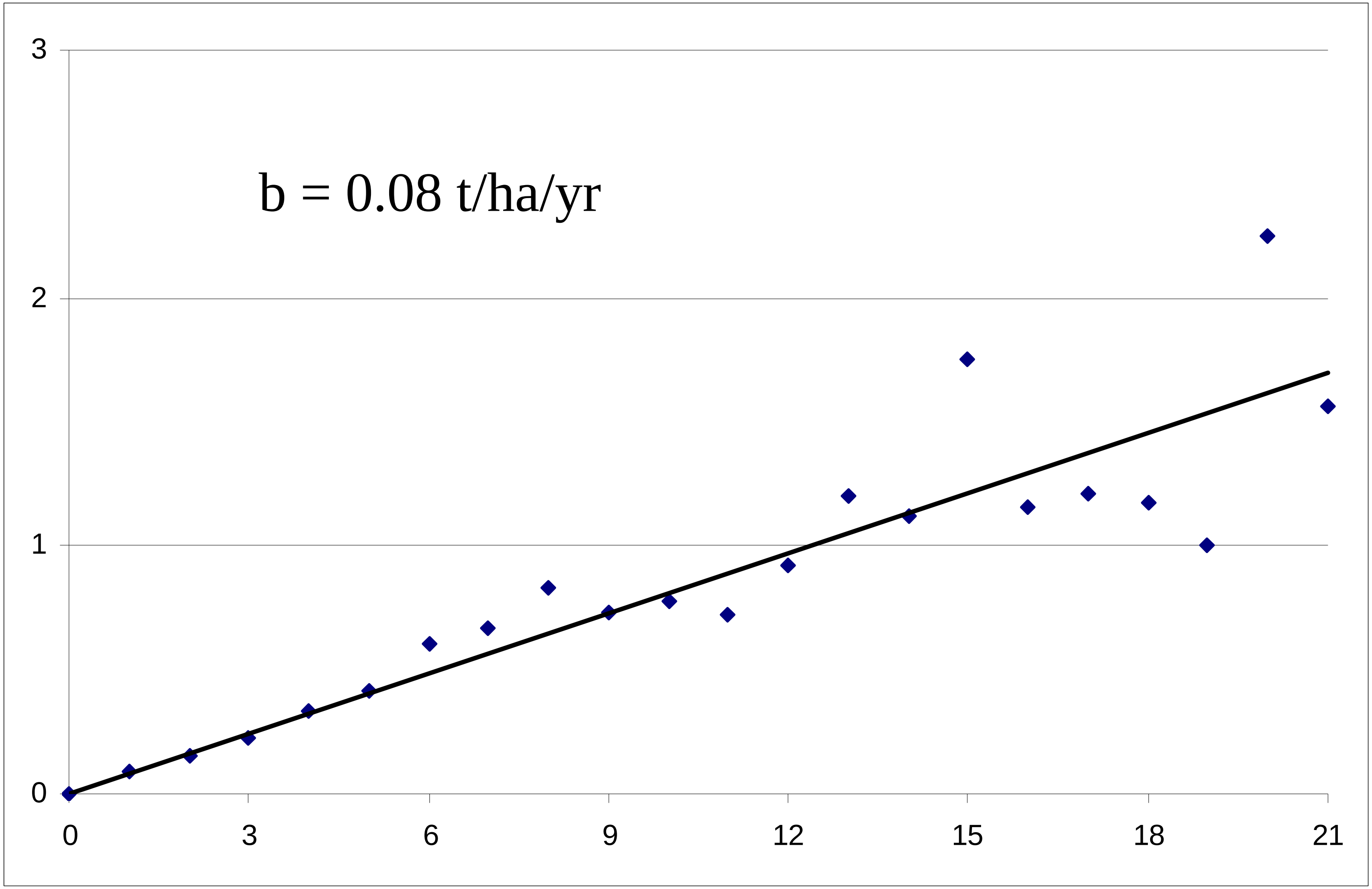
Estimated effect of trial year

T-U ↑

effect



Years in trial →

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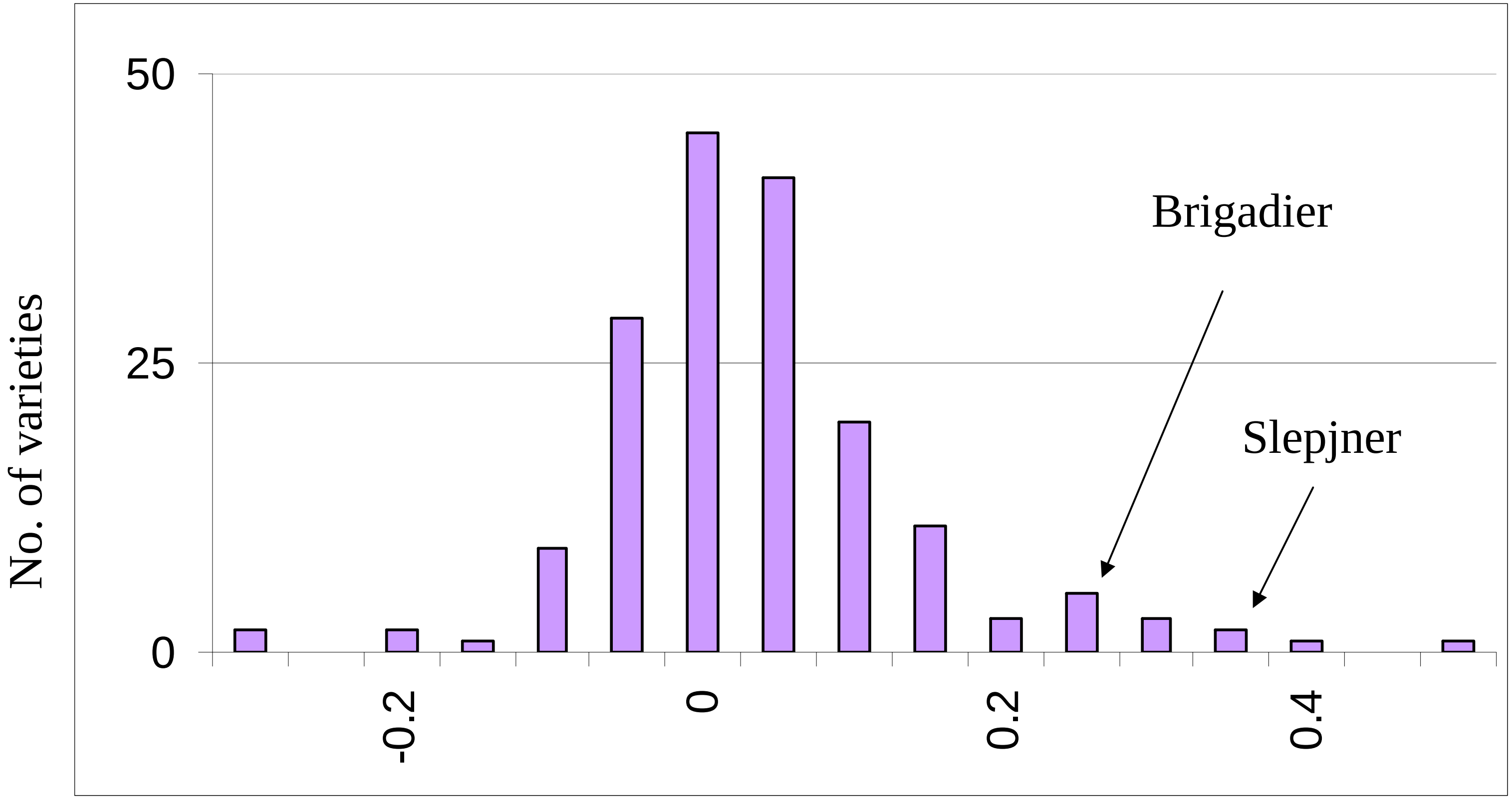
vars.trial year regressed on trial year

distribution of regression coefficients



Regression coefficient of T-U on years in trial

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GEI and climate

WW 1982- 2007 treated trials

8 climatic variables from the UK met office:

Central England av temp	Aut, Wint, Spr, Sum
England and Wales rainfall	Aut, Wint, Spr, Sum

Correlate var x years effects with climate

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Number of varieties with q-value <0.5

	Autumn	Winter	Spring	Summer
Rain	0	0	1	26
Temp	0	27	8	26

Greatest sensitivity is:

cold & wet summers

wet winters

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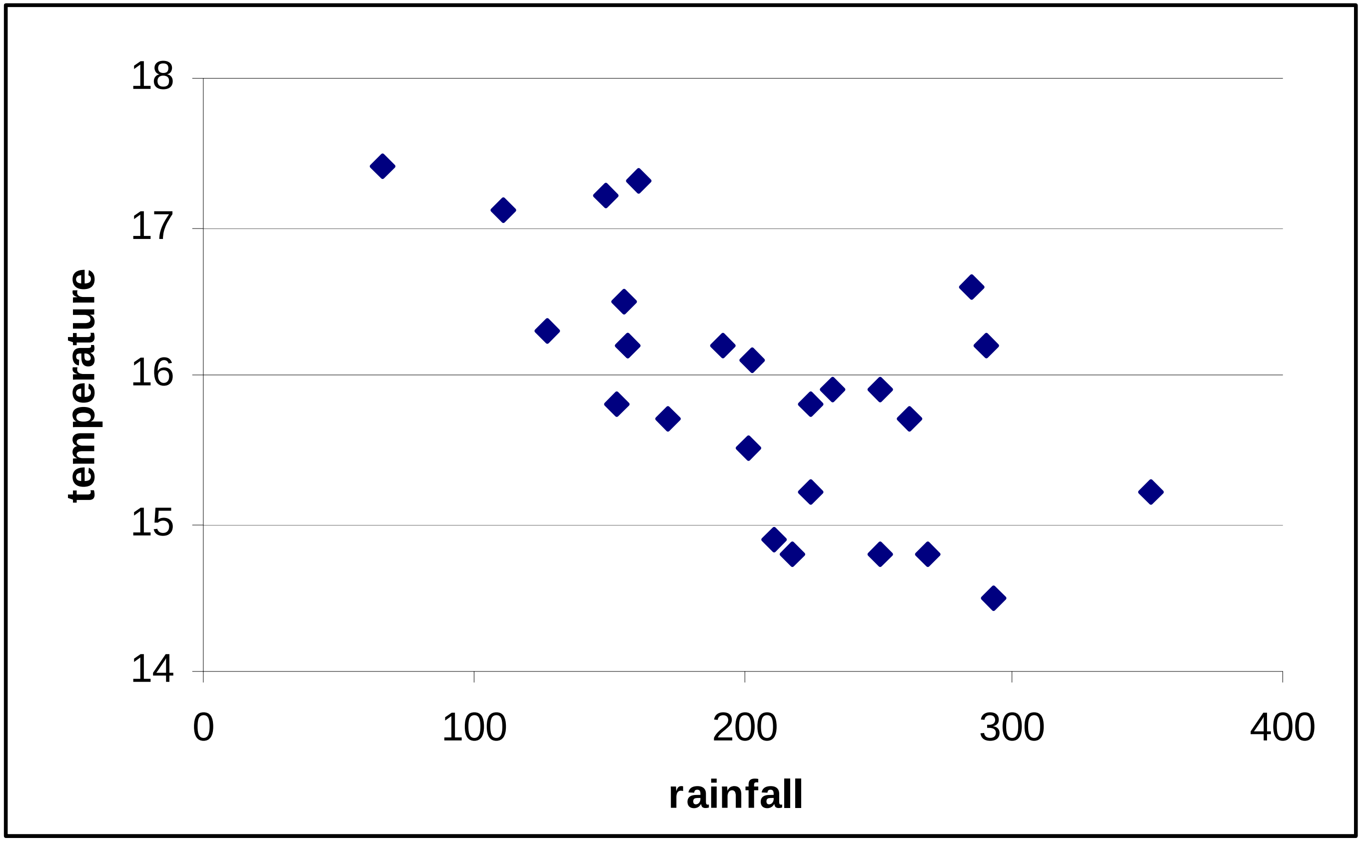
Wet summers are cold



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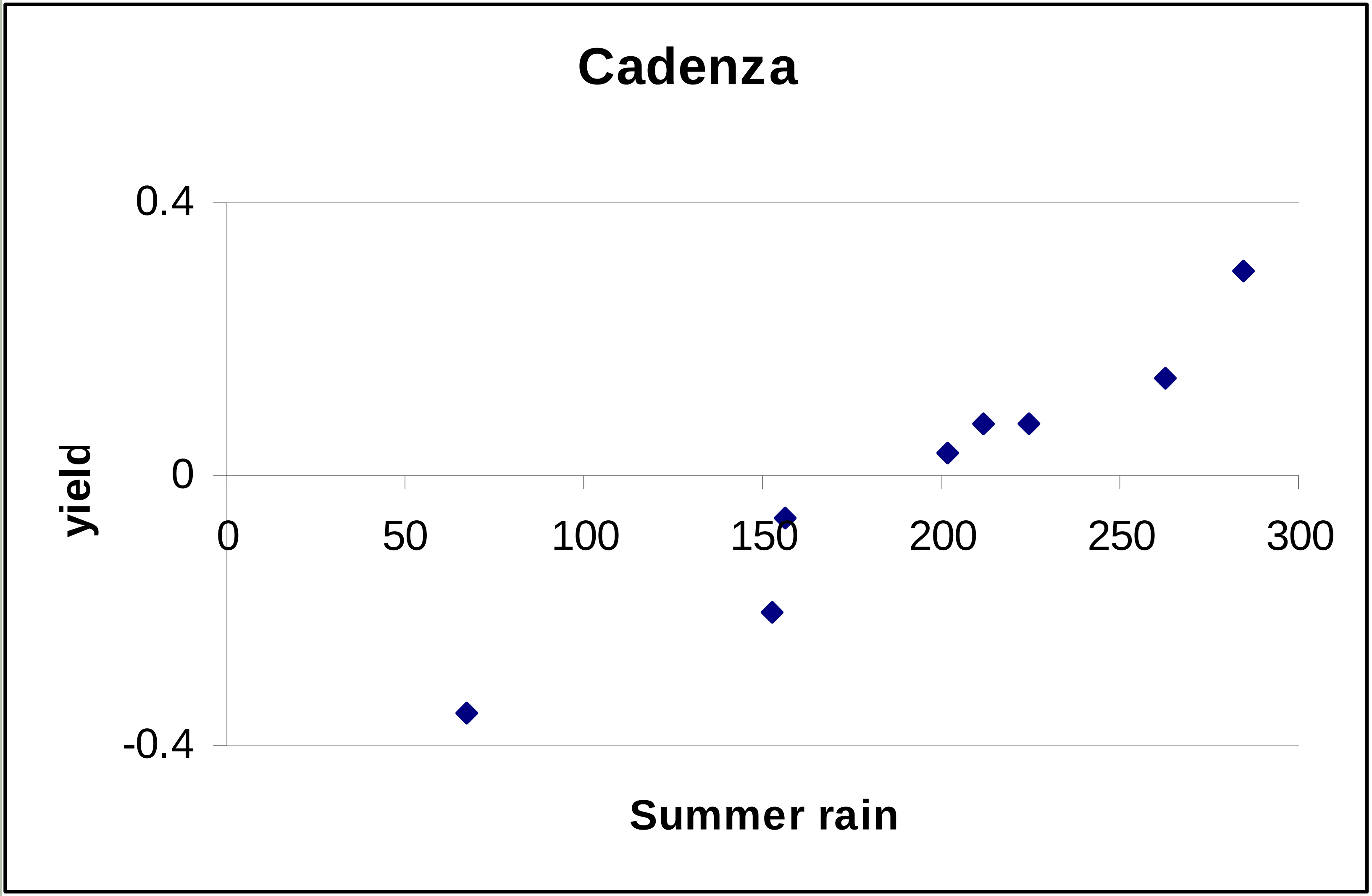

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Genomic selection in Winter wheat

159 varieties:1949 - 2004

217 mapped DArT markers

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Method

Split data into a training set and a test set:

a) uniformly w.r.t. age

b) on age

Regress yield on all markers in the training set.

More markers than varieties: use ridge regression (easy)

Predict yield in the test set.

Compare observed and predicted

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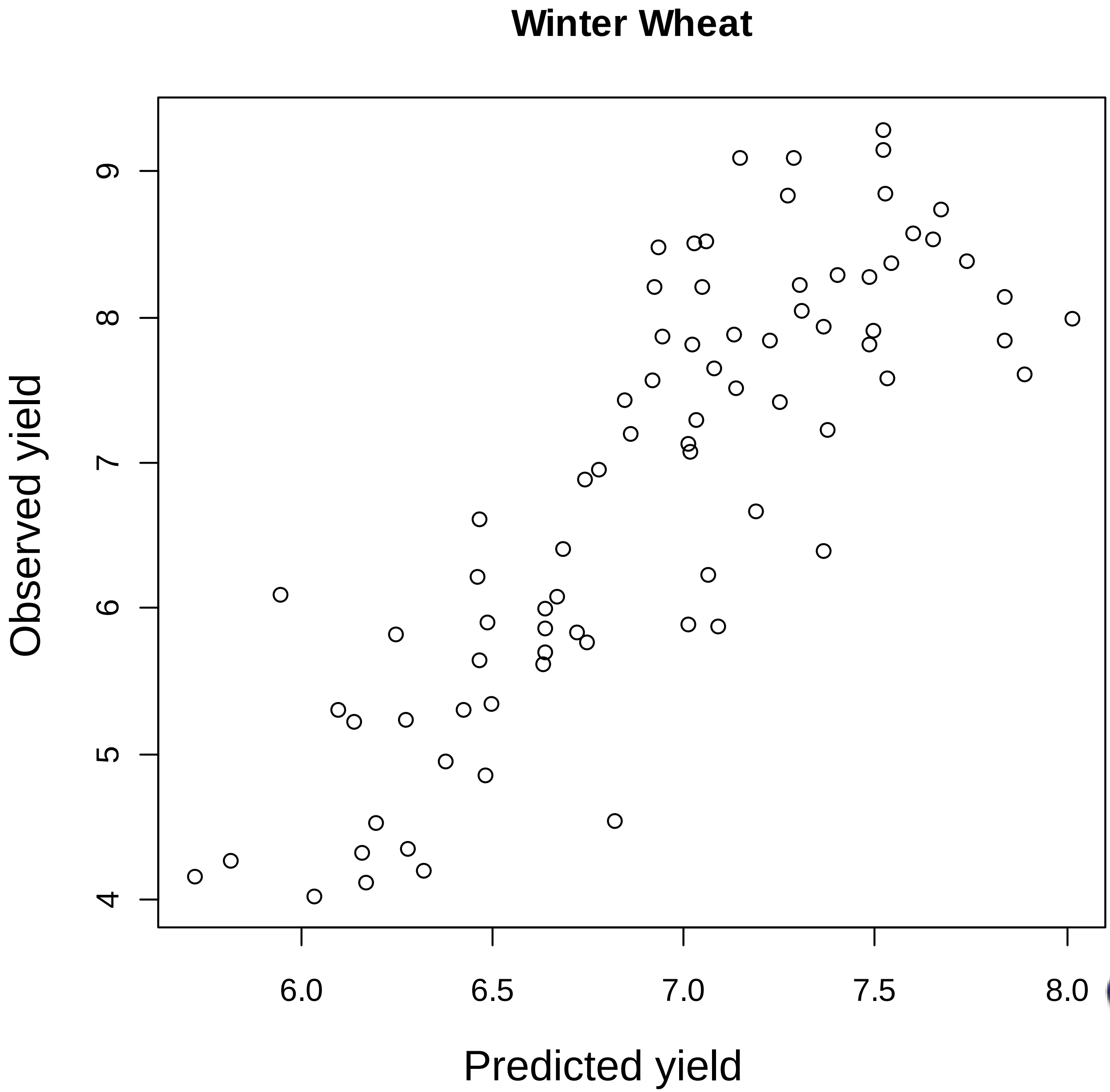
WW uniform split

r = 0.83



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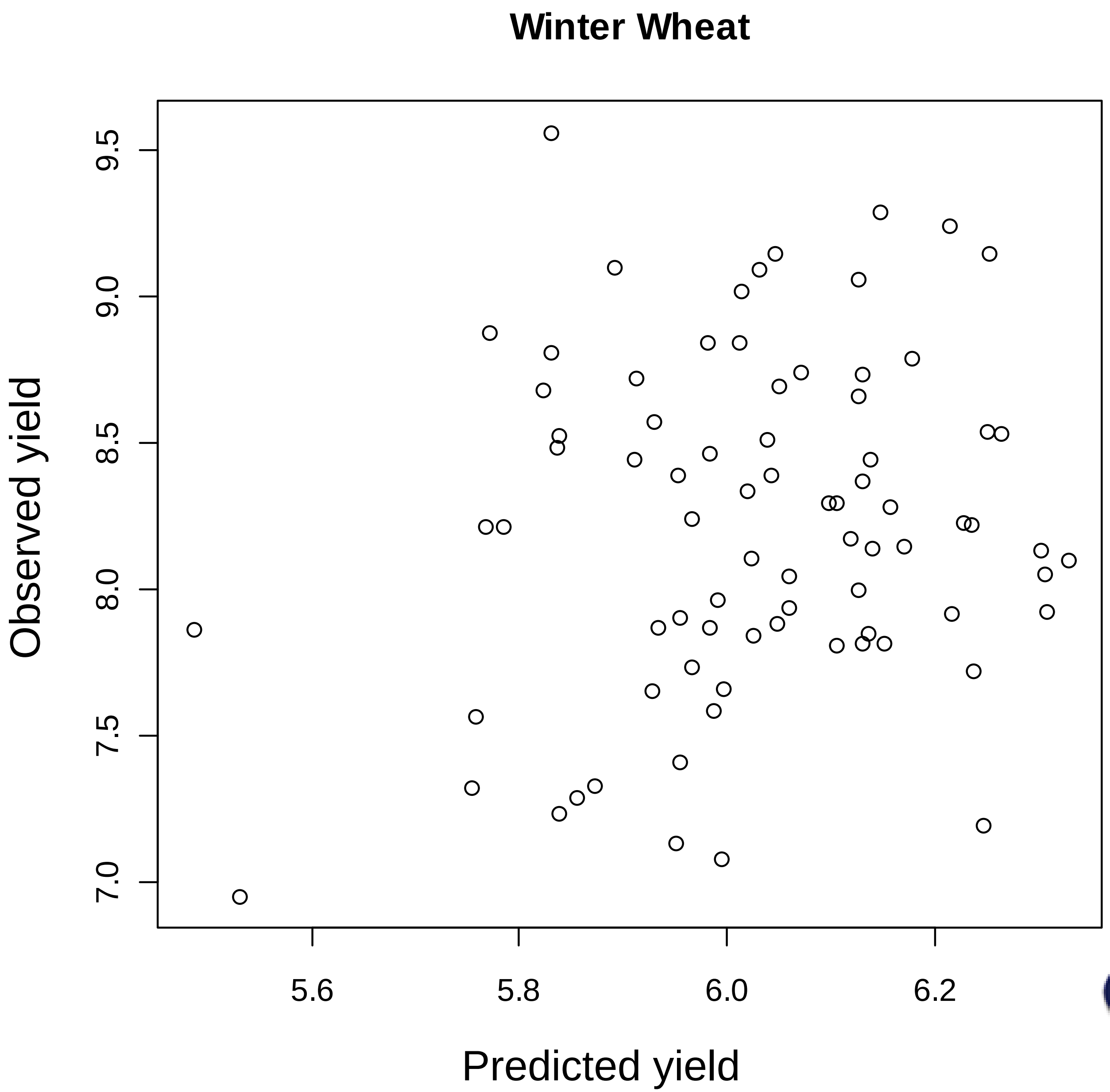
WW split on age

r = 0.17



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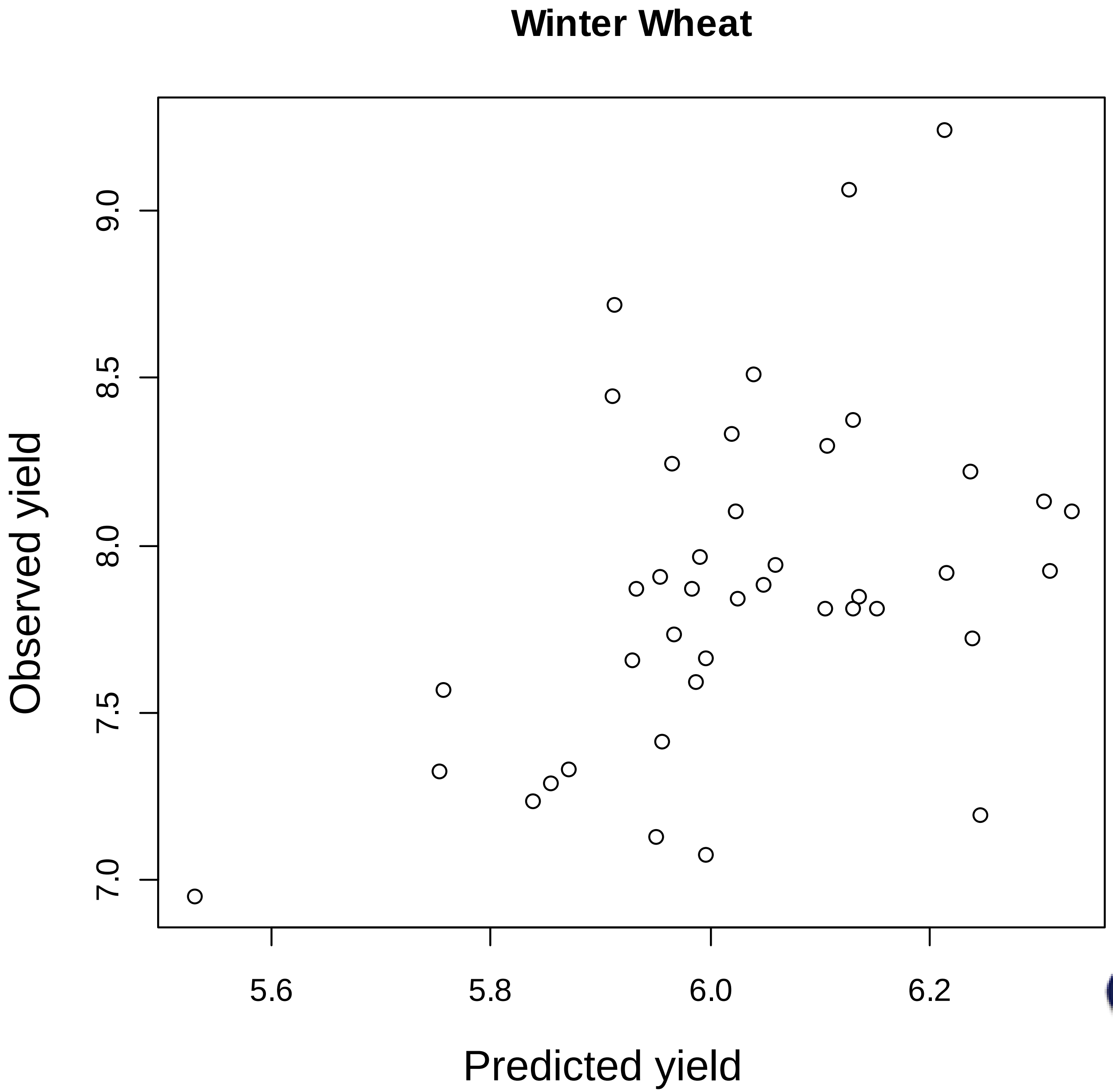
WW split on age – 10 years only

r = 0.44



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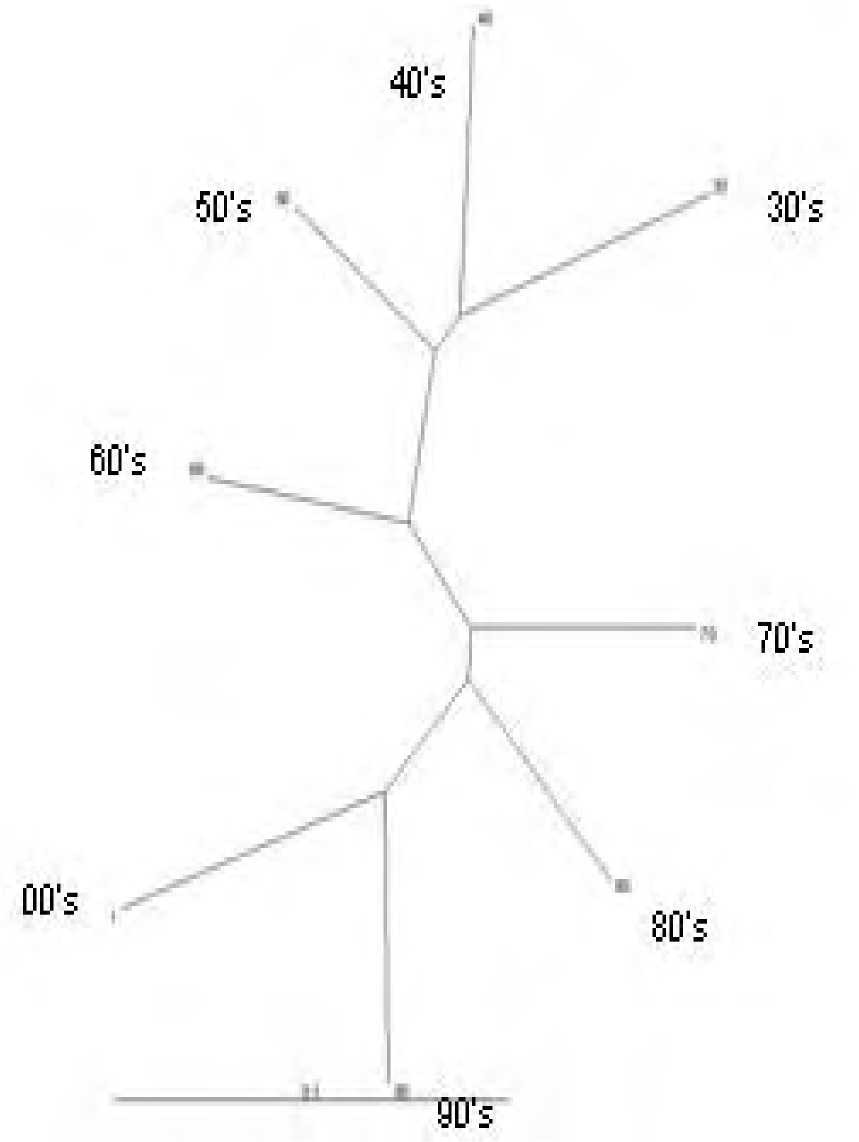
Changes in marker genotypes over time (UK)



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Results

Can predict yield

but correlation not great when predicting forward in time

predicting on kinship

Breeders already predict on kinship

cross the best with the best

Historical datasets are suitable to test methods

but mustn't get carried away by positive results.

Require experimental populations too

MAGIC

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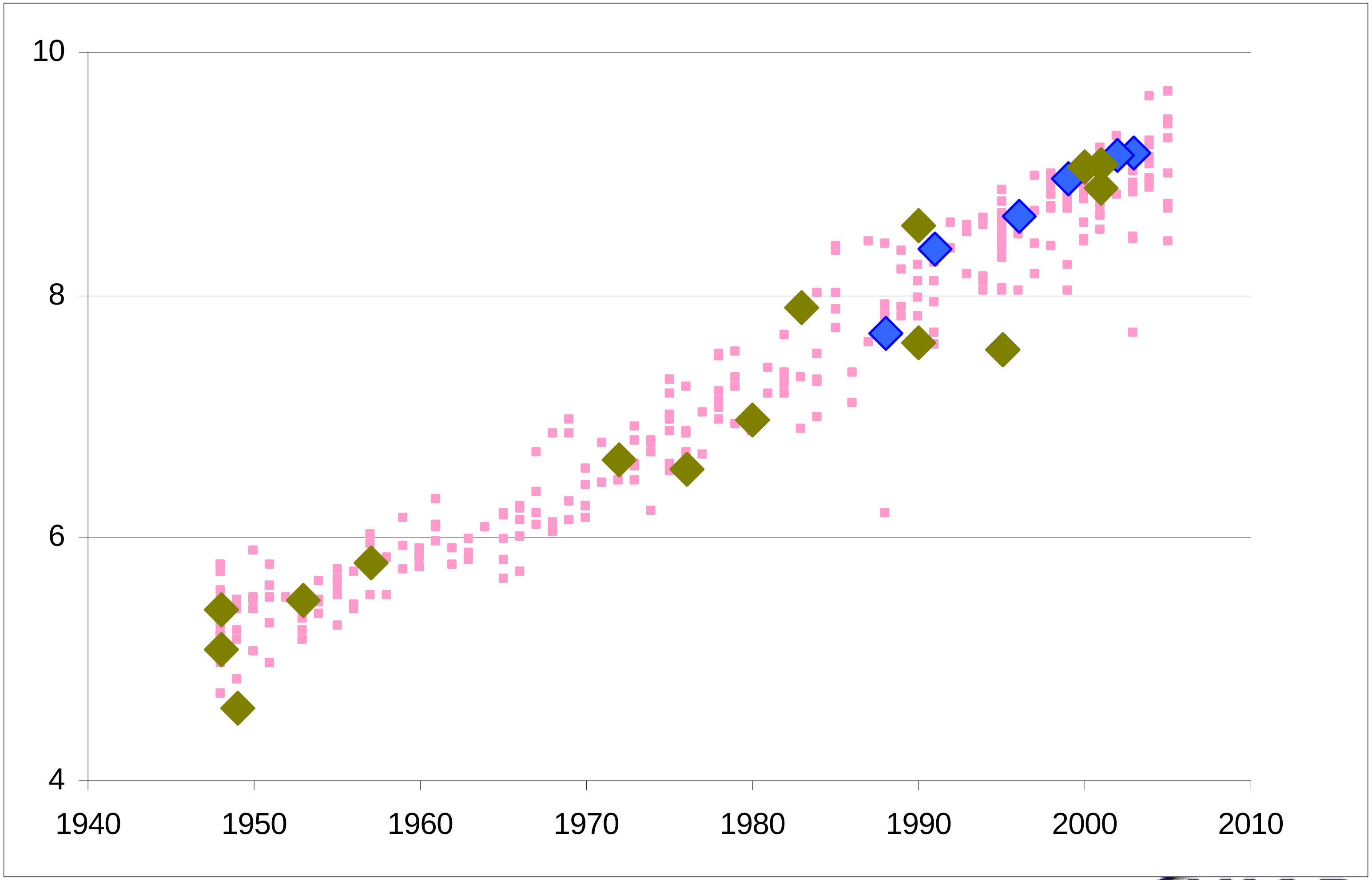
Founders of WW MAGIC populations



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Conclusion

There is more to historical datasets than just a source of free phenotypes for association mapping.

"Retrospective analysis of genetic gain and variance can be useful in designing strategies to manage genetic variation for target traits in breeding programs." Condóna et al *Crop Sci* 2009

Strength will come from exploiting links with experimental populations.

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Acknowledgements

NIAB

Jon White

Nick Gosman

Andy Greenland

Richard Hornsell

Andy Horwell

Phil Howell

Haidee Philpott

Claire Pumfrey

Others

David Balding	UCL / IC
Peter Craufurd	UoR
Tim Wheeler	UoR
Bill Thomas	SCRI
Eric Ober	BB