Optimization of breeding schemes with GS in R

Friedrich Longin

State Plant Breeding Institute, University of Hohenheim, Stuttgart, Germany;
https://lsa-weizen.uni-hohenheim.de

University of Hohenheim, Stuttgart

- **3 faculties**
  - 1 – life sciences (biology, physics, biotechnology, food production and ingredients); ~ 14 institutes
  - 2 – agriculture (breeding, quantitative genetics, molecular genetics, agronomy, plant health, agroeconomics, animal sciences,…); ~ 15 institutes
  - 3 – Economy (management, economics, law, social sciences…); ~ 8 institutes
- ~ **4000 students** per year, all B.Sc. and M.Sc.

  Master of crop science (english)
- **4 state institutes** incorporated into the University
- **Experimental station** for agriculture

Excellence Unit in Plant Breeding

Institute of Plant Breeding, Seed Science and Population Genetics

Subject Areas:

Applied Genetics and Plant Breeding
Prof. Dr. Albrecht E. Melchinger

Quantitative Genetics and Genomics

Prof. Dr. Scholten

Crop Biodiversity and Breeding Informatics

Prof Dr. Karl Schmid

Seed Science and Technology
Prof. Dr. Michael Kruse

State Plant Breeding Institute

Head: PD Dr. Tobias Würschum

Research groups:

Biotechnology and Mapping Strategies
Dr. Wilmar Leiser

Rye and Biotic Stress Resistance
Prof. Dr. Thomas Miedaner

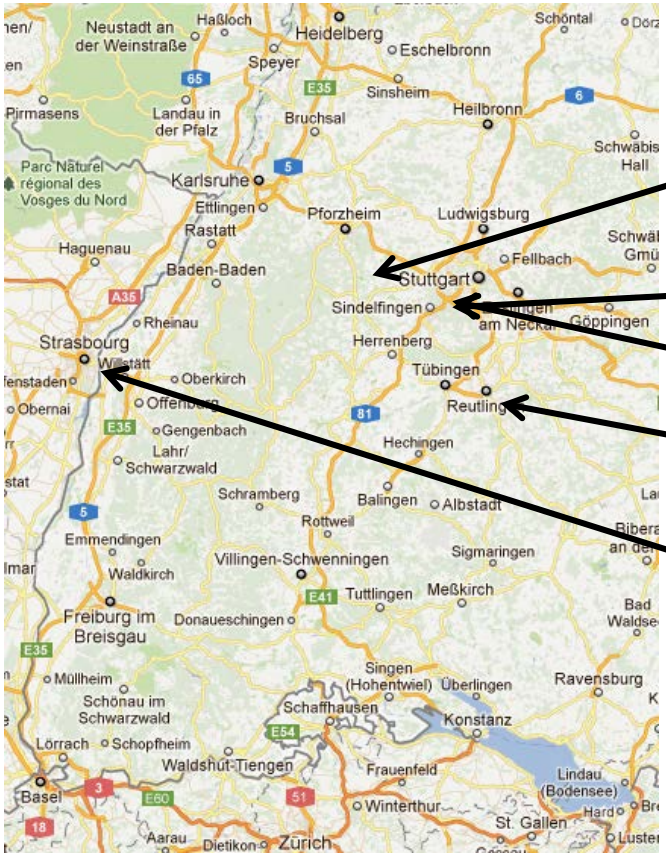
Triticale and Breeding Methodology
Dr. Hans P. Maurer

Wheat Breeding and Selection Theory
PD Dr. Friedrich Longin

Sunflower and Soybean Breeding
Dr. Volker Hahn

Experimental Station

Experimental stations



Ihinger Hof

Heidfeldhof/Hohenheim

Kleinhohenheim/organic

Lindenhöfe

Eckartsweier

Five **experimental stations** ensure **high-quality phenotyping**

which is the basis for breeding and science

State Plant Breeding Institute (LSA)

- Six **scientists** with **broad** range of **expertise,**
- PhD and PostDocs (from agronomy, bioinformatics, mathematics)
- Experienced **technical staff** (>20) with phenotyping facilities, green houses, climate chambers, biotechlab,…
- ~ 20 peer-reviewed **publications** per year in leading international journals
- ~ 1.800.000€ extramural **grants** per year
- **Cooperations** with leading international **agricultural research centers** (*e.g.* CAAS, CIMMYT, INRA, ACPFG, NIAB)

Breeding activities at the LSA

Einkorn

Emmer

Spelt

Durum

Wheat

Rye

Triticale

Soybean

Sunflower

LSA has competitive breeding programs

Wheat group - aims

- Elite **breeding in rare wheat species**

- **Breeding programs in T. aestivum**
  - Pre-Breeding for grain yield: aim to deliver material to community for elite breeding starts
  - Breeding hybrid male parents: aim to deliver elite males to community

- **Research accompanying** these efforts
  - Genetic architecture of regarded traits
  - Optimized breeding schemes

Wheat group

- 1 scientist – Dr. F. Longin
- **7 technicians**
- 2 PostDocs, 1 PhDs, studen
- ~ 8 ha of nurseries
- > 25 different field locations
- Special nurseries for stress - **FHB**, virus, frost
- **Quality lab** for b- value, sds, falling, GI, protein content, vitreousness and dark points
- Machinery for threshing and dehulling

https://lsa-weizen.uni-hohenheim.de/

You are a breeder

- Congratulations → **fantastic job!**
- A breeder is the **head of product development**
  - You must be **innovative**
  - You must be able to **rapidly take decisions**
  - You must **define the strategies**
  - You must have **success**
  - You are **responsible for whole product chain**

You have to decide = you‘re responsible

- Marketing tells you your **specific framework**

? Strategies ?

You have to decide = you‘re responsible

- Marketing tells you your **specific framework**

? Strategies ?

Which breeding scheme ?

Which quality lab analyses ?

Molecular markers ?

Trial management ?

Priorisation of traits ?

Orga of phenotyping ?

Disease management ?

...

You have to decide = you‘re responsible

- Marketing tells you your **specific framework**

? Strategies ?

Which breeding scheme ?

Which quality lab analyses ?

Molecular markers ?

Trial management ?

Priorisation of traits ?

Orga of phenotyping ?

Disease management ?

...

Other lectures

Let‘s start – what we will do

- Introduction: Breeding categories → focus line breeding
- Theorectical background of selection gain package: formula of selection gain
- Variables influencing the selection gain
  - Important existing results
  - Realization in R package
- GS breeding schemes
  - Important results
  - Realization in R package
- Run your own first simulations

Breeding categories

- Line breeding

Wheat

- Hybrid breeding

Maize

- Clone breeding

Potato

- Population breeding

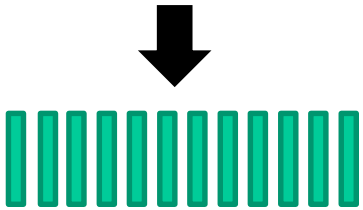
Rye

Source: Wikimedia

Line breeding based on per se performance

Line breeding

New breeding lines from DH, ssd,…



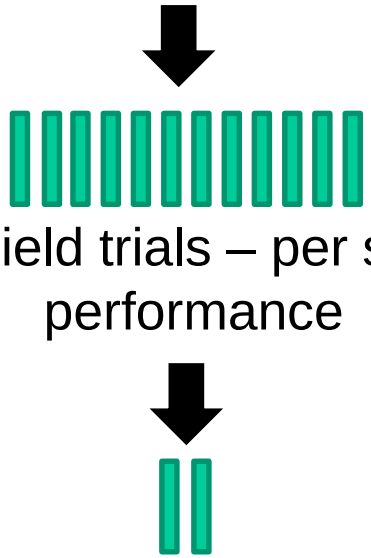
Field trials – per se performance

New line varieties

Hybrid breeding based on GCA

Line breeding

New breeding lines from DH, ssd,…



Field trials – per se performance

New line varieties

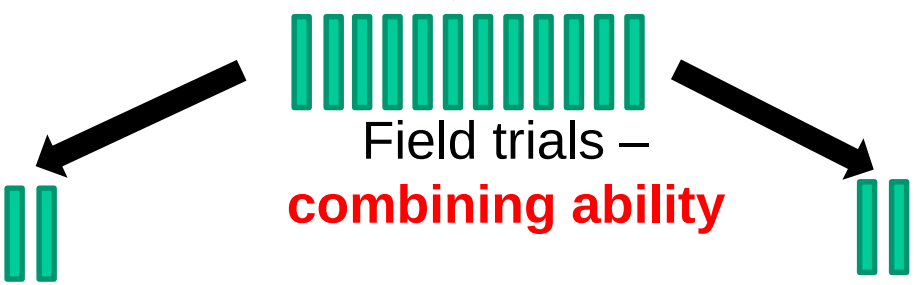
Hybrid breeding

New breeding lines in heterotic group 1

New breeding lines in heterotic group 2

GCA-Tester

GCA- Tester



Field trials – **combining ability**

New lines for hybrid production in heterotic group 1

New lines for hybrid production in heterotic group 2

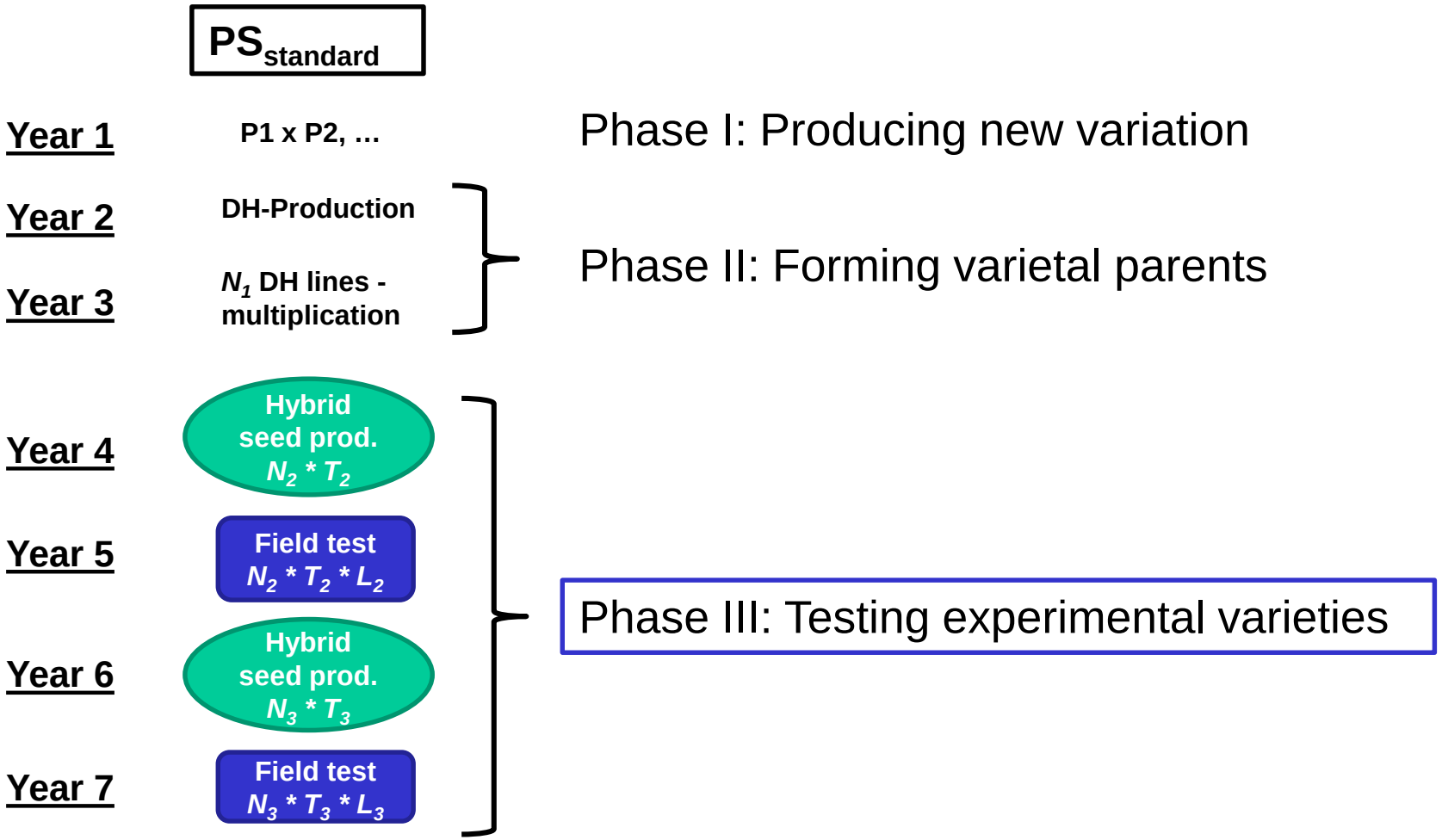
3 Phases in a breeding scheme

Example: phenotypic selection in hybrid breeding

Year 1	**P1 x P2, …**
Year 2	**DH-Production**
Year 3	**N_1 DH lines - multiplication**
Year 4	**Hybrid seed prod. $N_2 * T_2$**
Year 5	**Field test $N_2 * T_2 * L_2$**
Year 6	**Hybrid seed prod. $N_3 * T_3$**
Year 7	**Field test $N_3 * T_3 * L_3$**

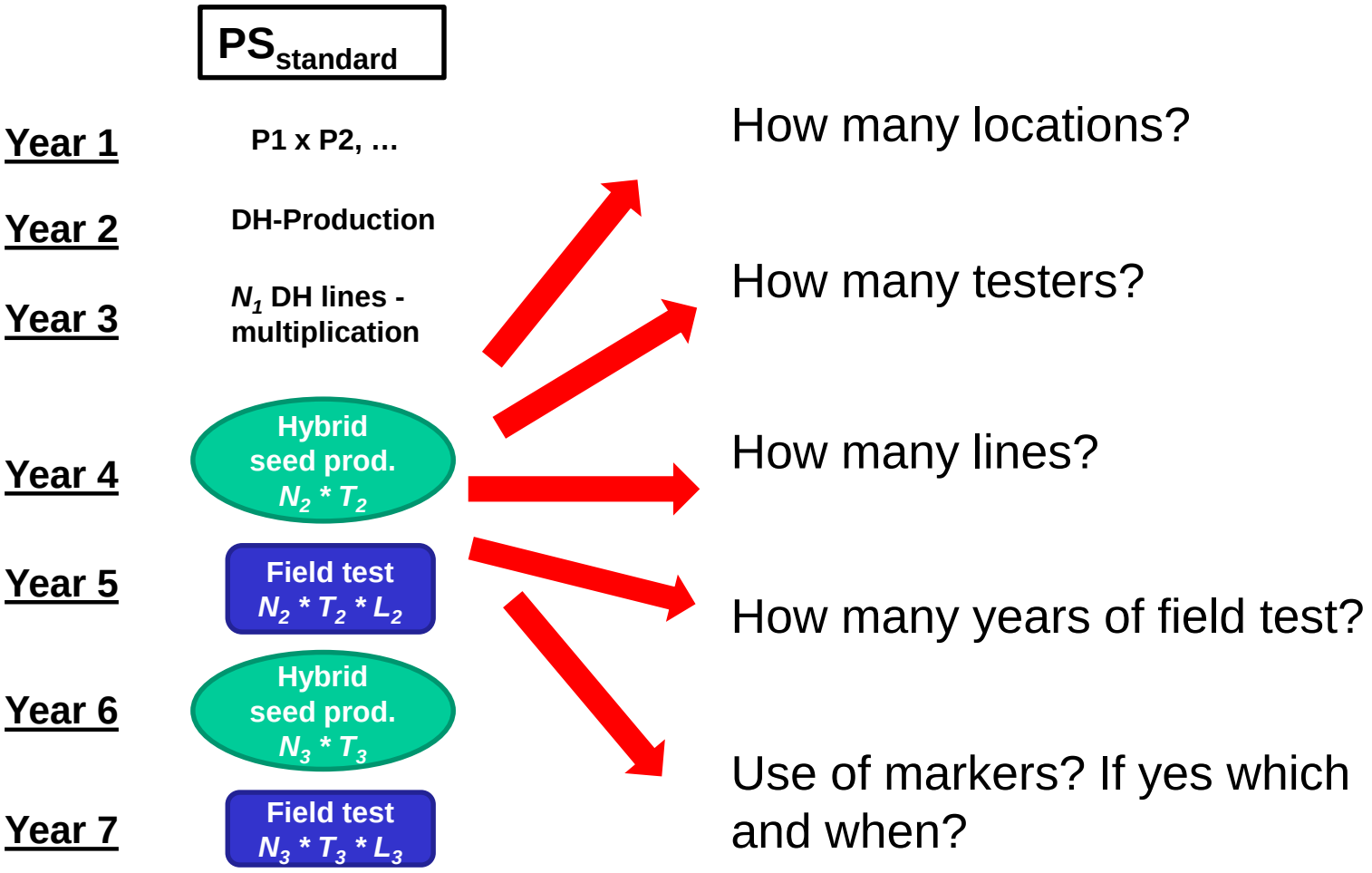
Source: Longin et al. 2015

3 Phases in a breeding scheme



Source: Longin et al. 2015

Many questions…



Source: Longin et al. 2015

Option 1: Field trials

Year 1 P1 x P2, …

Year 2 DH-Production

Year 3 N_1 DH lines - multiplication

Year 4 Hybrid seed prod. $N_2 * T_2$

Year 5 Field test $N_2 * T_2 * L_2$

Year 6 Hybrid seed prod. $N_3 * T_3$

Year 7 Field test $N_3 * T_3 * L_3$

e.g. 1: maximum N
→ minimum L

Source: Longin et al. 2015

Option 1: Field trials

Year 1	P1 x P2, …	P1 x P2, …
Year 2	DH-Production	DH-Production
Year 3	N_1 DH lines - multiplication	N_1 DH lines - multiplication
Year 4	Hybrid seed prod. $N_2 * T_2$	Hybrid seed prod. $N_2 * T_2$
Year 5	Field test $N_2 * T_2 * L_2$	Field test $N_2 * T_2 * L_2$
Year 6	Hybrid seed prod. $N_3 * T_3$	Hybrid seed prod. $N_3 * T_3$
Year 7	Field test $N_3 * T_3 * L_3$	Field test $N_3 * T_3 * L_3$

e.g. 1: maximum N
→ minimum L

e.g. 2: minimum N
→ maximum L

Source: Longin et al. 2015

Option 1: Field trials

Year 1	P1 x P2, …	P1 x P2, …	P1 x P2, …
Year 2	DH-Production	DH-Production	DH-Production
Year 3	N_1 DH lines - multiplication	N_1 DH lines - multiplication	N_1 DH lines - multiplication
Year 4	Hybrid seed prod. $N_2 * T_2$	Hybrid seed prod. $N_2 * T_2$	Hybrid seed prod. $N_2 * T_2$
Year 5	Field test $N_2 * T_2 * L_2$	Field test $N_2 * T_2 * L_2$	Field test $N_2 * T_2 * L_2$
Year 6	Hybrid seed prod. $N_3 * T_3$	Hybrid seed prod. $N_3 * T_3$	
Year 7	Field test $N_3 * T_3 * L_3$	Field test $N_3 * T_3 * L_3$	

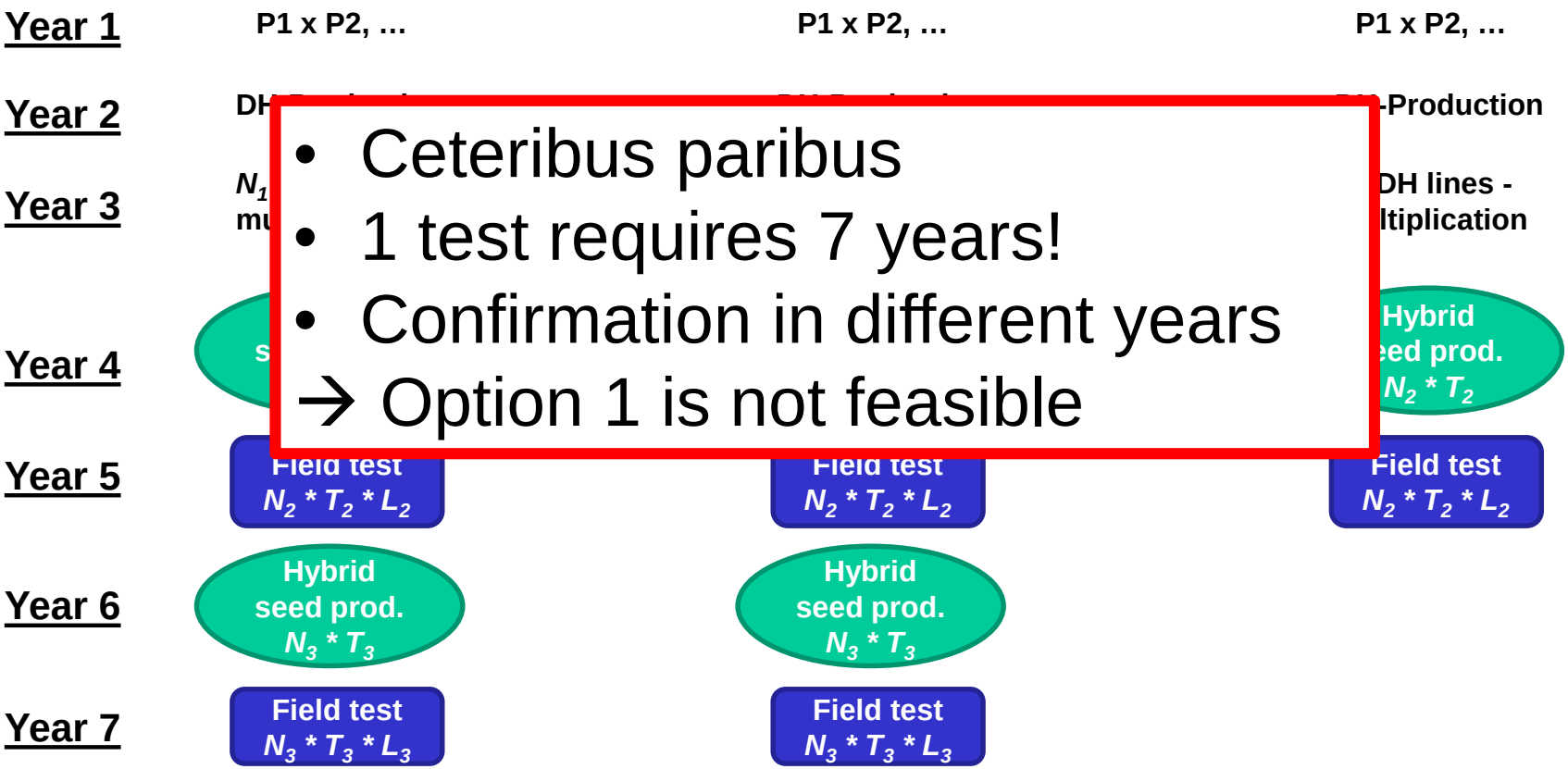
e.g. 1: maximum N → minimum L

e.g. 2: minimum N → maximum L

e.g. 3: 1 year less field trials

Source: Longin et al. 2015

Option 1: Field trials



- Ceteribus paribus
- 1 test requires 7 years!
- Confirmation in different years

→ Option 1 is not feasible

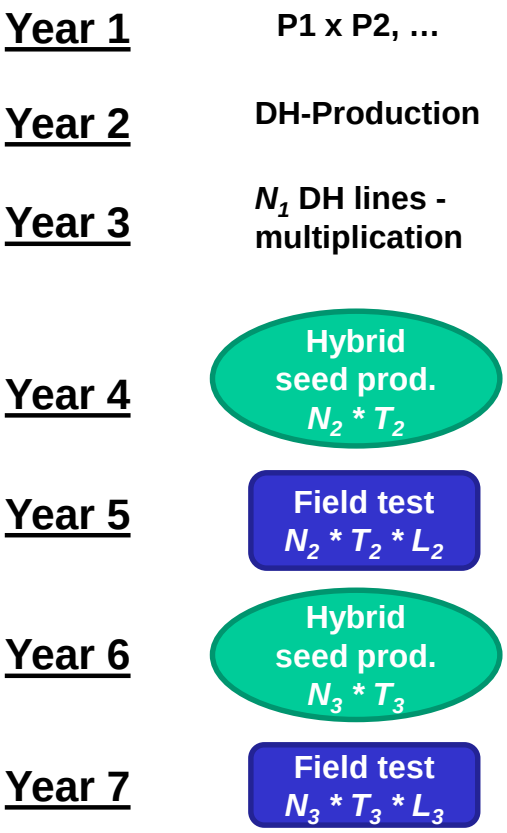
e.g. 1: maximum N
→ minimum L

e.g. 2: minimum N
→ maximum L

e.g. 3: 1 year less field trials

Source: Longin et al. 2015

Option 2: Simulation of breeding methods



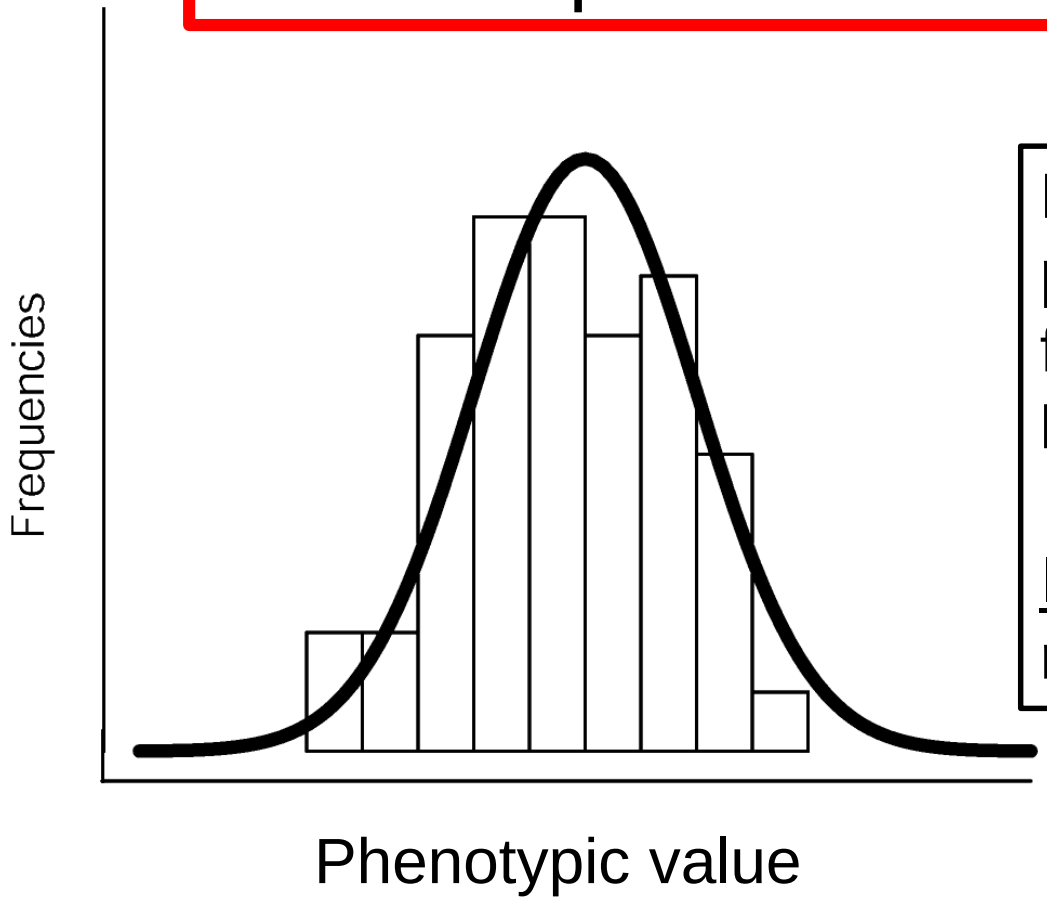
e.g. 1: maximum N
→ minimum L

- **Prediction the gain from selection** in breeding schemes → Breeder‘s equation
- **Simulation** of different breeding schemes
- **R Package „selection gain“**

Source: Longin et al. 2015

Choice of breeding method

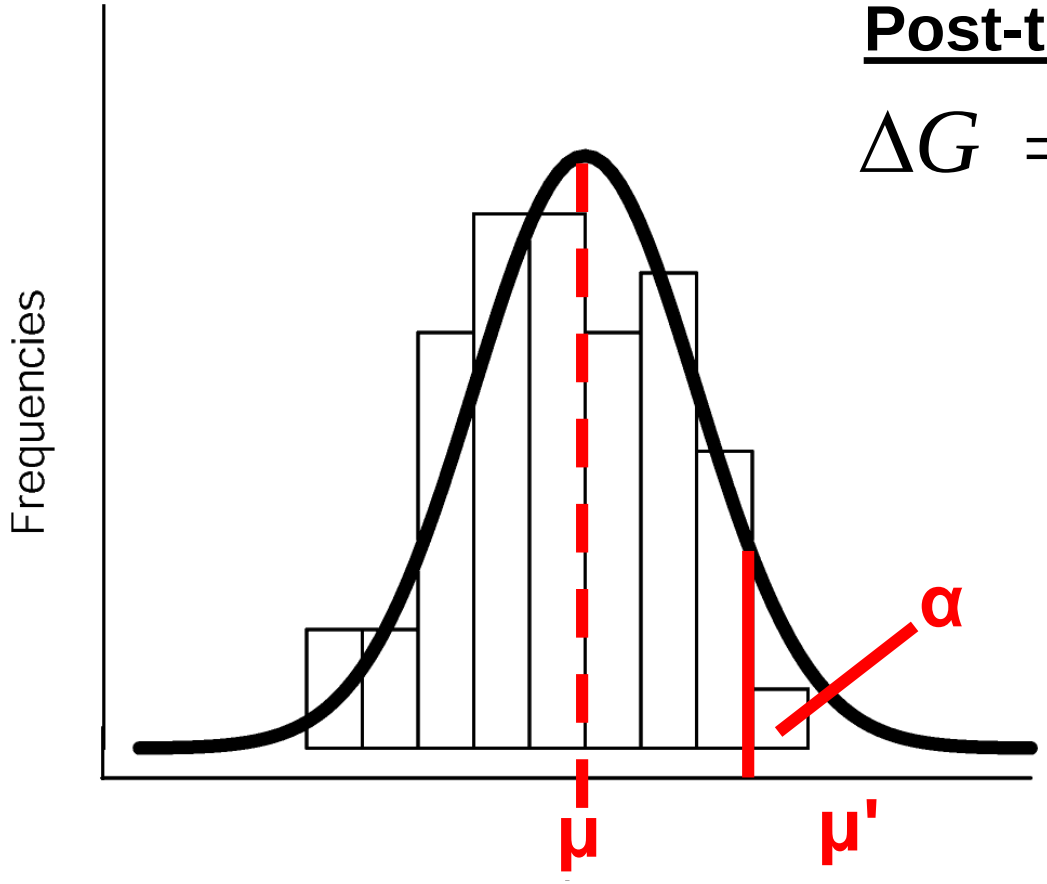
Concept of **selection gain**



Distribution of phenotypes in the field for quantitative traits:
P = G + E;

<u>In R:</u>
rnorm (N, 0, $\sigma^2_G + \sigma^2_E$)

Selection gain



Post-test = realized:

$$\Delta G = h^2(\mu' - \mu) = h^2 S$$

Prae-test = predicted:

$$\Delta G = ih\sigma_y$$

Prediction of selection gain

Selection gain

$$\Delta G = ih\sigma_y$$

- i = selection intensity,
- h = square root of the heritability,
- σ_y = square root of the genetic variance of the target variable

Annual selection gain

$$\Delta G_a = ih\sigma_y / Y$$

- Y = no. of years required to finish one breeding cycle

Variables influencing selection gain

Annual selection gain

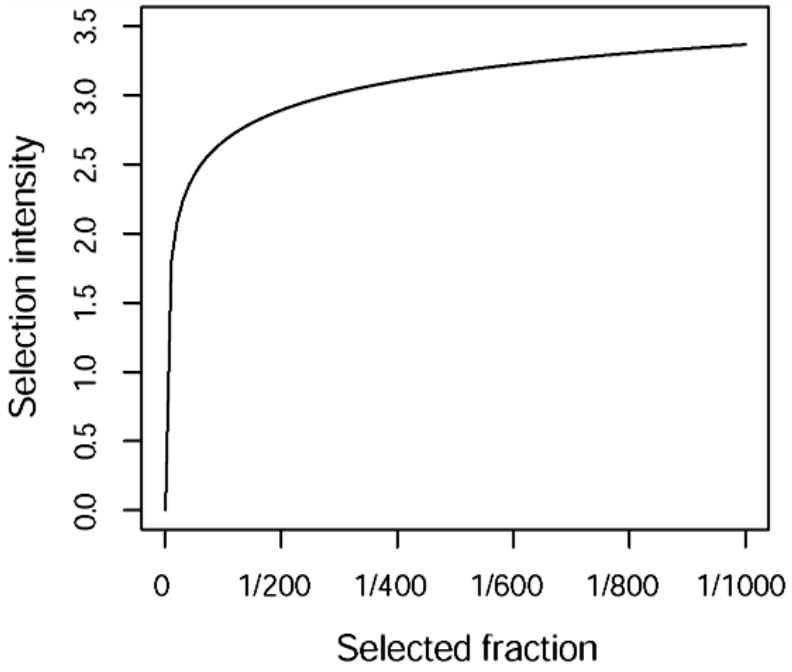
$$\Delta G_a = ih\sigma_y / Y$$

- i = selection intensity,
- h = square root of the heritability,
- σ_y = square root of the genetic variance of the target variable
- Y = no. of years required to finish one breeding cycle

Selection gain is maximized by an

- Increase of i → reduction of Y
- Increase of h
- Increase of σ_y

Increasing selection intensity



Selected fraction

$$\alpha = \frac{no.selected\ lines}{no.tested\ lines}$$

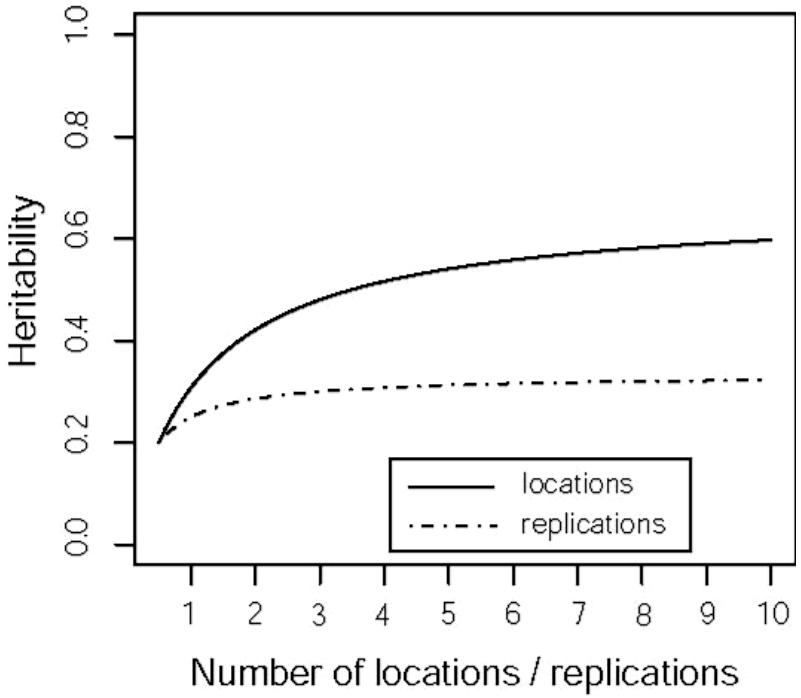
Selection intensity is increased by

- Increasing the number of tested lines
- Decreasing the number of selected lines

BUT: Increase is not linear

Source: Becker 1993

Increasing heritability



$$h^2 = \sigma_G^2 / \sigma_P^2$$

$$\sigma_P^2 = \sigma_G^2 + \sigma_{GxE}^2 / L + \sigma_e^2 / (L * R)$$

L = Locs, R = Reps, σ^2_G = genet. variance; σ^2_P = phenotyp. variance, σ^2_{GxE} = variance due to Genotyp-environment - interaction; σ^2_e = error variance

→ **estimated via ANOVA**

Heritability is increased by

- Increasing the number of locations
- Increasing the number of replications, but less than for locations!

BUT: Increase is not linear

Source: Becker 1993

Allocation of resources

$$\Delta G = ih\sigma_y / Y$$

Allocation of resources

i: function of **α = N_{sel} / N_1**

$$h^2 = \sigma_G^2 / \sigma_P^2 \rightarrow \sigma_P^2 = \sigma_G^2 + \sigma_{GxE}^2 / L + \sigma_e^2 / (L * R)$$

L = Locs, R = Reps, σ^2_G = genet. variance; σ^2_P = phenotyp. variance, σ^2_{GxE} = variance due to Genotyp-environment - interaction; σ^2_e = error variance

→ **estimated via ANOVA**

Optimize allocation of resources

- **Framework**
  - Target criteria: **maximize selection gain**
  - **Variables to optimze**:
    - No. of locations
    - No. of replications
    - No. of lines
    - No. of testers, type of tester
    - Splitting of lines on crosses and lines within crosses

→ **Fixed annual budget**

Budget of a breeding program = annual budget

Seed production		Seed stock		Breeding scheme					Special nurseries			
Resp.	Min trials	Ex of	Season	Prod.	Tests	Traits	Resp.	Allocation	Frost	WiSo	FHB	Virus
			Winter						HB	BY	BY	VL
BY			Summer	P1 x P2			BY	1 Loc				
			Winter									
BY			Summer	F1 self			BY	1 Loc				
			Winter									
BY			Summer	F2 self	Single plant	ear quality, kernel quality	BY	1 Loc				
		rest F1	Winter									
BY			Summer	F3 self	Ear to row	row obs, kernelquality, colour, sds	BY	1 Loc				
		rest F2	Winter									
BY			Summer	F4 self	Ear to row	row obs, kernelquality, colour, sds	BY	1 Loc	25 K			
		rest F3	Winter			heading, lodging, height, diseases,						
BY	1200g		Summer	F5 self	LP1	yield, colour, sds, protein, vitreousity	BH	4 Loc, 2 reps	25 K	1 row	3 rows	2 Loc, 2 rows
		rest F4	Winter			heading, lodging, height, diseases,						
BY	2500g		Summer	F6 self	LP2	yield, colour, sds, Protein, vitreousity	BH	10 Loc, 2 reps		1 row	3 rows	2 Loc, 2 rows

Official offer

	Breeding scheme	
Season	Prod.	Tests
2013/14	P1 x P2	
2014/15	F1 self	
2015/16	F2 self	Single plant
2016/17	F3 self	Ear to row
2017/18	F4 self	Ear to row
2018/19	F5 self	LP1
2019/20	F6 self	LP2

Breeding scheme	
Prod.	Tests
P1 x P2	
F1 self	
F2 self	Single plant
F3 self	Ear to row
F4 self	Ear to row
F5 self	LP1

Breeding scheme	
Prod.	Tests
P1 x P2	
F1 self	
F2 self	Single plant
F3 self	Ear to row
F4 self	Ear to row

Breeding scheme	
Prod.	Tests
P1 x P2	
F1 self	
F2 self	Single plant
F3 self	Ear to row

Breeding scheme	
Prod.	Tests
P1 x P2	
F1 self	
F2 self	Single plant

Breeding scheme	
Prod.	Tests
P1 x P2	
F1 self	

Breeding scheme	
Prod.	Tests
P1 x P2	

Budget: horizontal and vertical!

Examples for budgets per program

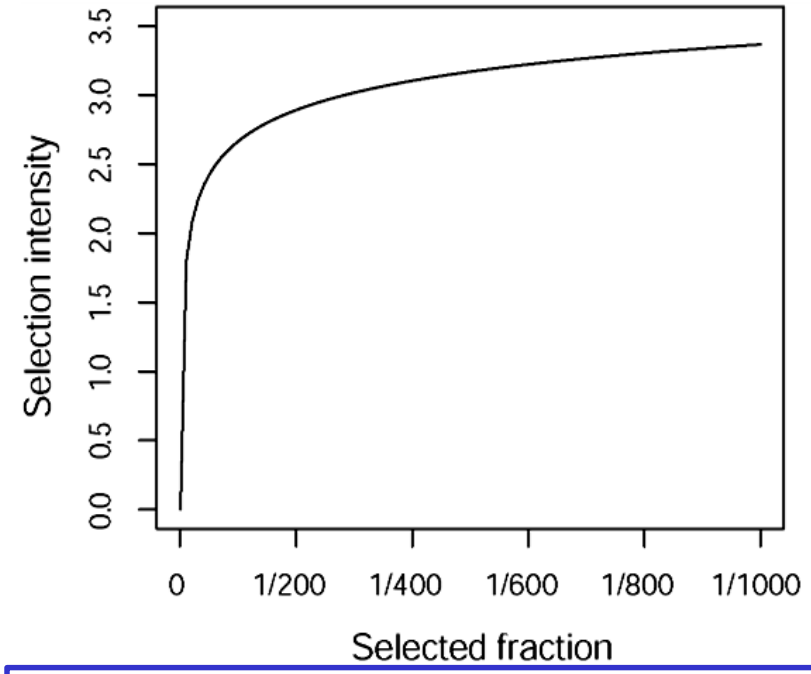
- **Maize**
  - Large: >1.000.000€
  - Small: ~ 500.000€
- **Wheat**
  - Large: 600.000€
  - Small: 200.000€
- **Barley**
  - Large: 400.000€
  - Small: 100.000€

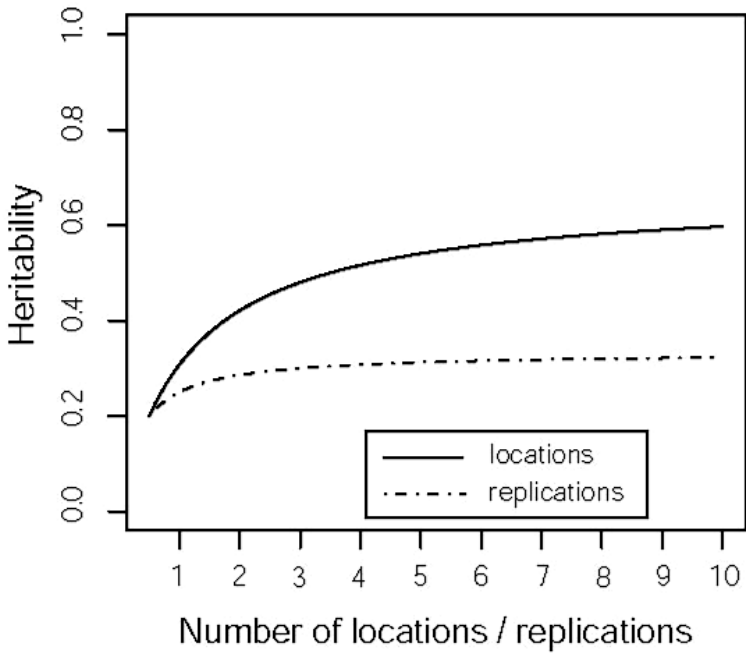
Simple budget formula

Budget = N*L*R (*T) + Production of N

- N = no. of test candidates
- L = no. of test locations
- R = no. of replications
- T = no. of testers

Selection intensity *vs.* heritability

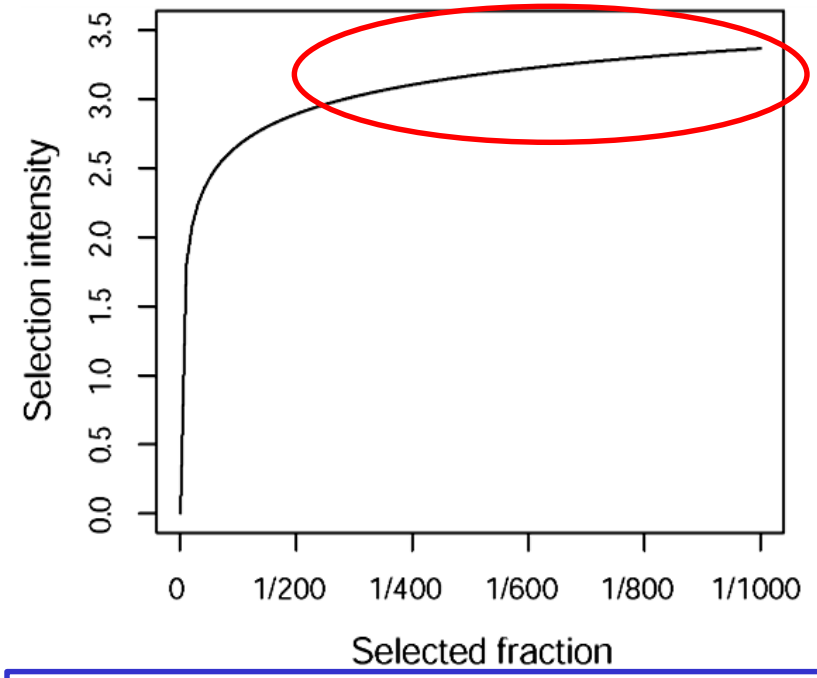


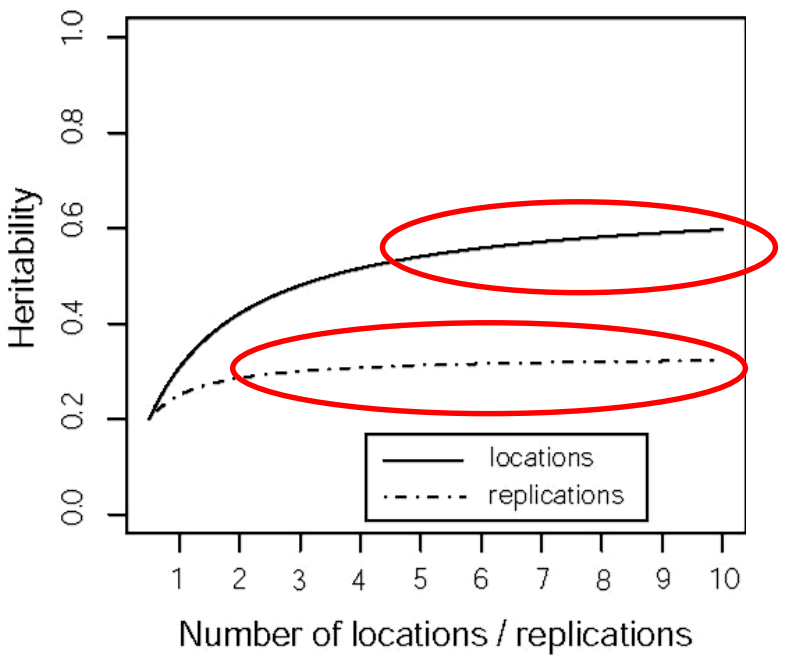


For a fixed budget, maximization of ΔG represents a compromise between a high number of test candidates and a high intensity of testing.

Quelle: Becker 1993

Golden rule





For a fixed budget, maximization of ΔG represents a compromise between a high number of test candidates and a high intensity of testing.

Golden rule: Curves of i and h^2 level off and increase by L > than in R

Quelle: Becker 1993

Variables influencing selection gain

Annual selection gain

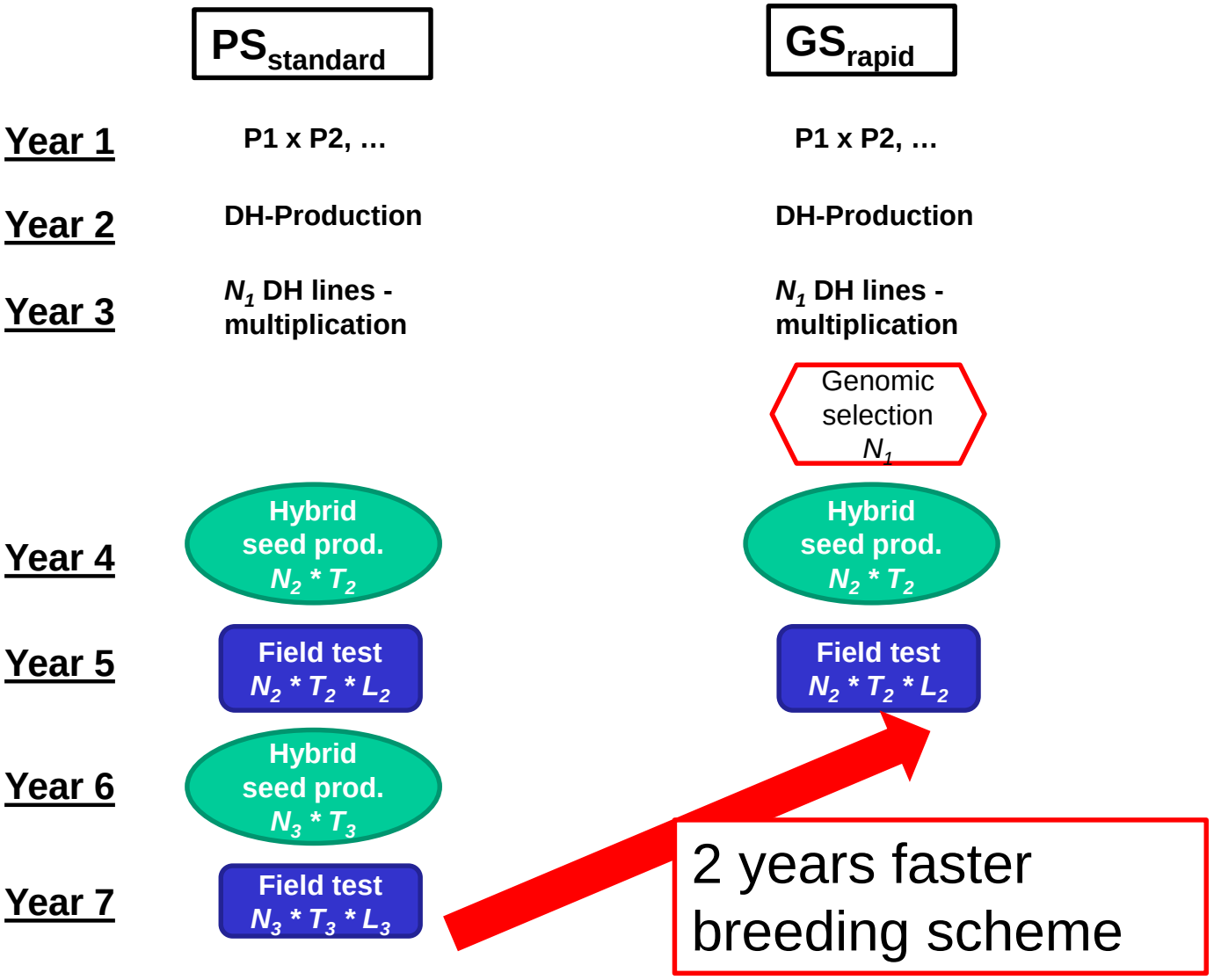
$$\Delta G_a = ih\sigma_y / Y$$

- i = selection intensity,
- h = square root of the heritability,
- σ_y = square root of the genetic variance of the target variable
- Y = no. of years required to finish one breeding cycle

Selection gain is maximized by an

- Increase of i → **reduction of Y**
- Increase of h
- Increase of σ_y

Reduce cycle length



Source: Longin et al. 2016

Annual selection gain

$$\Delta G_a = ih\sigma_y / Y$$

Assumptions:

- $i = 2$
- $h = 0.7$
- $\sigma_y = 5$ dt/ha

Example:

$$\Delta G = 2 * 0.7 * 5 / 7 = 1$$

$$\Delta G = 2 * 0.7 * 5 / 5 = 1.4$$

> 40 % higher annual selection gain

Cycle length has very strong effect on annual selection gain

→You must be faster than your competitor

Variance components

Crop	Variance components due to				
	G	GxL	GxY	GxLxY	E
Winter wheat	14.2	2.4	2.4	9.2	14.4
Winter barley	6.1	1.6	1.6	6.7	13
Grain maize early	19.6	6.1	5.1	11.7	27.1
Forage maize early	38.7	15.6	8.6	17.8	80.8
Winter oil seed rape	3.3	1.7	2	3.8	9.7
Sugarbeet	33.6	9.1	1.7	4.8	35.2

Source: Laidig et al. 2008

Variance components

Crop	Variance components due to				
	G	GxL	GxY	GxLxY	E
Winter wheat	14.2	2.4	2.4	9.2	14.4
Winter barley	6.1	1.6	1.6	6.7	13
Grain maize early	19.6	6.1	5.1	11.7	27.1
Forage maize early	38.7	15.6	8.6	17.8	80.8
Winter oil seed rape	3.3	1.7	2	3.8	9.7
Sugarbeet	33.6	9.1	1.7	4.8	35.2

High variance due to

- genotype x year and
- genotype x year x location interaction

Source: Laidig et al. 2008

Year → large effect on genotype ranking

Genotyp	Rank 2015	Rank 2016	Yield 2016	Yield 2015
	21	1	58,71	77,10
Miradoux		2	58,66	
W-10066-217-316/14/3-512-2/1	8	3	58,57	82,33
W-10037-210-309/17/1-487-1/3	2	4	58,03	86,39
W-10021-204-307/4/3-468-2/1	1	5	57,89	90,33
W-10029-207-305/11/1-439-4/1	17	6	57,22	79,24
W-10066-217-316/9/2-511-3/1	6	7	57,02	83,49
W-10013-202-302/9/1-408-2/1	16	8	56,44	79,45
Lupidur	10	9	55,87	81,85
W-10058-214-313/21/2-501-1/3	9	10	55,68	82,07
W-10033-209-308/3/1-474-1/3	19	11	55,00	78,42
W-10064-216-315/10/3-506-2/1	13	12	54,97	80,86
W-10021-204-307/2/2-466-6/3	18	13	54,97	79,24
W-10058-214-313/11/1-499-1/3	15	14	54,89	80,46
W-10031-208-306/22/1-460-3/1	5	15	54,87	84,43
W-10066-217-316/23/3-514-6/3	4	16	54,65	84,81
W-10064-216-315/17/3-507-1/1	3	17	54,54	86,30
W-10043-211-310/19/2-494-3/3	12	18	54,34	81,28
W-10033-209-308/10/3-476-6/3	23	19	54,32	76,02

Further advantages of multiple year testing

- Disease resistance (natural occurring)
- Frost
- Drought, heat

→ Speed of the program is also a compromise between a maximum annual selection gain and a security of the results

Compromise necessary

Annual selection gain

$$\Delta G_a = ih\sigma_y / Y$$

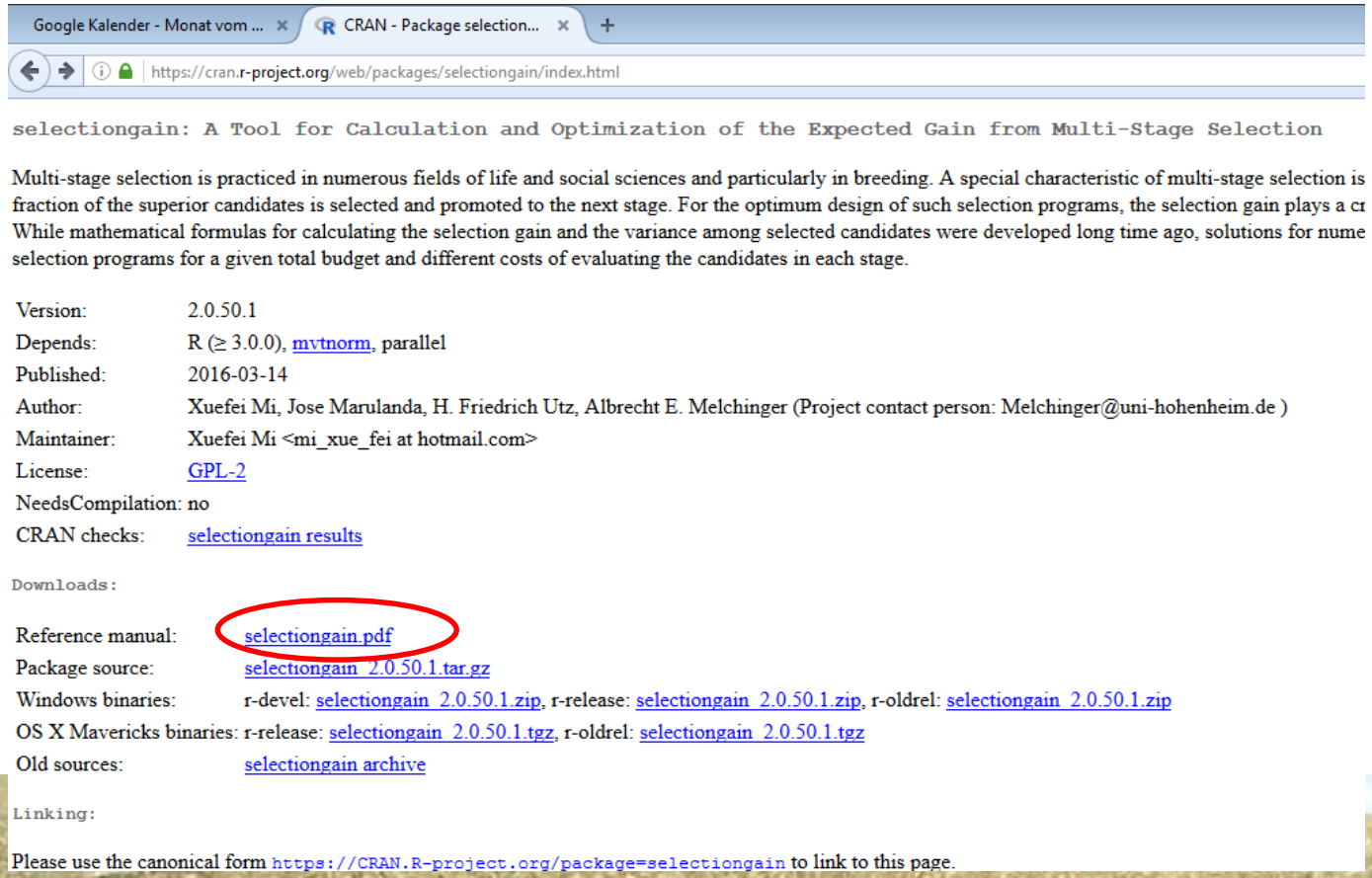
Annual selection gain is maximized by an

- increase of i → reduction of Y
- increase of h
- increase of σ_y

Compromise necessary between theory and practice!

R package „selection gain“

- Open source software package R (www.r-project.org)
- Package selectiongain
- https://cran.r-project.org/web/packages/selectiongain/index.html



Google Kalender - Monat vom ... | CRAN - Package selection...

https://cran.r-project.org/web/packages/selectiongain/index.html

selectiongain: A Tool for Calculation and Optimization of the Expected Gain from Multi-Stage Selection

Multi-stage selection is practiced in numerous fields of life and social sciences and particularly in breeding. A special characteristic of multi-stage selection is fraction of the superior candidates is selected and promoted to the next stage. For the optimum design of such selection programs, the selection gain plays a cr While mathematical formulas for calculating the selection gain and the variance among selected candidates were developed long time ago, solutions for nume selection programs for a given total budget and different costs of evaluating the candidates in each stage.

Version:	2.0.50.1
Depends:	R (≥ 3.0.0), mvtnorm, parallel
Published:	2016-03-14
Author:	Xuefei Mi, Jose Marulanda, H. Friedrich Utz, Albrecht E. Melchinger (Project contact person: Melchinger@uni-hohenheim.de)
Maintainer:	Xuefei Mi <mi_xue_fei at hotmail.com>
License:	GPL-2
NeedsCompilation:	no
CRAN checks:	selectiongain results

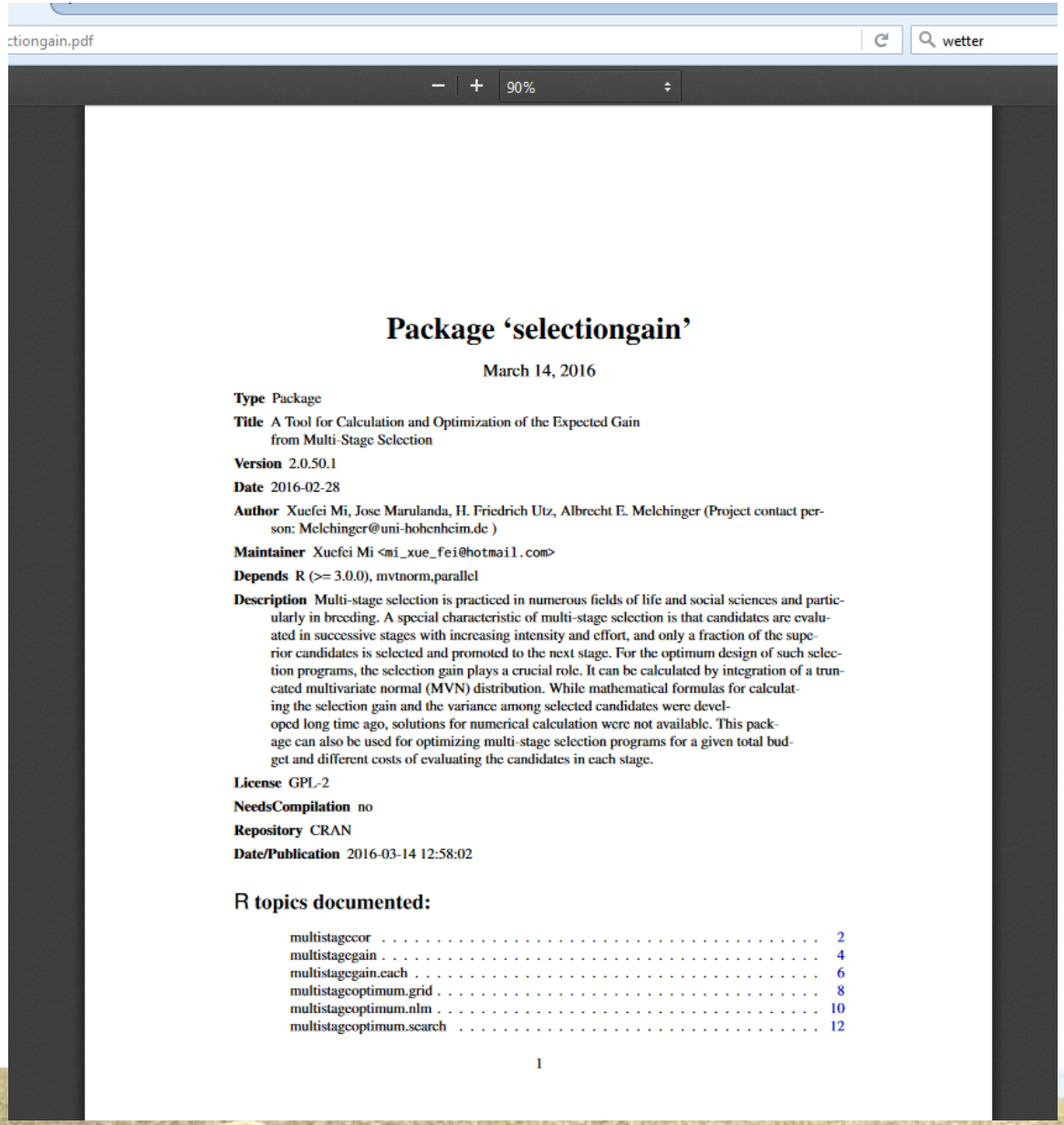
Downloads:

Reference manual:	selectiongain.pdf
Package source:	selectiongain_2.0.50.1.tar.gz
Windows binaries:	r-devel: selectiongain_2.0.50.1.zip, r-release: selectiongain_2.0.50.1.zip, r-oldrel: selectiongain_2.0.50.1.zip
OS X Mavericks binaries:	r-release: selectiongain_2.0.50.1.tgz, r-oldrel: selectiongain_2.0.50.1.tgz
Old sources:	selectiongain archive

Linking:

Please use the canonical form https://CRAN.R-project.org/package=selectiongain to link to this page.

Selectiongain - Manual



tiongain.pdf

wetter

90%

Package 'selectiongain'

March 14, 2016

Type Package

Title A Tool for Calculation and Optimization of the Expected Gain from Multi-Stage Selection

Version 2.0.50.1

Date 2016-02-28

Author Xuefei Mi, Jose Marulanda, H. Friedrich Utz, Albrecht E. Melchinger (Project contact person: Melchinger@uni-hohenheim.de)

Maintainer Xuefei Mi <mi_xue_fei@hotmail.com>

Depends R (>= 3.0.0), mvtnorm,parallel

Description Multi-stage selection is practiced in numerous fields of life and social sciences and particularly in breeding. A special characteristic of multi-stage selection is that candidates are evaluated in successive stages with increasing intensity and effort, and only a fraction of the superior candidates is selected and promoted to the next stage. For the optimum design of such selection programs, the selection gain plays a crucial role. It can be calculated by integration of a truncated multivariate normal (MVN) distribution. While mathematical formulas for calculating the selection gain and the variance among selected candidates were developed long time ago, solutions for numerical calculation were not available. This package can also be used for optimizing multi-stage selection programs for a given total budget and different costs of evaluating the candidates in each stage.

License GPL-2

NeedsCompilation no

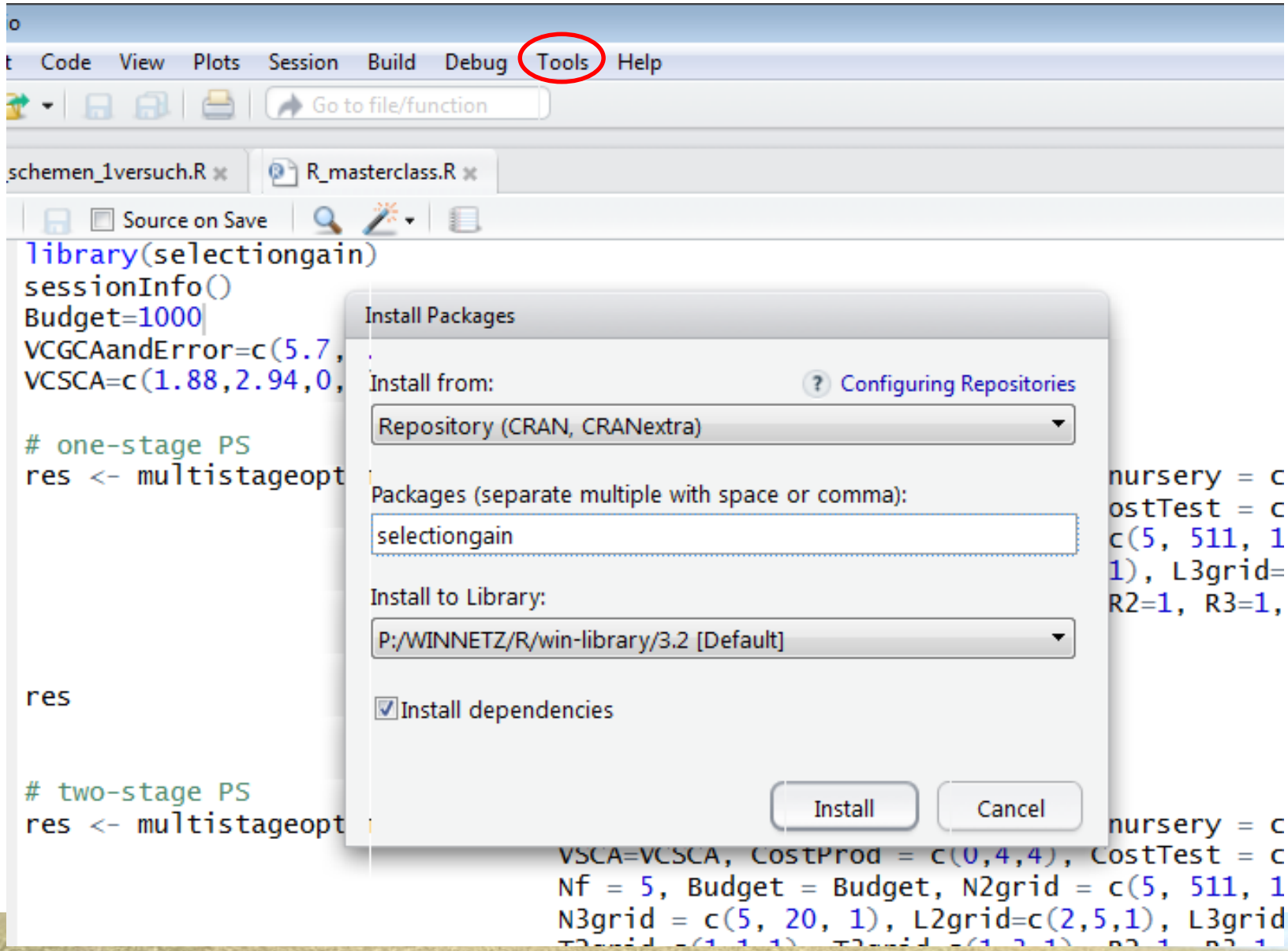
Repository CRAN

Date/Publication 2016-03-14 12:58:02

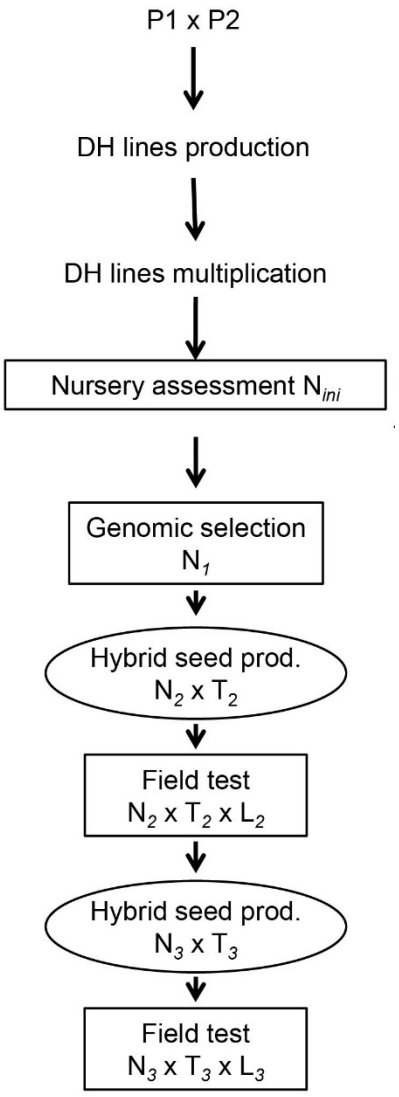
R topics documented:

1

Selectiongain - download



What is possible? – Breeding scheme



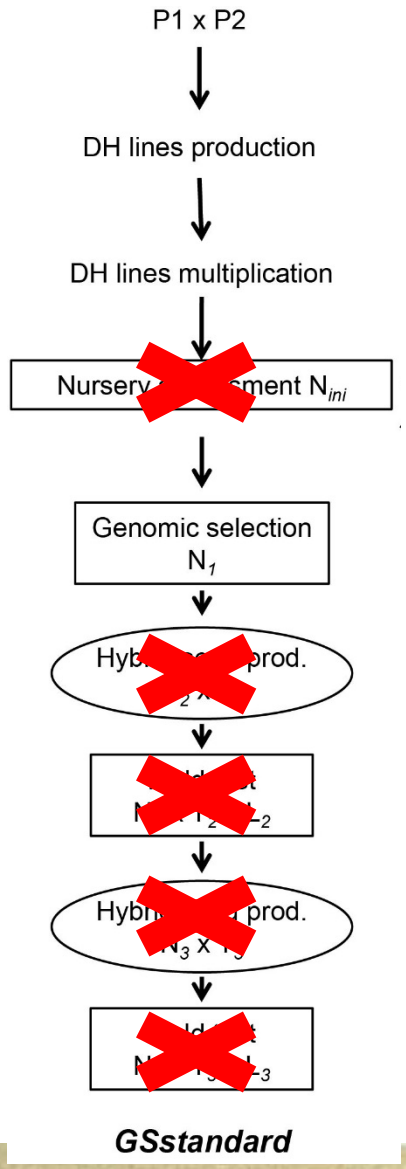
GSstandard

Breeding scheme:

- DH production
- Nursery selection on traits not correlated to yield
- GS on yield
- 2 stage phenotypic selection on yield

N_i , L_i , R_i , T_i = number of lines, locations, replications and testers used in stage i → *optimized*

What is possible? – Breeding scheme



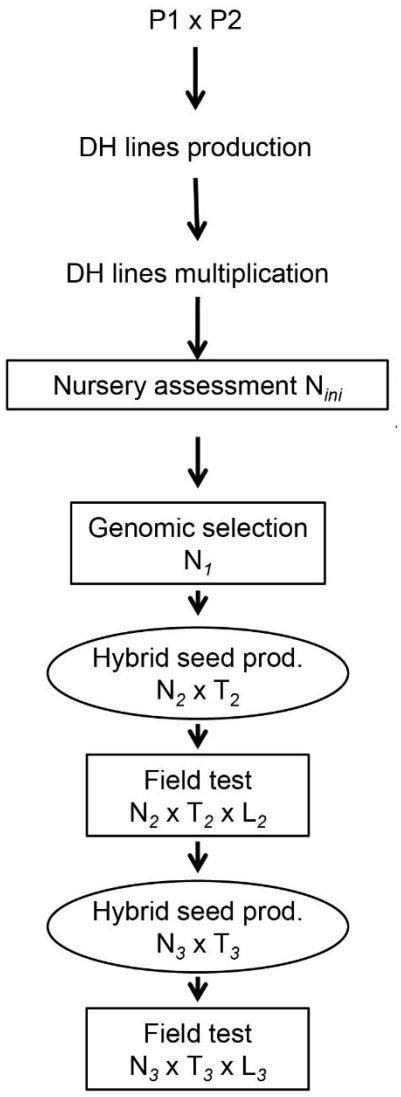
Breeding scheme:

- DH production
- Nursery selection on traits not correlated to yield
- GS on yield
- 2 stage phenotypic selection on yield

Breeding scheme - modifications

- Each test stage can be witched off
- You can enter maximum nubers in each test stages of N, L, R, T
- GS → yes/no

Budget & Costs



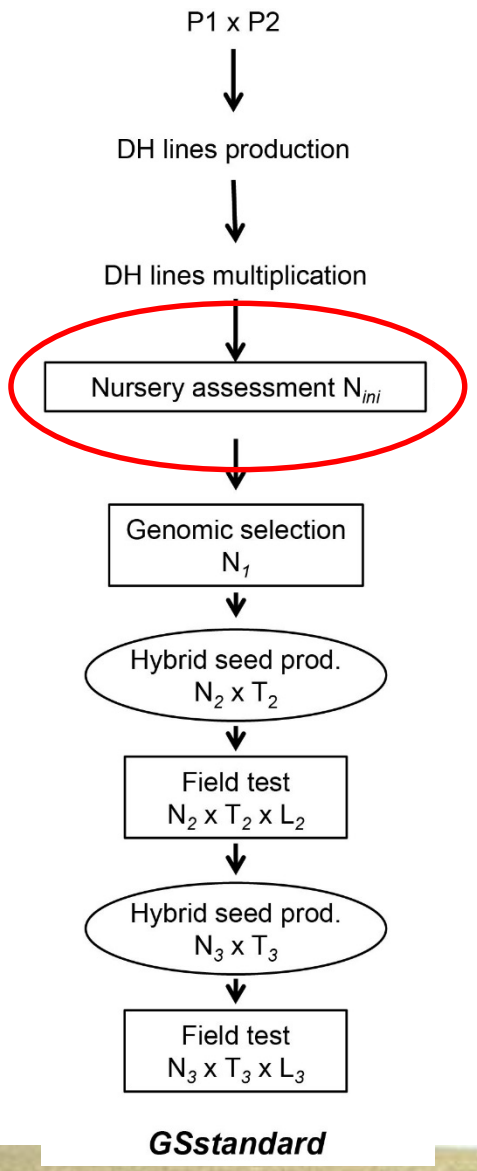
$$Budget = N_{ini}(Cost_{DH} + Cost_{nursery\ test}) + N_1(Cost_{Genotyping}) + N_2 T_2 Cost_{Hybridseed} + N_2 T_2 L_2 R_2 + N_3(T_3 - T_2) Cost_{Hybridseed} + N_3 T_3 L_3 R_3$$

Costs for:

- DH production
- Nursery selection
- GS
- Hybrid seed production
- Field plot,….

→ All „redefined“ in field plot equivalents

Nursery selection



We assume:

Nursery selection on traits not correlated to yield (e.g. lodging, leaf rust resistance, SDS,…)

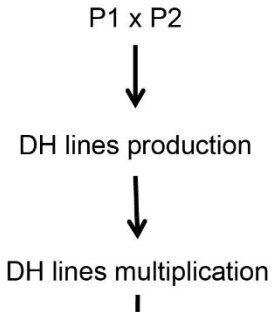
→ Nursery selection will not impact the selection gain formula

→ Nursery selection: costs money (budget impact)

→ Affects number of test lines

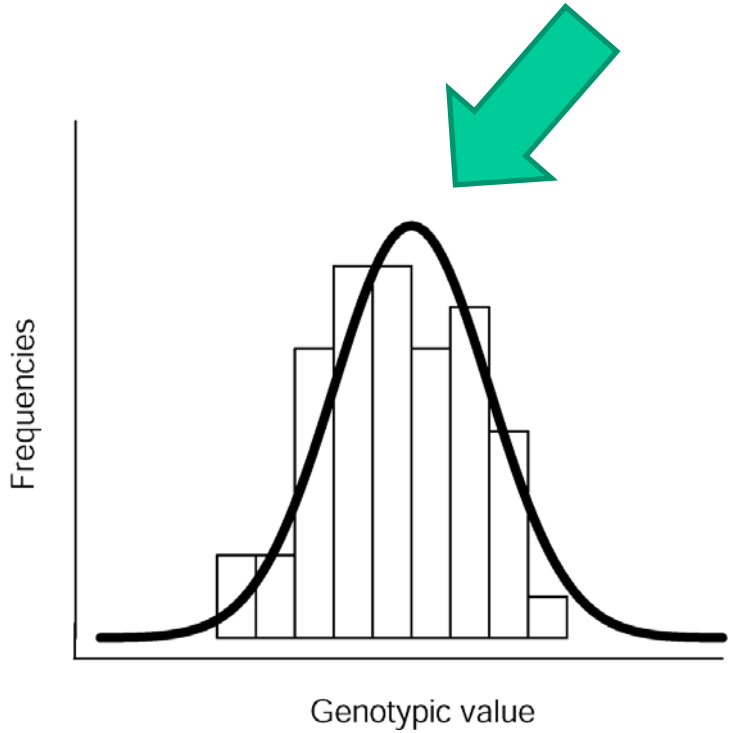
→ Nursery selection intensity is predefined (not optimized!) as $\alpha = \frac{N_{ini}}{N_1}$

First step of simulations



We define basics:

- Budget (for crossing, line development, GS, field tests) in field plot equivalents
- Crop & Trait to select for → variance components



$$\sigma_P^2 = \sigma_{GCA}^2 + \sigma_{GCAxy}^2 + \sigma_{GCAxl}^2 / L + \sigma_{GCAxlxy}^2 / L +$$
$$\sigma_{SCA}^2 / TM + \sigma_{SCAxy}^2 / TM + \sigma_{SCAxl}^2 / TML + \sigma_{SCAxlxy}^2 / TML$$
$$\sigma_e^2 / (TLR)$$

σ^2_{GCA} = GCA variance; σ^2_{SCA} = SCA variance ; σ^2_P = phenotyp. variance, $\sigma^2_{GCAx...}$ = variance due to Genotyp-environment - interaction; σ^2_e = error variance

→ **estimated via ANOVA**

Getting started with the code

library(selectiongain) → load the package

sessionInfo() → Info on the version you use

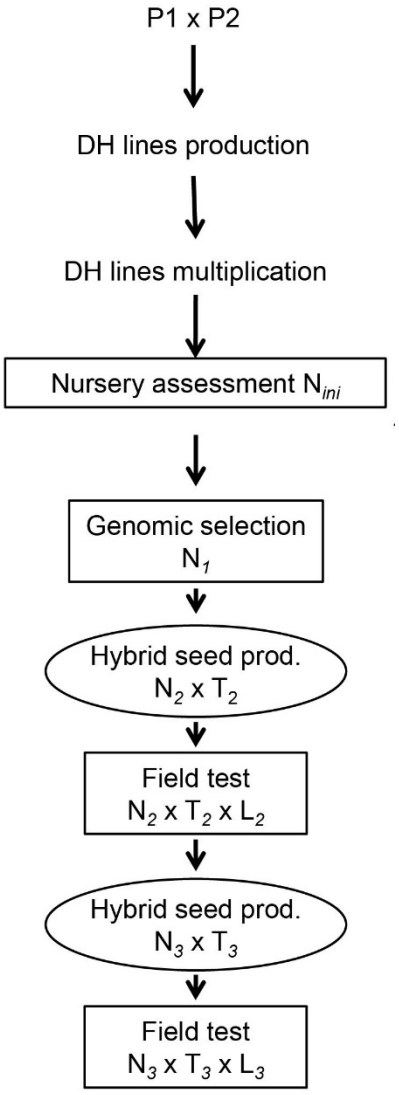
Important input parameters

- Budget = in field plot eqivalents
- VCGCAandError = c(GCA,GCA*loc, GCA*year, GCA*loc*year, error)
- VCSCA = c(SCA, SCA*loc, SCA*year, SCA*loc*year)

Example for hybrid wheat:

- Budget =10 000
- VCGCAandError=c(5.7, 5.19, 0, 0, 24.37)
- VCSCA=c(1.88, 2.94, 0,0)

Second step of simulations



GSstandard

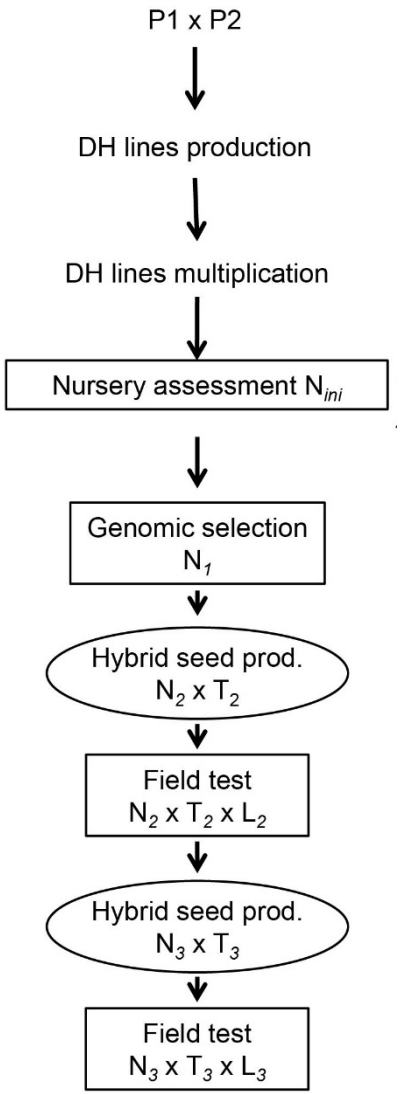
We define breeding operations:

- Intensity of nursery selection
- GS: yes/no; predictive ability
- Number of test stages in field
- Maximum numbers of testers, locations,…
- Costs for each operation

Most important code

```
Budget = 10000
VCGCAandError = c(5.7,5.19,0,0,24.37)
VCSCA = c(1.88,2.94,0,0)

multistageoptimum.search (
          maseff=NA, alpha.nursery = 1,
        VGCAandE=VCGCAandError, VSCA=VCSCA,
          cost.nursery = c(1,0.3), CostProd = c(0,4,4),
          CostTest = c(2,1,1), t2free = T,
          Nf = 5, Budget = Budget,
        N2grid = c(5, 511, 10), N3grid = c(5, 20, 1),
        L2grid=c(2,5,1), L3grid=c(1,5,1),
        T2grid=c(1,1,1), T3grid=c(1,5,1),
        R2=1, R3=1, alg = Miwa(),
        detail=FALSE, fig=FALSE)
```



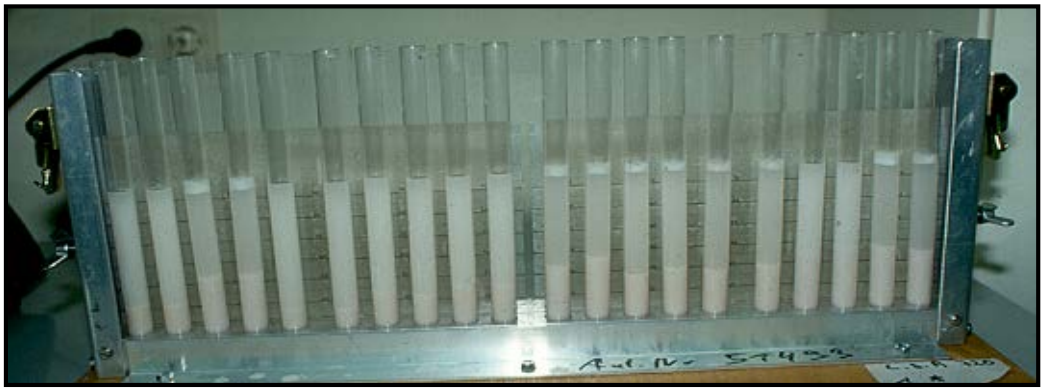
GSstandard

Most important code - explained

multistageoptimum.search (

maseff = GS pred. accuracy,
alpha.nursery = selected fraction in disease nursery,
VGCAandE=VCGCAandError, **VSCA**=VCSCA,
cost.nursery = c(line prod., test in nursery),
CostProd = c(0, hybrid seed prod., hybrid seed prod.),
CostTest = c(GS, yield plot, yield plot), **t2free** = T,
Nf = no. finally selected lines, **Budget** = Budget,
N2grid = c(5, 511, 10), N3grid = c(5, 5, 1),
L2grid=c(1,5,1), L3grid=c(1,5,1),
T2grid=c(1,1,1), T3grid=c(1,3,1),
R2=1, R3=1, alg = Miwa(),
detail=FALSE, fig=FALSE)

Let‘s go into breeding world



Modeling the optimum allocation

1. Basic level
- Target criterion
- Trait

2. Breeding level
- Scheme
- Scenario

3. Optimization level
- Test resources

Modeling the optimum allocation

1. Basic level

- Target criterion = selection gain
- Trait = grain yield in wheat

2. Breeding level

- Scheme = PS standard
- Scenario = variance components, budget, selected fraction, technical requirements,...

3. Optimization level

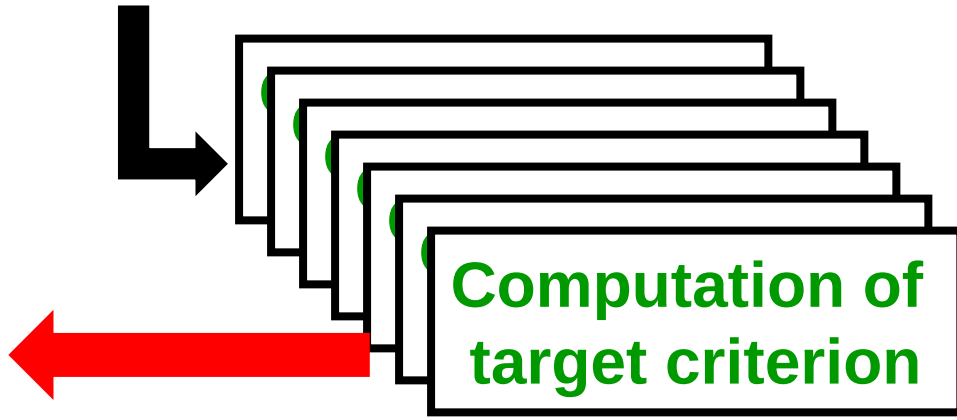
- Test resources = number of test locations, testers, replications, DH lines

Determining the opt. allocation within a given model framework

1. Basic level
- Selection gain
- Maize grain yield

2. Breeding level
- PSstandard
- **Given scenario**

3. Optimization level
specific allocation of the number of testers, test locations, DH lines, replications



AIM: Find the allocation maximizing selection gain for that specific def. of level 1 and 2

= optimum allocation

Use of molecular markers

Nothing else than indirect selection

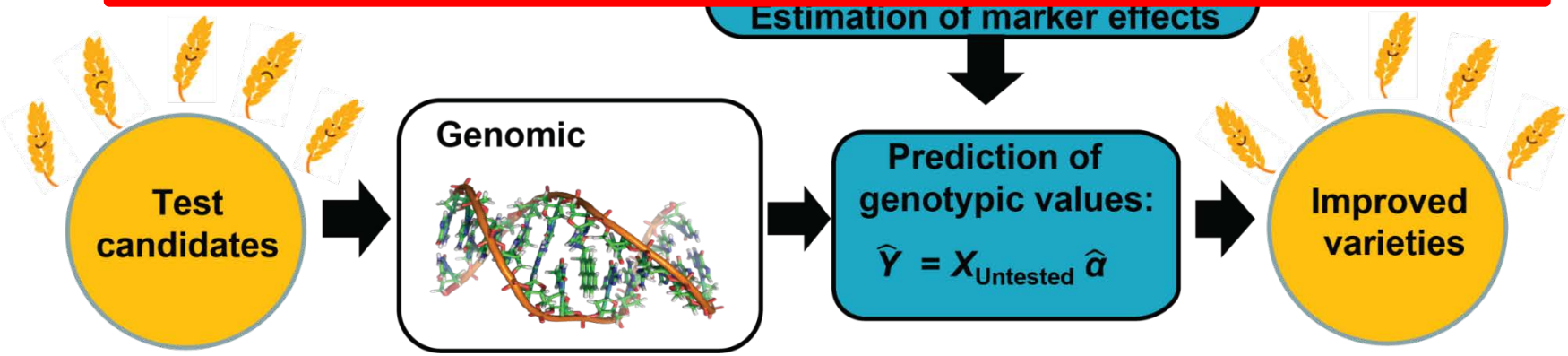
$$\Delta G = ih\rho\sigma_y / Y$$

- $0 < \rho < 1$: **selection gain is only increased if** the use of the test criteria enables
  - **Increase of i → high throughput: N_1**
  - **Increase of h**
  - **Increase of σ_y**
  - **Decrease of Y → fast recycling**

Genomic selection

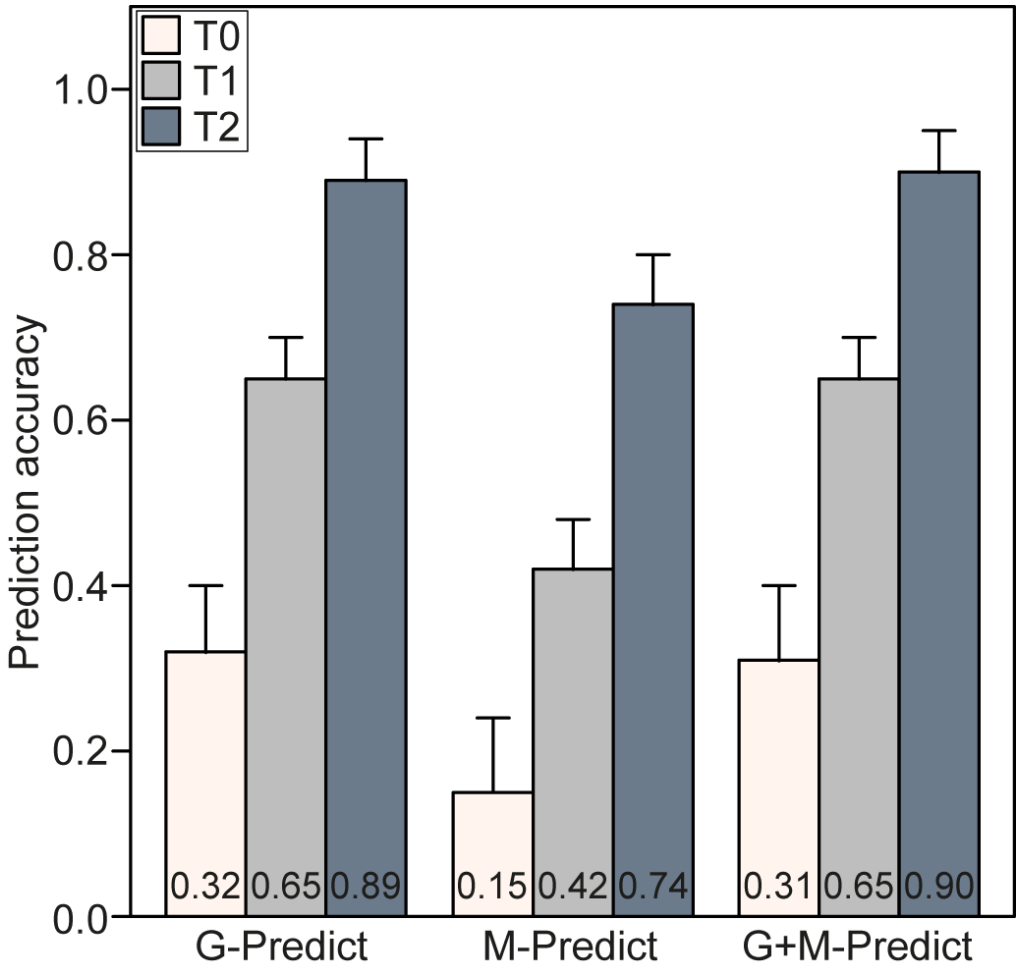
We assume, that

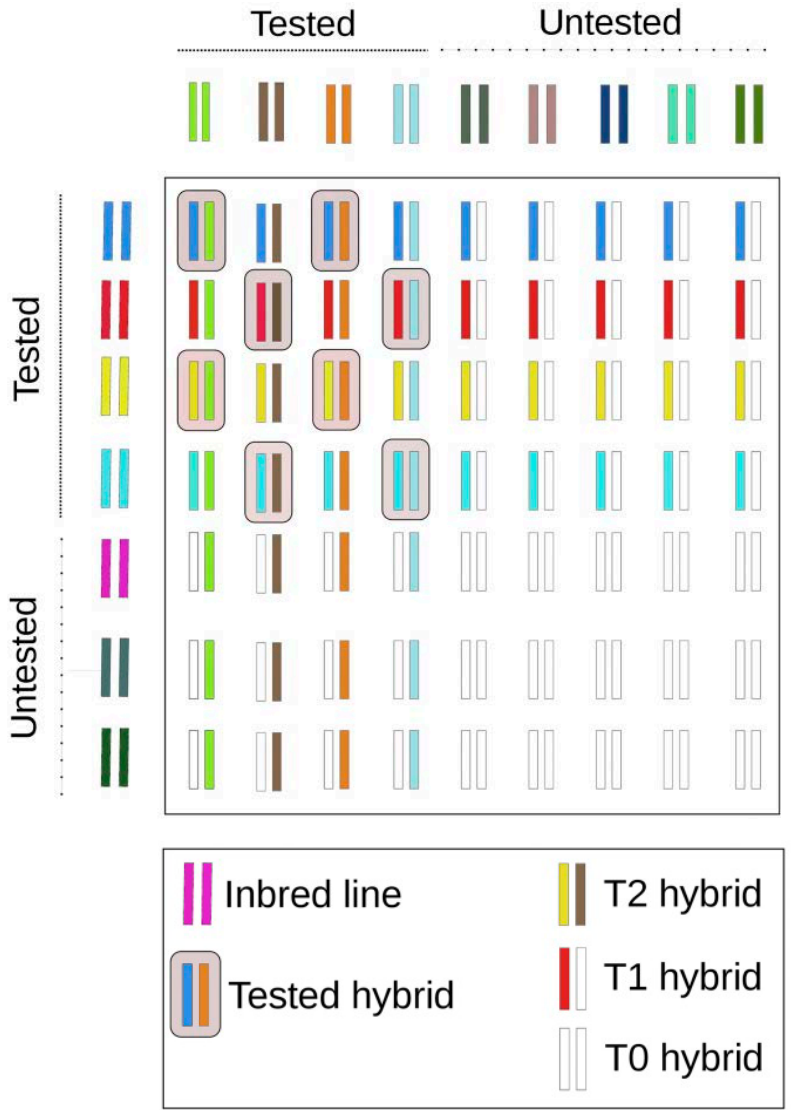
- **prediction models have been developed in previous projects → no budget required for it now!**
- **Retraining of the model is done with routine field trials → no additional budget required for it!**



Source: Zhao et al. 2015

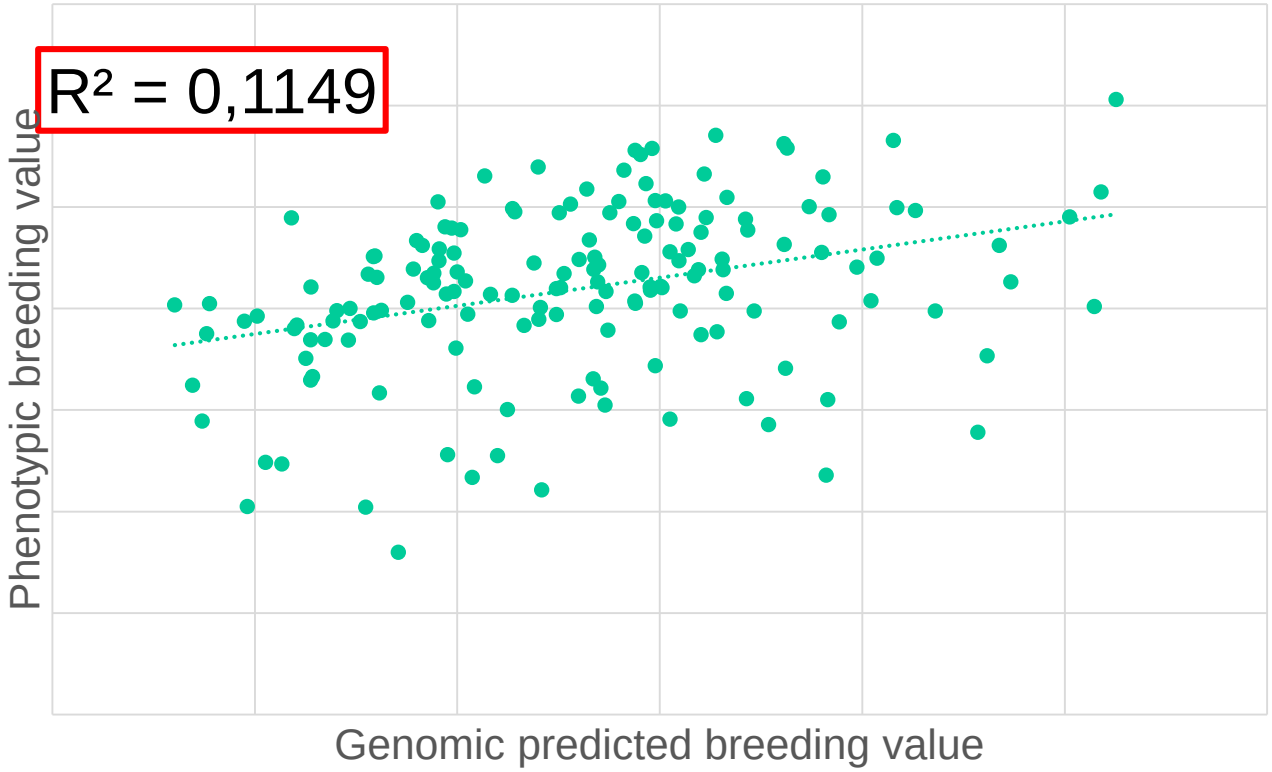
Prediction accuracy for hybrids





Source: Zhao et al. 2015, Technow et al. 2015

We need prediction ability



Correlation between observed and predicted breeding value = prediction ability
→ that‘s what we need for our simulations

$$Prediction\ accuracy = \frac{prediction\ ability}{h}$$

Modifications of the framework

Besides budget, variance components, costs for line production and phenotyping we need further data:

- Correlation GS with GCA: ρ(GS, GCA)= 0.3 (for T0 scenario; Zhao et al. 2014)
- Costs GS = high density genotyping of 1 line costs as much as 2 field plots

- (data is shown for wheat with framwork based on papers below)

Source: Longin et al. 2016, Marulanda et al. 2016

Breeding schemes

$PS_{standard}$

Year 1 P1 x P2, …

Year 2 DH-Production

Year 3 N_1 DH lines - multiplication

Year 4 Hybrid seed prod. $N_2 * T_2$

Year 5 Field test $N_2 * T_2 * L_2$

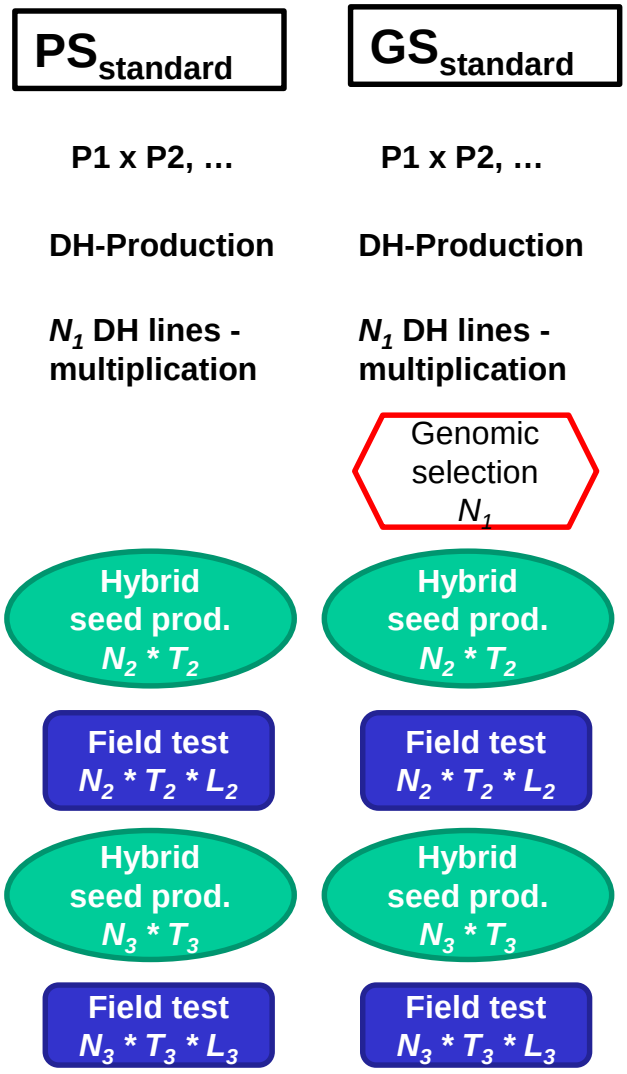
Year 6 Hybrid seed prod. $N_3 * T_3$

Year 7 Field test $N_3 * T_3 * L_3$

Year 8, 9,… Pre-registration trials

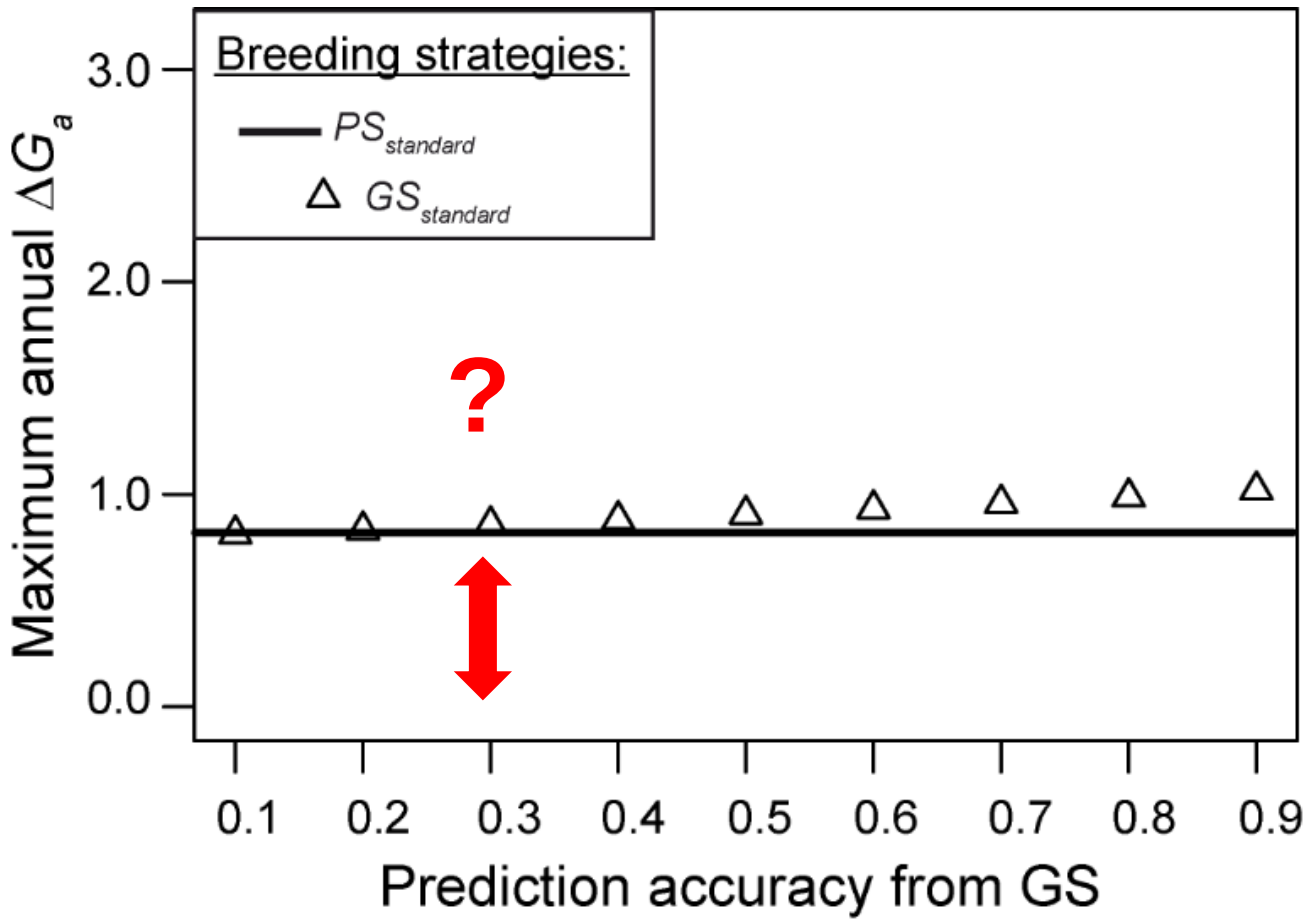
Source: Longin et al. 2015

Breeding schemes



Source: Longin et al. 2015

Increase in selection gain with GS



The higher the prediction accuracy the larger is the advantage of GS schemes

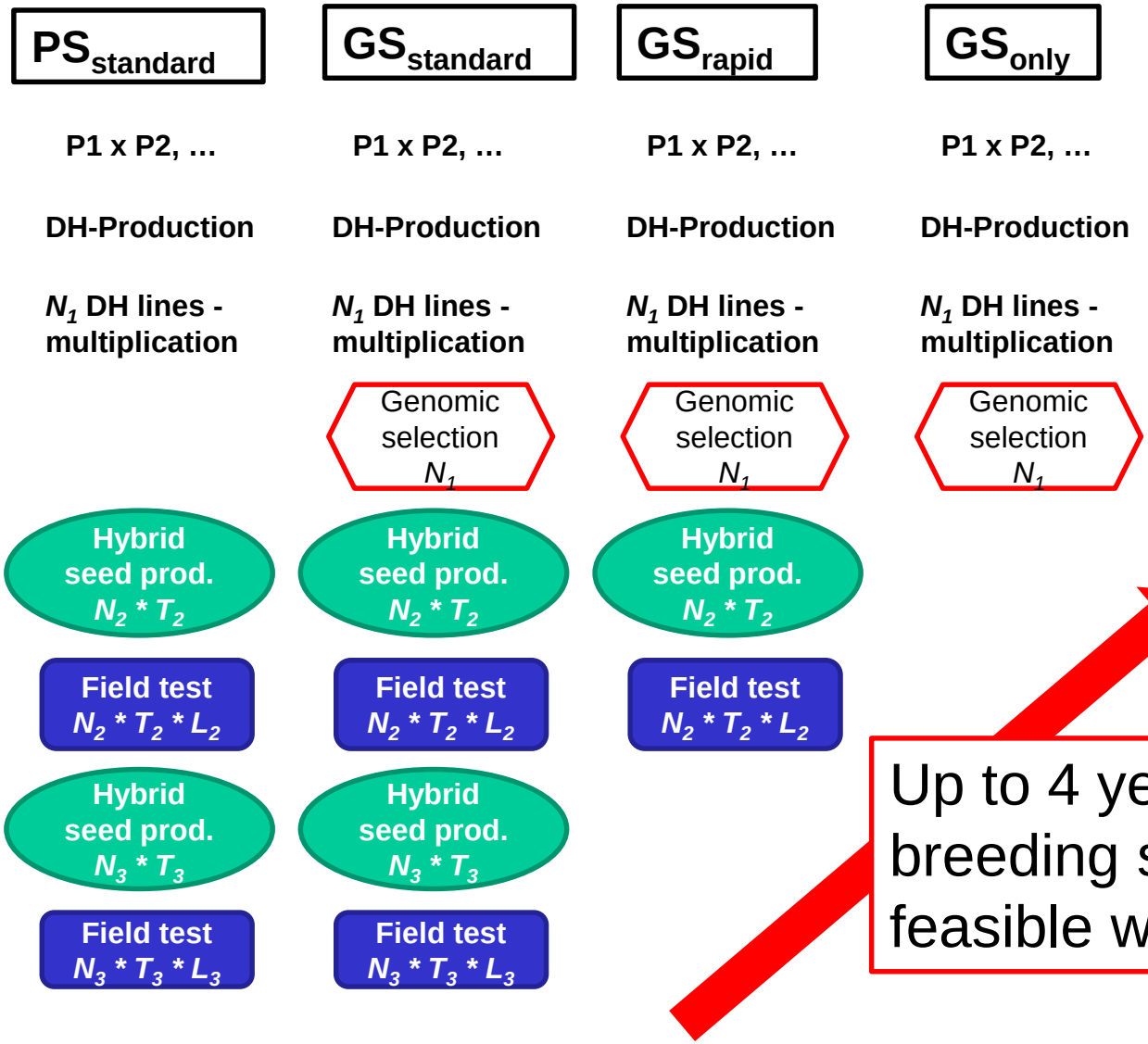
Source: Longin et al. 2015

Reduce cycle length with GS

	$PS_{standard}$	$GS_{standard}$	GS_{rapid}	GS_{only}
Year 1	P1 x P2, …	P1 x P2, …	P1 x P2, …	P1 x P2, …
Year 2	DH-Production	DH-Production	DH-Production	DH-Production
Year 3	N_1 DH lines - multiplication	N_1 DH lines - multiplication	N_1 DH lines - multiplication	N_1 DH lines - multiplication
		Genomic selection N_1	Genomic selection N_1	Genomic selection N_1
Year 4	Hybrid seed prod. $N_2 * T_2$	Hybrid seed prod. $N_2 * T_2$	Hybrid seed prod. $N_2 * T_2$	
Year 5	Field test $N_2 * T_2 * L_2$	Field test $N_2 * T_2 * L_2$	Field test $N_2 * T_2 * L_2$	
Year 6	Hybrid seed prod. $N_3 * T_3$	Hybrid seed prod. $N_3 * T_3$		
Year 7	Field test $N_3 * T_3 * L_3$	Field test $N_3 * T_3 * L_3$		

Source: Longin et al. 2015

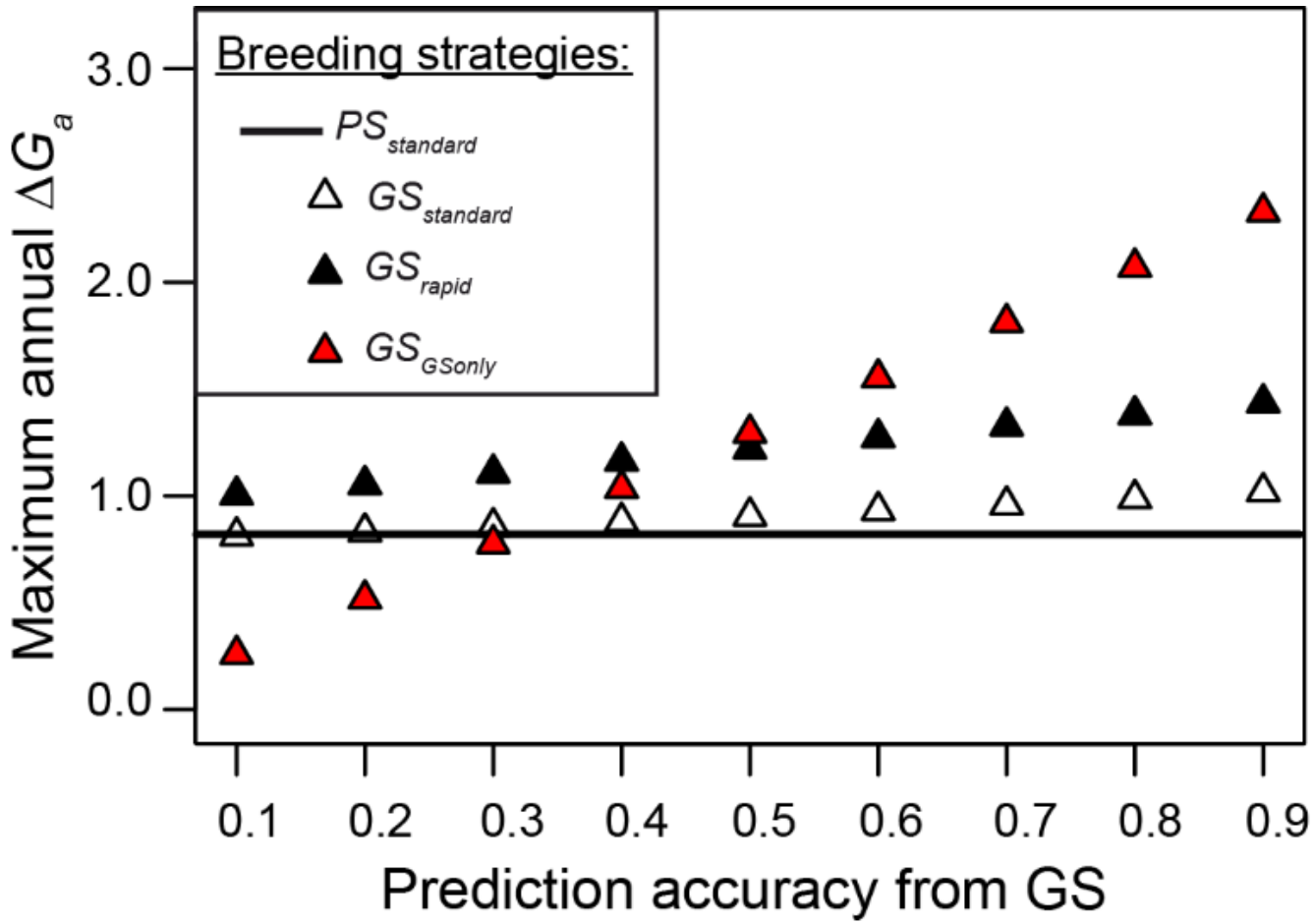
Reduce cycle length with GS



Up to 4 years faster breeding schemes feasible with GS

Source: Longin et al. 2015

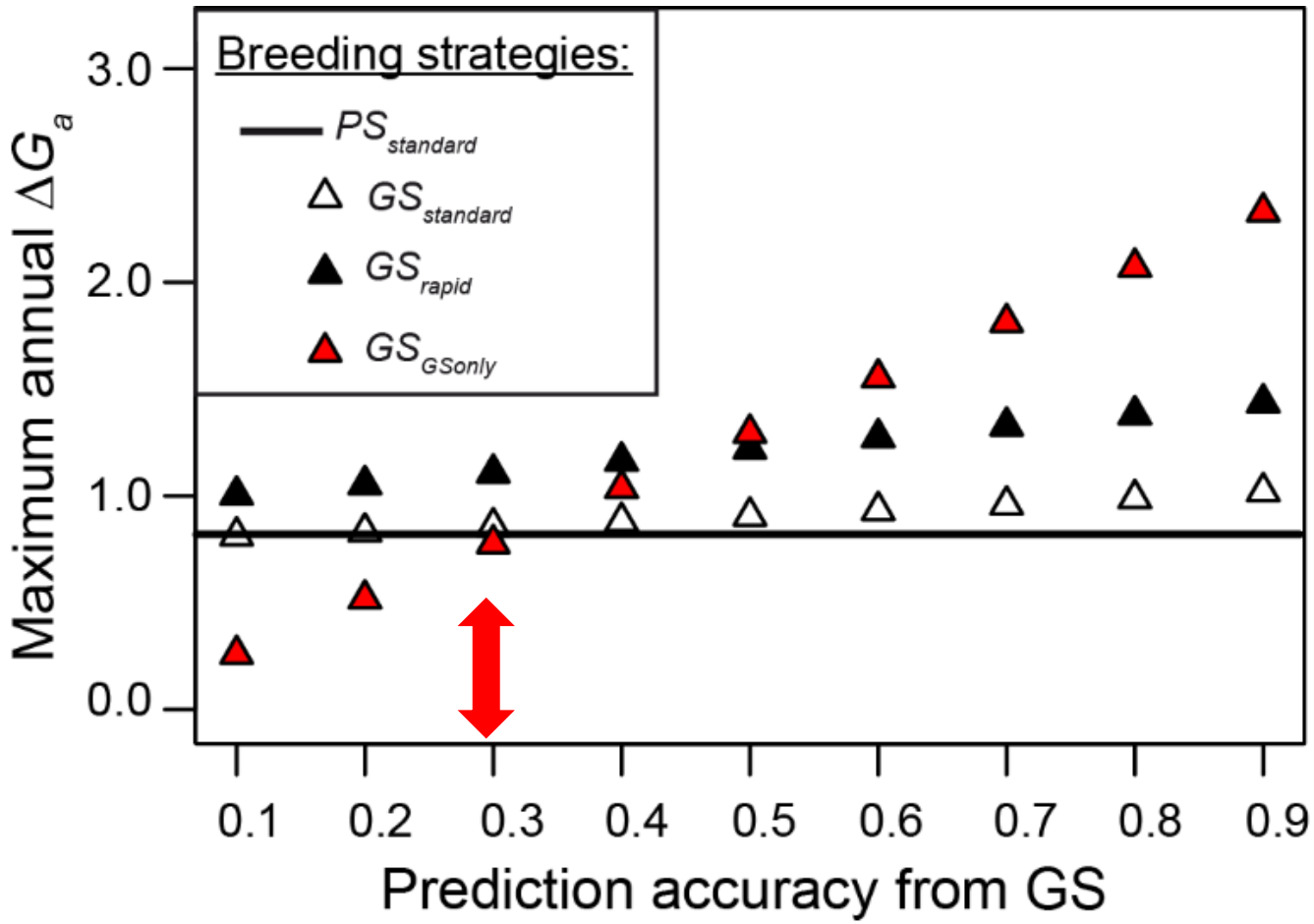
GS for yield is interesting



Genomic selection is promising for grain yield especially when used to shorten breeding cycle length

Source: Longin et al. 2015

GS for yield is interesting



With recent GS accuracy breeding scheme GS_{rapid} seems most promising: + 35% in annual selection gain

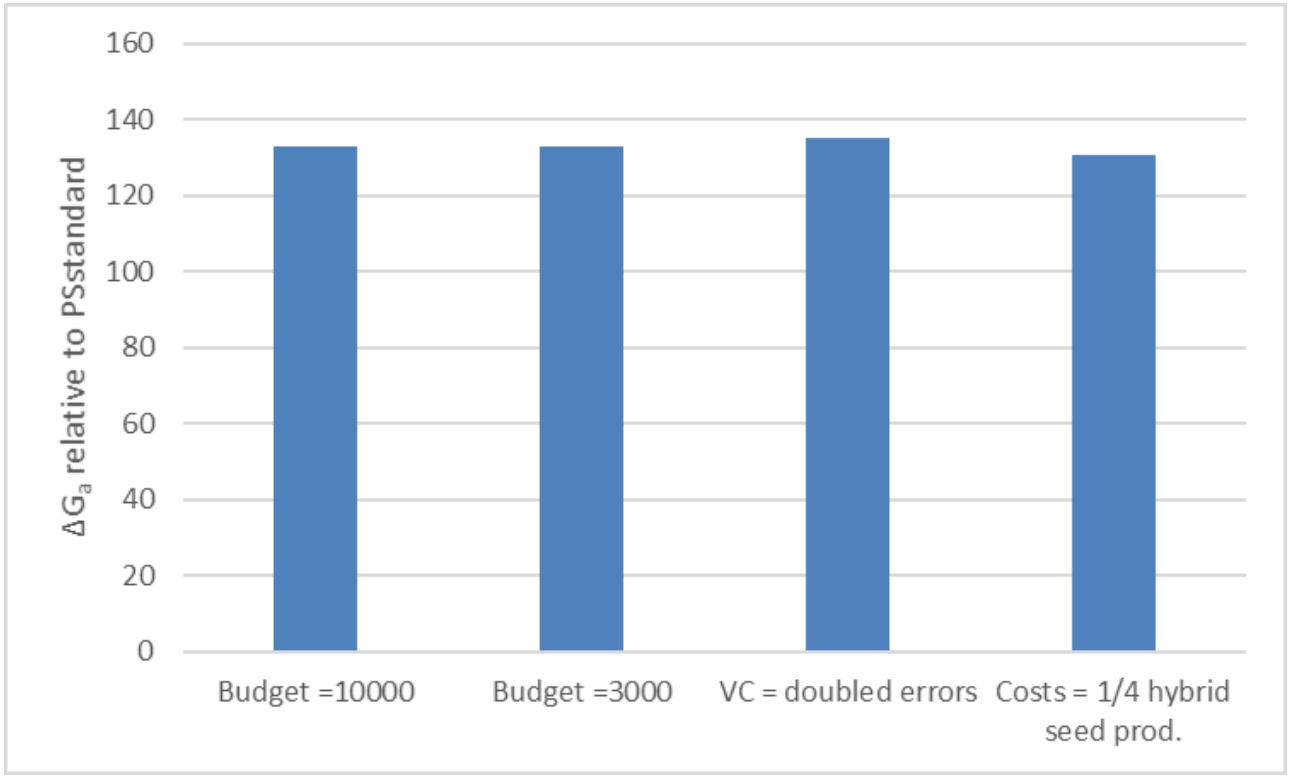
Source: Longin et al. 2015

Generalisation of results

We state that a breeding scheme using GS, namely Gsrapid, is top and should be used; but is it also the truth for

- small budgets ?
- different variance components ?
- reduced hybrid seed production costs ?

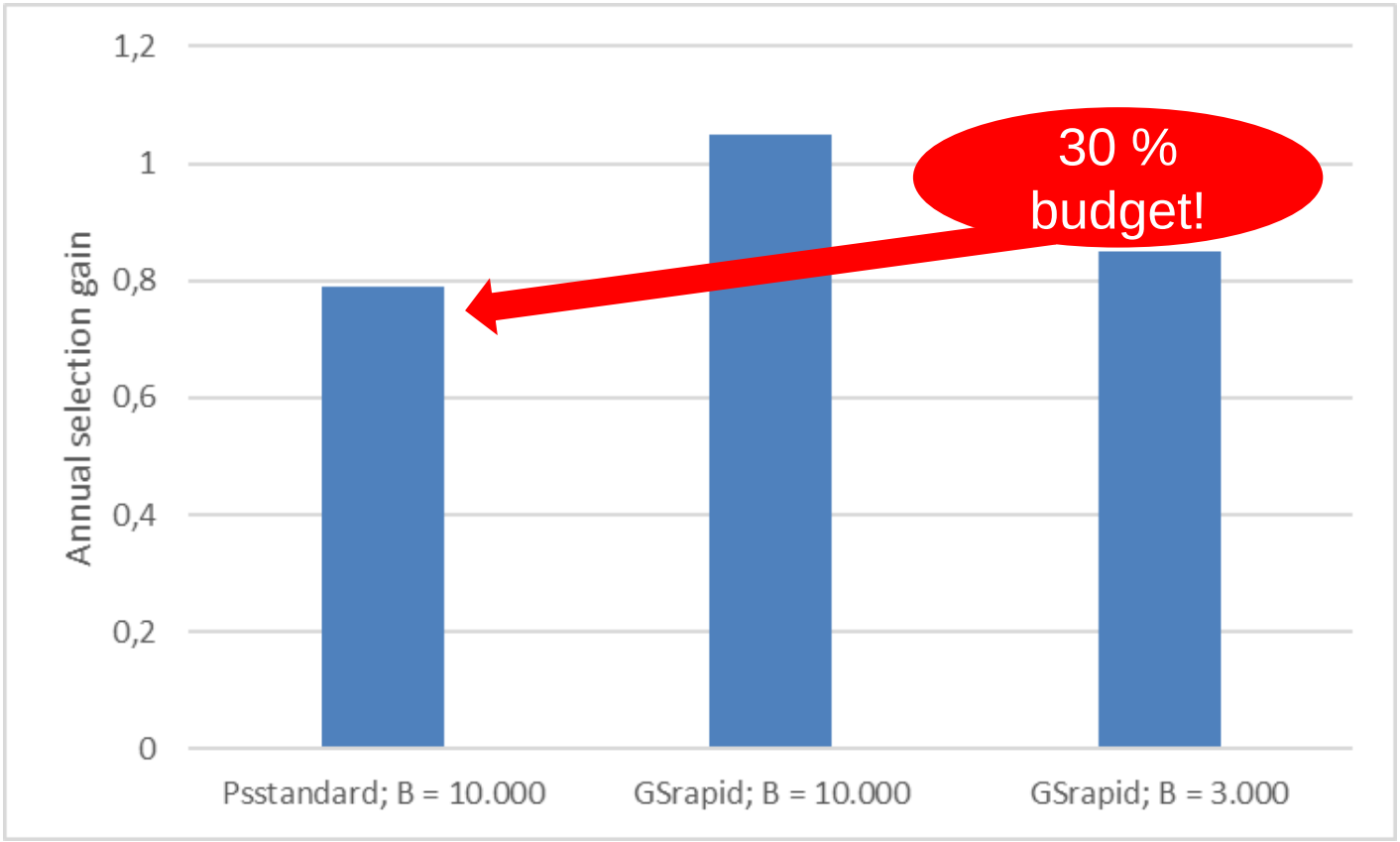
Broad advantage of *GSrapid*



The use of GS in elite breeding is recommended for a broad range of scenarios; also for small breeding programs!

Source: Marulanda et al. 2016

Think about….



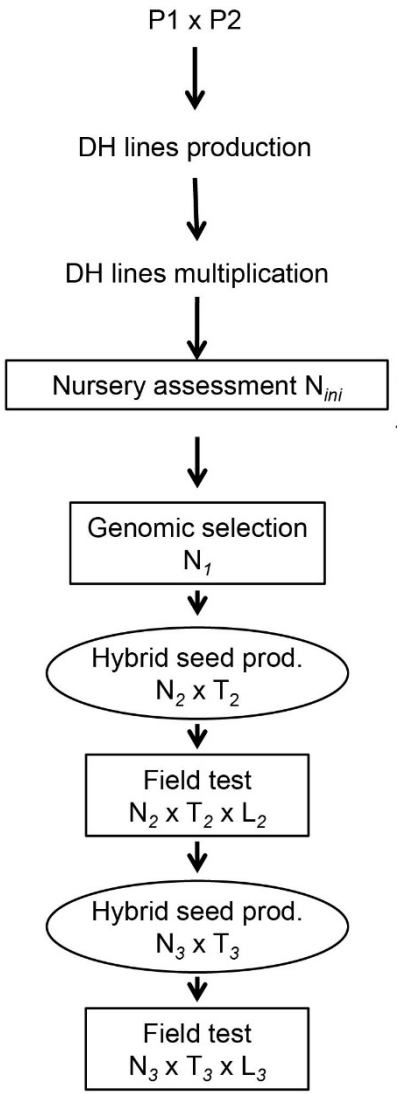
Using **GSrapid** with a budget of 3.000 field plots has a 7.6 % higher annual selection gain than PSstandard with a budget of 10.000 field plots!

Source: Marulanda et al. 2016

Realization of GSrapid

```
Budget = 10000
VCGCAandError = c(5.7,5.19,0,0,24.37)
VCSCA = c(1.88,2.94,0,0)

multistageoptimum.search (
          maseff=0.3, alpha.nursery = 0.25,
        VGCAandE=VCGCAandError, VSCA=VCSCA,
          cost.nursery = c(1,0.3), CostProd = c(0,4,0),
          CostTest = c(2,1,0), t2free = T,
          Nf = 5, Budget = Budget,
        N2grid = c(5, 511, 10), N3grid = c(5, 5, 1),
        L2grid=c(1,5,1), L3grid=c(0,0,1),
        T2grid=c(1,3,1), T3grid=c(0,0,1),
        R2=1, R3=1, alg = Miwa(),
        detail=FALSE, fig=FALSE)
```



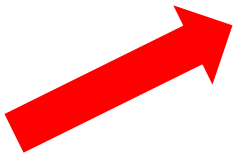
GSstandard

Student simulations

?

Line breeding

	$PS_{standard}$	GS_{rapid}
Year 1	P1 x P2, …	P1 x P2, …
Year 2	DH-Production	DH-Production
Year 3	Nursery with N_{nurs} DH lines	Nursery with N_{nurs} DH lines
		Genomic selection N_{GS}
Year 4	Field test $N_1 * L_1$	Field test $N_1 * L_1$
Year 5	Field test $N_2 * L_2$	



1 year faster

Questions

- Is Gsrapid better than PS standard also **for line breeding**?
- Does **nursery selection** impacts the ranking fo the breeding schemes?
- Is **SSD competitive to DH**?

→ Look on annual and absolute selection gain and elaborate potential differences in the allocation of resources

Questions

- Is Gsrapid better than PS standard also **for line breeding**?
- Does **nursery selection** impacts the ranking fo the breeding schemes?
- Is **SSD competitive to DH**?

→ Look on annual and absolute selection gain and elaborate potential differences in the allocation of resources

- **<u>Three student groups</u>**
  - Optimize both breeding schemes for line breeding and different budgets
  - Optimize both breeding schemes for different intensity of nursery selection for ρ(GS, per se) = 0.3, 0.5, 0.7
  - Optimize both breeding schemes for SSD and DH

How to realize

Examples for wheat:

- Budget: large =12 000; small = 5 000
- VCGCAandError=c(14.06, 22.27, 0, 0, 24.37)
- VCSCA=c(0, 0, 0,0)
- Cost DH = 1
- Cost nursery = 0.3
- Cost GS = 3 versus 1
- GS prediction ability for yield = 0.3, 0.4, 0.5

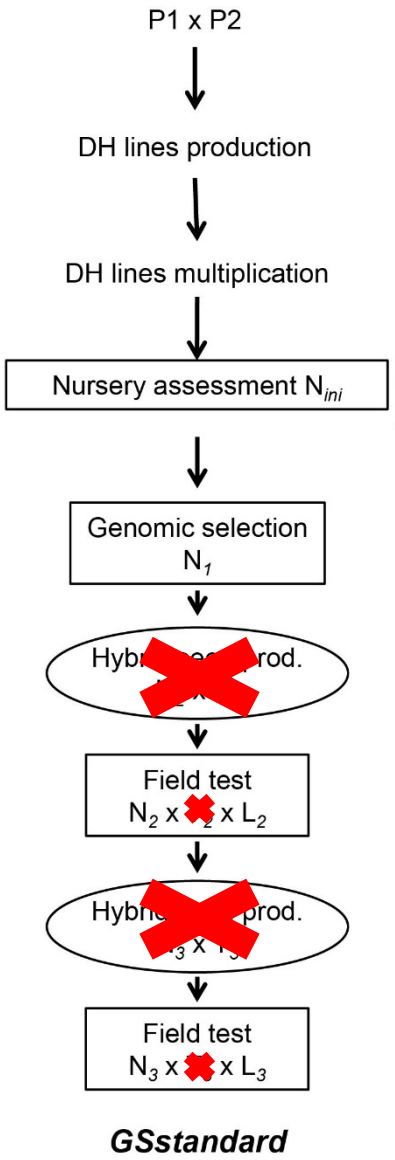
Compare SSD with DHs: play around with

- Cost SSD = 0.1
- σ^2_G (SSD) =0.88 * σ^2_G (DH)
- Cycle length DH versus SSD

Changes in code

```
Budget = 10000
VCGCAandError = c(14.06,22.27,0,0,24.37)
VCSCA = c(0,0,0,0)

multistageoptimum.search (
        maseff=NA, alpha.nursery = 0.25,
      VGCAandE=VCGCAandError, VSCA=VCSCA,
        cost.nursery = c(1,0.3), CostProd = c(0,0,0),
        CostTest = c(2,1,1), t2free = T,
        Nf = 5, Budget = Budget,
      N2grid = c(5, 6011, 40), N3grid = c(5, 1511, 5),
      L2grid=c(1,5,1), L3grid=c(2,10,1),
      T2grid=c(1,1,1), T3grid=c(1,1,1),
      R2=1, R3=1, alg = Miwa(),
      detail=FALSE, fig=FALSE)
```



SSD better than DH?

Breeding schemes with phenotypic selection in 2 years on yield

	DH-fast	DH-slow	SSD	Pedigree
Year 1	Cross	Cross	Cross	Cross
Year 2	DH	DH	SSD	F1
Year 3	Multiplication	DH	SSD	F2
Year 4	Yield test	Multiplication	Multi	F3
Year 5	Yield test	Yield test	Yield test	F4
Year 6		Yield test	Yield test	Yield test
Year 7				Yield test

- DH fast: able to realize?
- DH slow: realizable for all crosses

Contact

PD Dr. Friedrich Longin

State Plant Breeding Institute, University of Hohenheim,

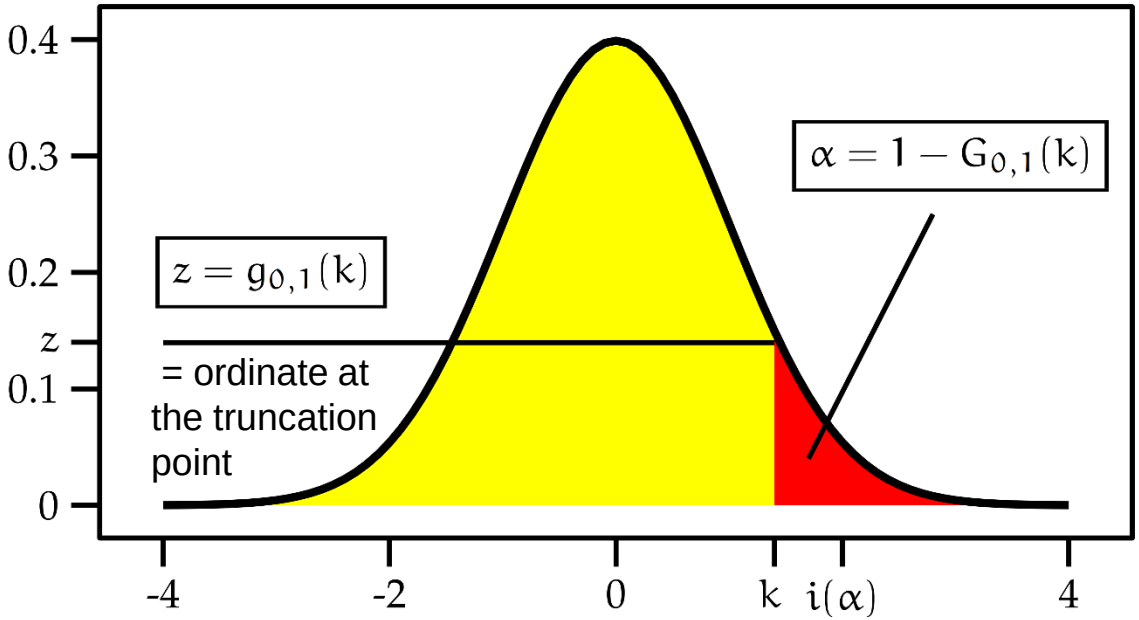
Fruwirthstrasse 21

70593 Stuttgart, Germany

Phone: (++49) 0711 459 23846

friedrich.longin@uni-hohenheim.de

Prediction of selection intensity



$$S = i(\alpha)\sigma_P$$

$$\alpha = \frac{no.selected\ lines}{no.tested\ lines}$$

$k = G_{0,1}^{-1}(1-\alpha)$ = truncation point calculated by the cumulative density function

$$i(\alpha) = \frac{z(\alpha)}{\alpha} = \frac{g_{0,1}(k)}{\alpha} = \frac{g_{0,1}[G_{0,1}^{-1}(1-\alpha)]}{\alpha}$$

Source: Schrag/Frisch

Realisation in R

Numerical calculation:

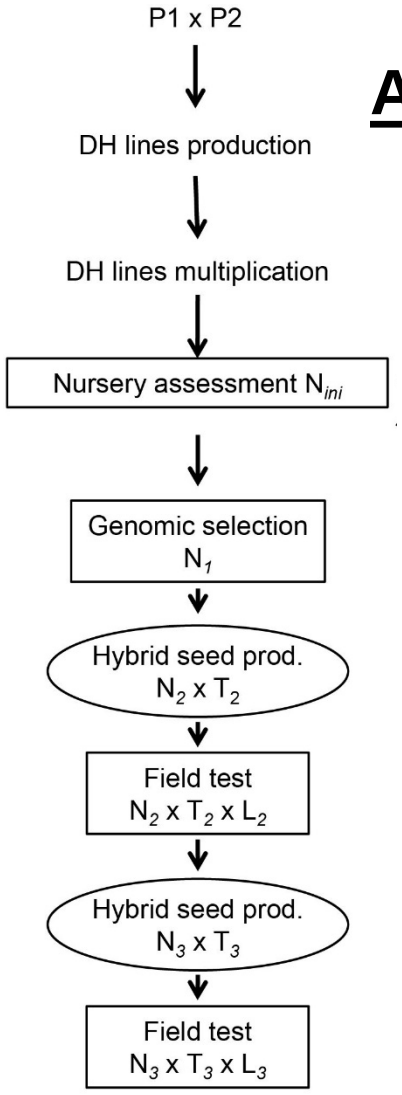
$$i(\alpha) = \frac{z(\alpha)}{\alpha} = \frac{g_{0,1}(k)}{\alpha} = \frac{g_{0,1}[G_{0,1}^{-1}(1-\alpha)]}{\alpha}$$

	R	Excel
$g_{\mu,\sigma^2}(x)$	`dnorm(x,mu,sigma)`	`=NORMVERT(x;mu;sigma;0)`
$G_{\mu,\sigma^2}(x)$	`pnorm(x,mu,sigma)`	`=NORMVERT(x;mu;sigma;1)`
$G^{-1}_{\mu,\sigma^2}(1-\alpha)$	`qnorm(1-alpha,mu,sigma)`	`=NORMINV(1-alpha;mu;sigma)`

Keep in mind:

- these formula assume infinite number of candidates
- for exact calculation → order statistics but difficult to realize for multistage selection
- no difference in allocation of resources and selection gain only slightly overestimated by infinitessimal model

Multistage selection = multivariate distributions



GSstandard

Approximation from Dickerson and Hazel 1944

$$\Delta G = i_1 \rho_1 \sigma_y + i_2 \rho_2' \sigma_y'$$

- ρ_1 = heritability
- σ_y' = genetic variance after first selection = $\sqrt{\sigma_y^2 (1 - \rho_1^2 (i_1 (i_1 - k_1))}$ → **> for decreased α**
- $\rho_2' = \frac{\rho_2 - \rho_1 \rho_{12} i_1 (i_1 - k_1)}{\sqrt{(1 - \rho_1^2 i_1 (i_1 - k_1)(1 - \rho_{12}^2 i_1 (i_1 - k_1))}}$

Interested in more details?

Vortr. Pflanzenzüchtg. 7, 30-40 (1984)

Calculating and maximizing the gain from selection

H.F. Utz

Institute of Plant Breeding, Seed Science, and Population Genetics, University of Hohenheim

1. Introduction

The breeder must often predict the gain due to selection. As early as 1934, STUDENT used the gain to interpret a selection experiment. With the aid of the expected gain, SMITH (1936) derived the optimum weighting of characters, i.e. the selection index. In the meantime, this equation has become a standard instrument in deciding which alternative selection procedure is better or in answering questions such as how many replications or candidates would be needed to reach a maximum of gain. KEMPTHORNE (1977) succinctly stated that the expected gain is "the 'work horse' formula of quantitative selection".

Whoever calculates expected gains will be confronted with certain numerical problems. It will therefore be useful to discuss the calculation and maximization of such gains. In the following paper, the basic formulae will be presented and some helpful approximations given for the cases of one-stage and multi-stage selection.

2. Predicting gain from selection

where σ_y is the standard deviation of the genetic values y of the candidates,

$\rho_{y\eta}$ is the correlation coefficient between y and the phenotypic measurement η, which can be a single observation, a mean of values, or a selection index criterion, and

$i_{(\alpha)}$ is the selection intensity or the standardized selection differential.

The determination of σ_y and $\rho_{y\eta}$ is rather a problem of estimation, since the parameters of the population undergoing selection are usually unknown. The size of $\rho_{y\eta}$ depends on the test situation, the number of replications, of locations, and also which parts of the genetic variance can be exploited. A detailed discussion of these topics can be found in the textbook of HALLAUER and MIRANDA (1981) or in SCHNELL (1982).

Assuming a normal distribution for y and a great population of candidates, then the selection intensity can be obtained as

$$i_{(\alpha)} = z_{(\alpha)} / \alpha \qquad (2)$$

where $z_{(\alpha)}$ is the ordinate of the standardized normal distribution at the point of truncation, and

α is the selected fraction.

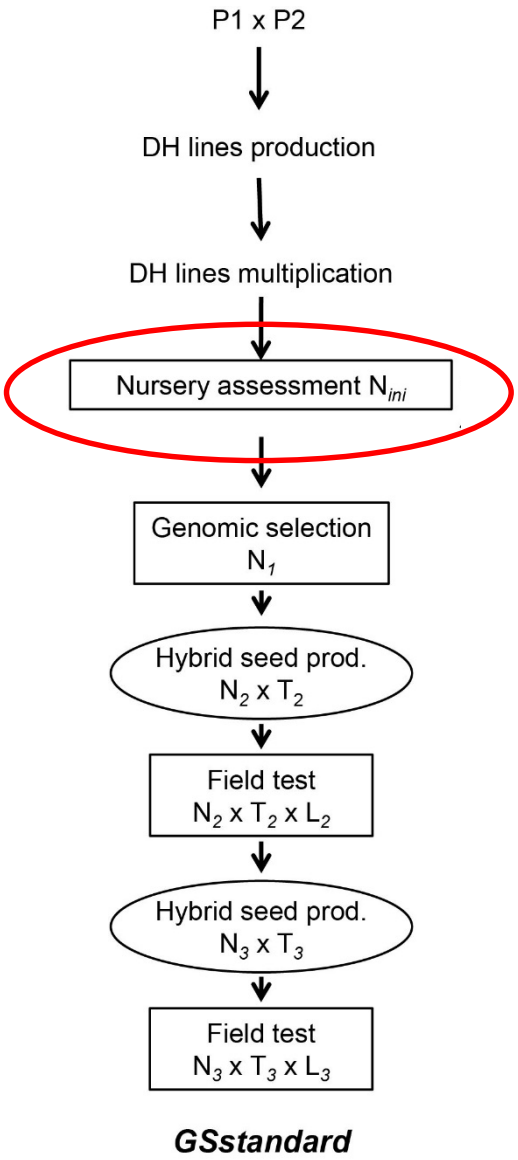
The ordinate $z_{(\alpha)}$ for certain α is tabulated in standard statistical tables (cf. PEARSON and HARTLEY, 1970). The direct use of tables of $i_{(\alpha)}$ is more convenient. KONDO and ELDERTON (1931) tabulated $i_{(\alpha)}$ for $\alpha = 0.001(0.001)1$ with 10 decimals. BECKER (1975) gives tables for the same steps

- For exact formulas: Mi Papers, Cochran (1951),…
- For finite sample size: MC simulations or order statistics

Nursery selection

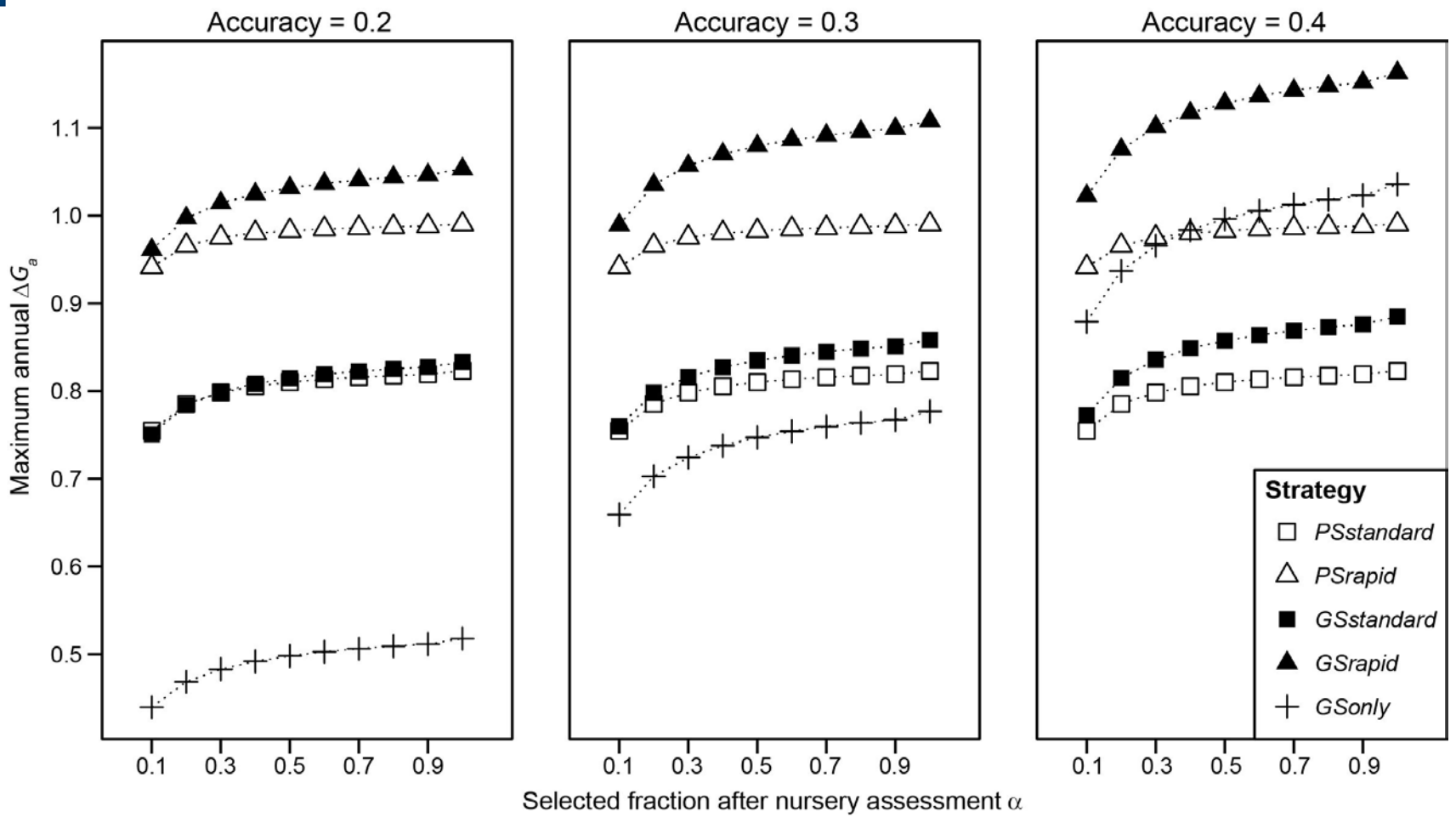
Further data required:

- Breeders usually select lines first based on high heritable traits (diseases, qualities,…)
- Assumption: traits observed in nursery do **not correlate with target trait, eg. GCA for grain yield**
- Cost for nursery selection = 0.3 yield plots



Source: Marulanda et al. 2016

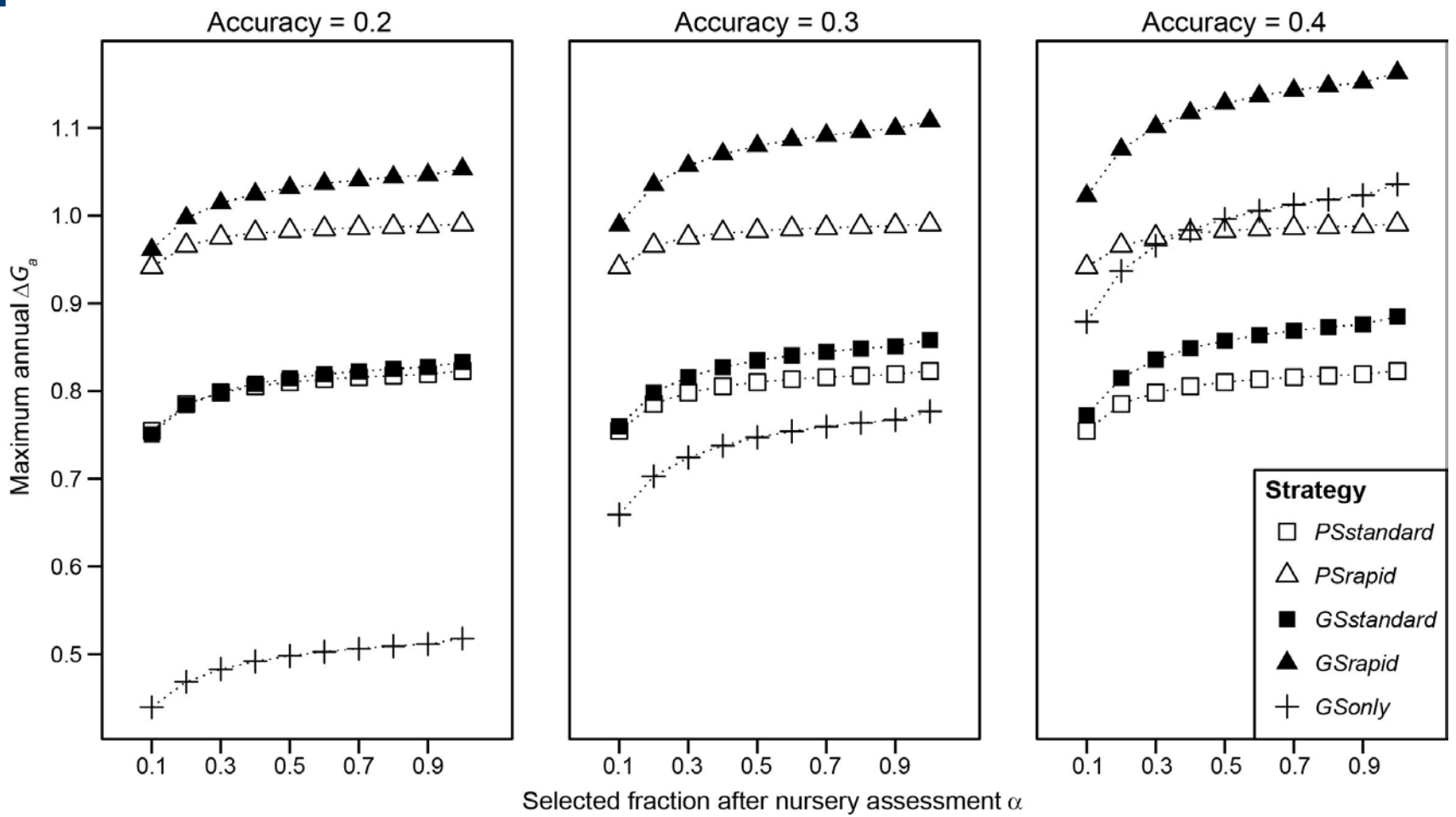
Impact of nursery selection



1. Ranking of schemes nearly not affected by nursery selection → GSrapid is top!

Source: Marulanda et al. 2016

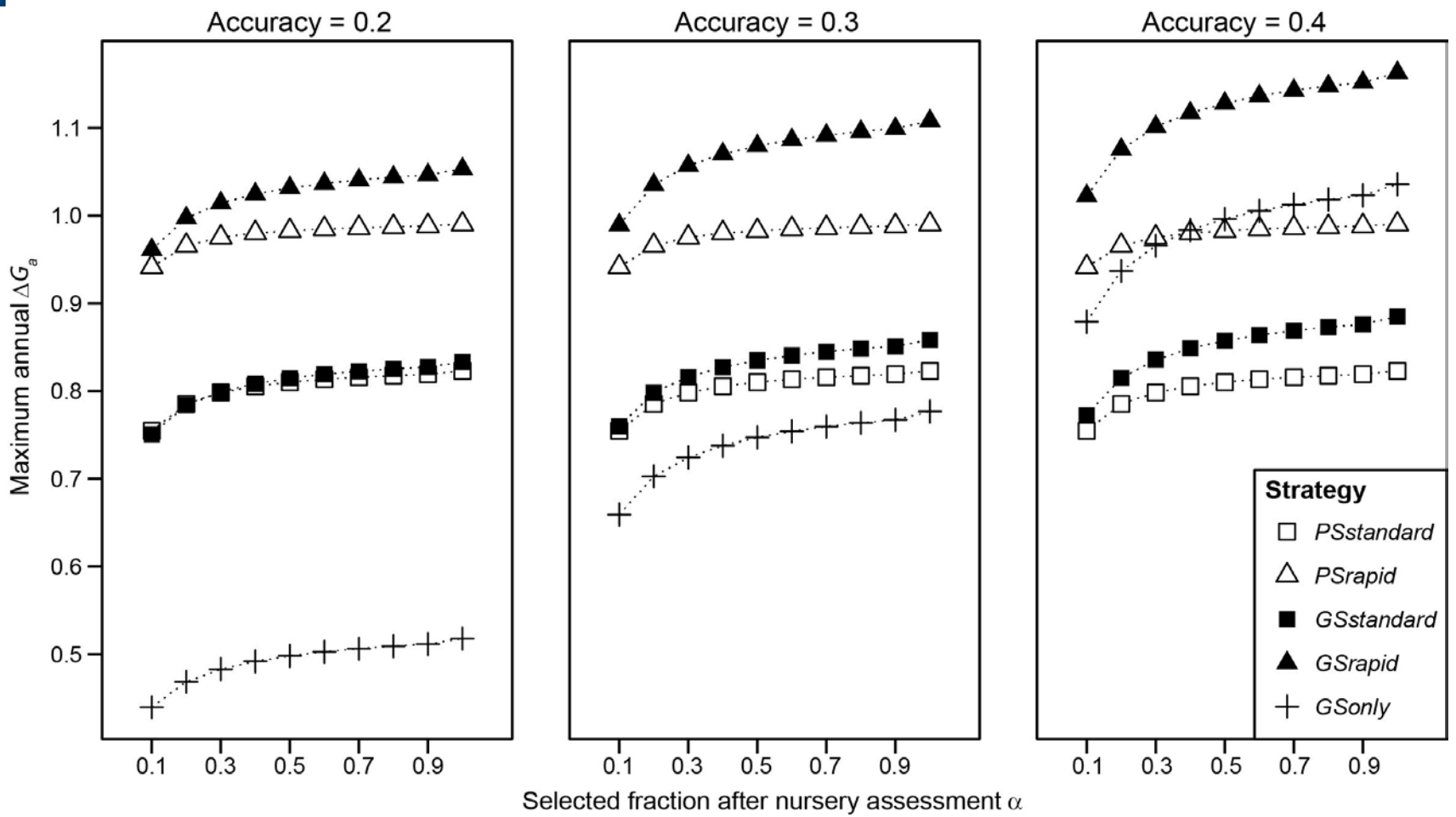
Impact of nursery selection



2. With increasing nursery selection (smaller α), ΔG_a for grain yield is reduced

Source: Marulanda et al. 2016

Impact of nursery selection



3. This reduction is larger for GS schemes and for increased GS prediction accuracy

Source: Marulanda et al. 2016