

Implementation of genetic gain assessment using the BRRI data

Overview

Two datasets

- Aman & Boro
- Get mean yield for each genotype at each environment

Genetic gain assessment

1. Incorporating regression terms in basic MET mixed model
 - Genetic trend: βr_i
 - Per group
 - Agronomic trend: γt_k

Two datasets

- Aman & Boro

Data

Data

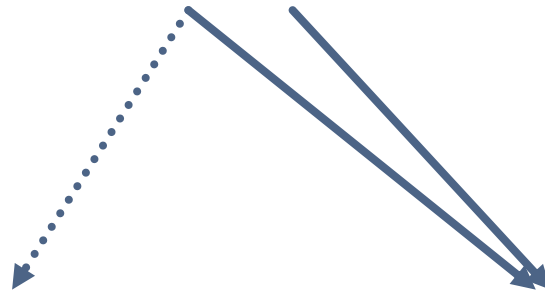
Original

SL	Year	Location	Year of release	Rep	Variety	Group	Yield
1	2001	Barisal	1980	1	BR10	Long	3.5
2	2001	Comilla	1980	1	BR10	Long	5.01104651
3	2001	Gazipur	1980	1	BR10	Long	4.28023256
4	2001	Rajshahi	1980	1	BR10	Long	4.48

Data

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4	2001	Rajshahi	1980	1	BR10	Long	4.48



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	Y	t.k	r.i	L	Env	G	Rep	Group	Yield
1:	2001	2001	1980	Barisal	2001-Barisal	BR10	1	Long	3.500000
2:	2001	2001	1980	Comilla	2001-Comilla	BR10	1	Long	5.011047
3:	2001	2001	1980	Gazipur	2001-Gazipur	BR10	1	Long	4.280233
4:	2001	2001	1980	Rajshahi	2001-Rajshahi	BR10	1	Long	4.480000
5:	2001	2001	1980	Rangpur	2001-Rangpur	BR10	1	Long	3.176419

7631:	2015	2015	2014	Comilla	2015-Comilla	BRR1	3	Stress	5.219160
7632:	2015	2015	2014	Gazipur	2015-Gazipur	BRR1	3	Stress	1.988598
7633:	2015	2015	2014	Rajshahi	2015-Rajshahi	BRR1	3	Stress	4.926488
7634:	2015	2015	2014	Rangpur	2015-Rangpur	BRR1	3	Stress	2.200000
7635:	2015	2015	2014	Satkhira	2015-Satkhira	BRR1	3	Stress	3.820000

Numeric

New columns

Data

Table: Number of unique entries per column

Aman		Boro	
	number		number
Y	15	Y	15
t.k	15	t.k	15
r.i	18	r.i	16
L	9	L	10
Env	116	Env	137
G	29	G	31
Rep	3	Rep	3
Group	5	Group	3

Data

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Aman		Boro	
	number		number
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t.k	15	t.k	15
r.i	18	r.i	16
L	9	L	10
Env	116	Env	137
G	29	G	31
Rep	3	Rep	3
Group	5	Group	3

Basic model for long-term MET data

$$y_{ijk} = \mu + G_i + L_j + Y_k + (LY)_{jk} + (GL)_{ij} + (GY)_{ik} + (GLY)_{ijk} \quad (1)$$

y_{ijk} = mean yield of the i -th genotype in the j -th location and k -th year

μ = overall mean

Two datasets

- Aman & Boro
- Get mean yield for each genotype at each environment

GxE means

GxE means

Goal: Obtain yield per genotype and environment averaged over replicates

Option 1: Arithmetic means

```
dat[, ari.mean := mean(Yield), by=c("Env", "G")]
```

GxE means

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Option 1: Arithmetic means

```
dat[, ari.mean := mean(Yield), by=c("Env", "G")]
```

Option 2: Adjusted means

For each environment separately:

1. Fit simple linear model: $y_{ij} = \mu + g_i + rep_j + e_{ij}$
2. Calculate adj. means per genotype
3. Calculate Smith's weights (Smith et al., 2001)

```
mod <- lm(formula = Yield ~ G + Rep,  
          data     = subset(dat, Env==dat$Env[sel.env]))  
adj.mean <- emmeans(mod, "G")  
weight   <- diag(solve(vcov(adj.mean)))
```

GxE means

	Y	L	Env	t.k	r.i	Group	G	G.ari.mean	G.adj.mean	w.G
1:	2001	Barisal	2001-Barisal	2001	1980	Long	BR10	3.873333	3.873333	58.926346
2:	2001	Barisal	2001-Barisal	2001	1980	Medium	BR11	3.743333	3.743333	58.926346
3:	2001	Barisal	2001-Barisal	2001	1988	Long	BR22	4.236667	4.236667	58.926346
4:	2001	Barisal	2001-Barisal	2001	1988	Long	BR23	4.710000	4.710000	58.926346
5:	2001	Barisal	2001-Barisal	2001	1992	Medium	BR25	4.086667	4.086667	58.926346

2542:	2015	Sonagazi	2015-Sonagazi	2015	2011	Short	BRR1 dhan57	2.372395	2.372395	15.605064
2543:	2015	Sonagazi	2015-Sonagazi	2015	2011	Stress	BRR1 dhan57	2.372395	2.372395	15.605064
2544:	2015	Sonagazi	2015-Sonagazi	2015	2013	Short	BRR1 dhan62	2.784334	2.784334	7.802532
2545:	2015	Sonagazi	2015-Sonagazi	2015	2014	Short	BRR1 dhan66	3.523763	3.523763	15.605064
2546:	2015	Sonagazi	2015-Sonagazi	2015	2014	Stress	BRR1 dhan66	3.523763	3.523763	15.605064

Aman

Boro

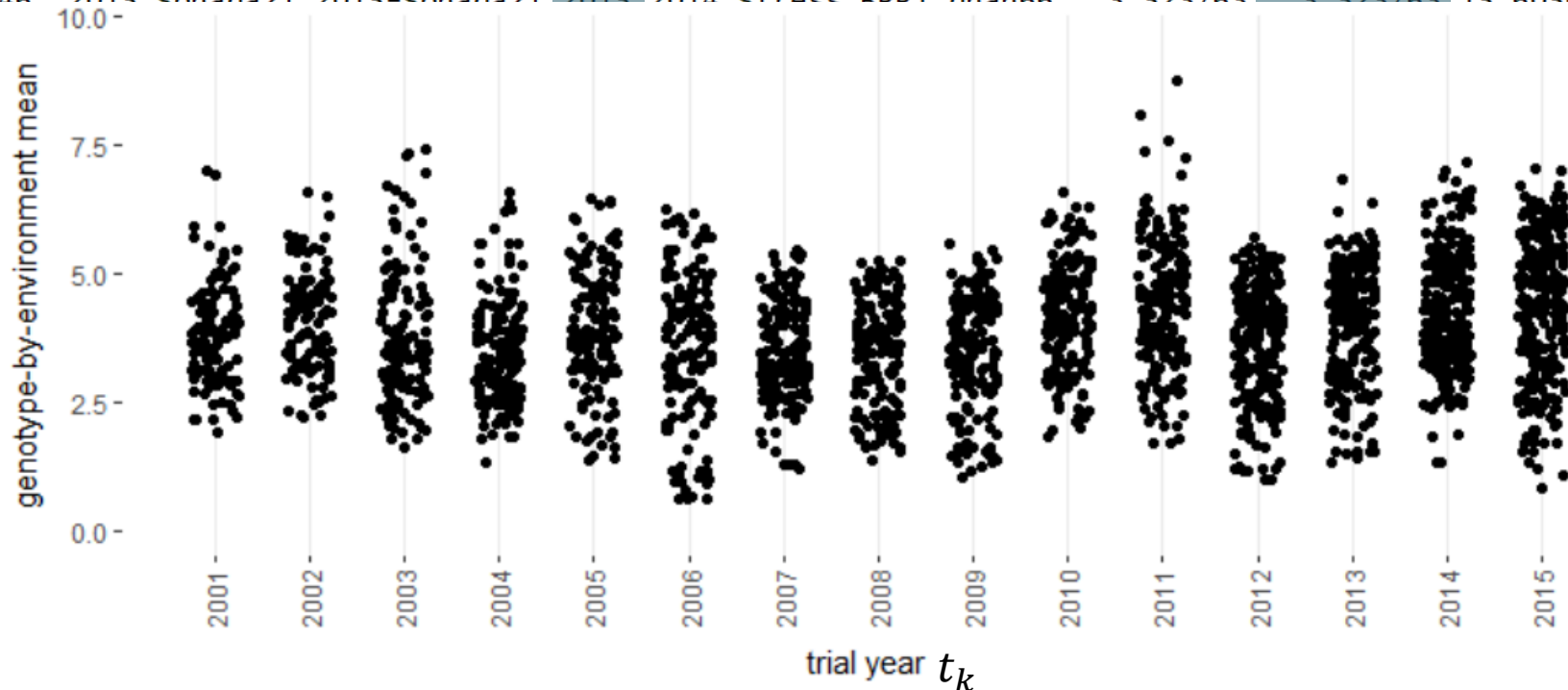
	Y	L	Env	t.k	r.i	Group	G	G.ari.mean	G.adj.mean	w.G
1:	2001-2002	Barisal	2001-2002-Barisal	2001	1970	Short	BR1	6.556667	6.556667	16.369190
2:	2001-2002	Barisal	2001-2002-Barisal	2001	1983	Long	BR12	7.556667	7.556667	16.369190
3:	2001-2002	Barisal	2001-2002-Barisal	2001	1983	Long	BR14	6.390000	6.390000	16.369190
4:	2001-2002	Barisal	2001-2002-Barisal	2001	1983	Long	BR15	6.820000	6.820000	16.369190
5:	2001-2002	Barisal	2001-2002-Barisal	2001	1983	Long	BR16	7.073333	7.073333	16.369190

2909:	2015-2016	Sonagazi	2015-2016-Sonagazi	2015	2014	Short	BRR1 dhan63	3.930000	3.930000	4.818834
2910:	2015-2016	Sonagazi	2015-2016-Sonagazi	2015	2014	Long	BRR1 dhan64	6.000000	6.000000	4.818834
2911:	2015-2016	Sonagazi	2015-2016-Sonagazi	2015	2014	Stress	BRR1 dhan67	3.956667	3.956667	4.818834
2912:	2015-2016	Sonagazi	2015-2016-Sonagazi	2015	2014	Short	BRR1 dhan68	6.056667	6.056667	4.818834
2913:	2015-2016	Sonagazi	2015-2016-Sonagazi	2015	2014	Long	BRR1 dhan69	5.140000	5.140000	4.818834

GxE means

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1:	2001	Barisal	2001-Barisal	2001	1980	Long	BR10	3.873333	3.873333	58.926346
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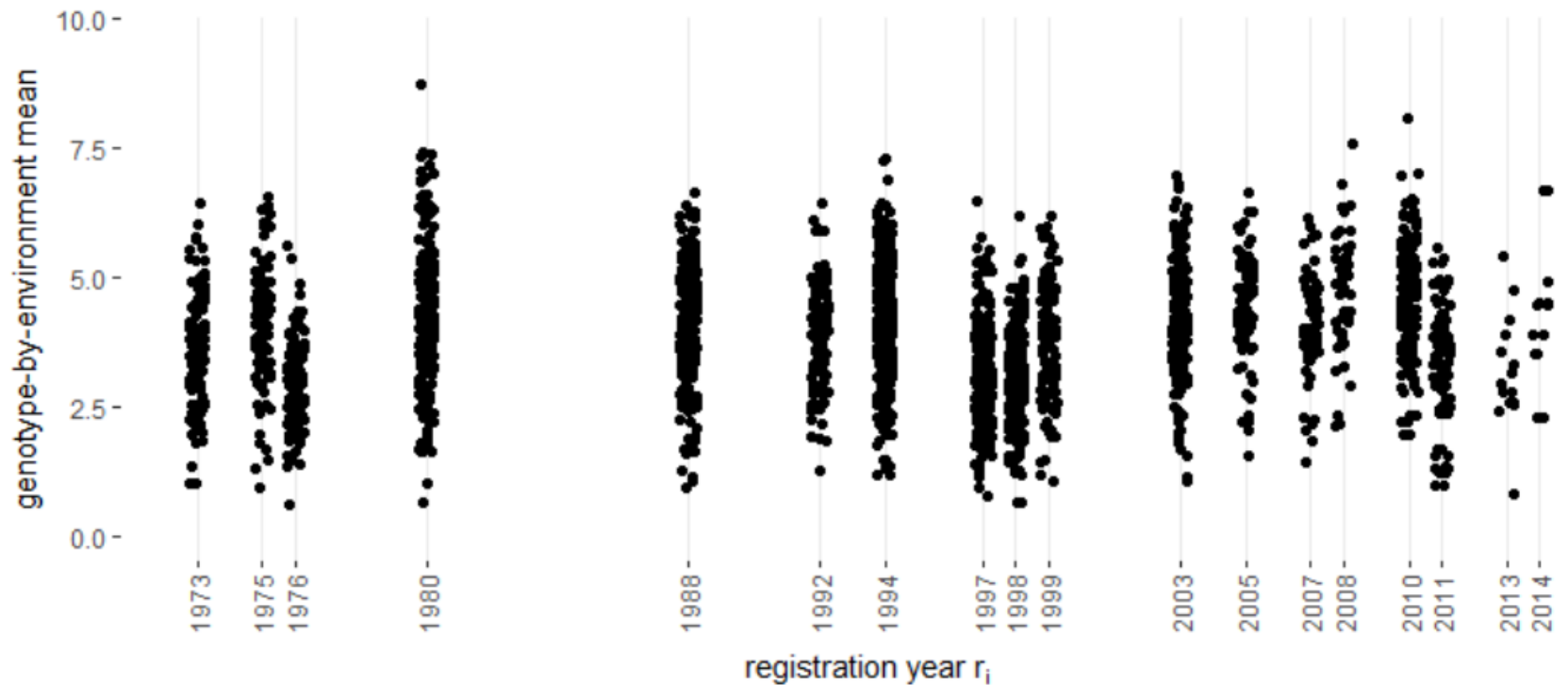


Genotype-by-environment means from aman dataset.

GxE means

	Y	L	Env	t.k	r.i	Group	G	G.ari.mean	G.adj.mean	w.G
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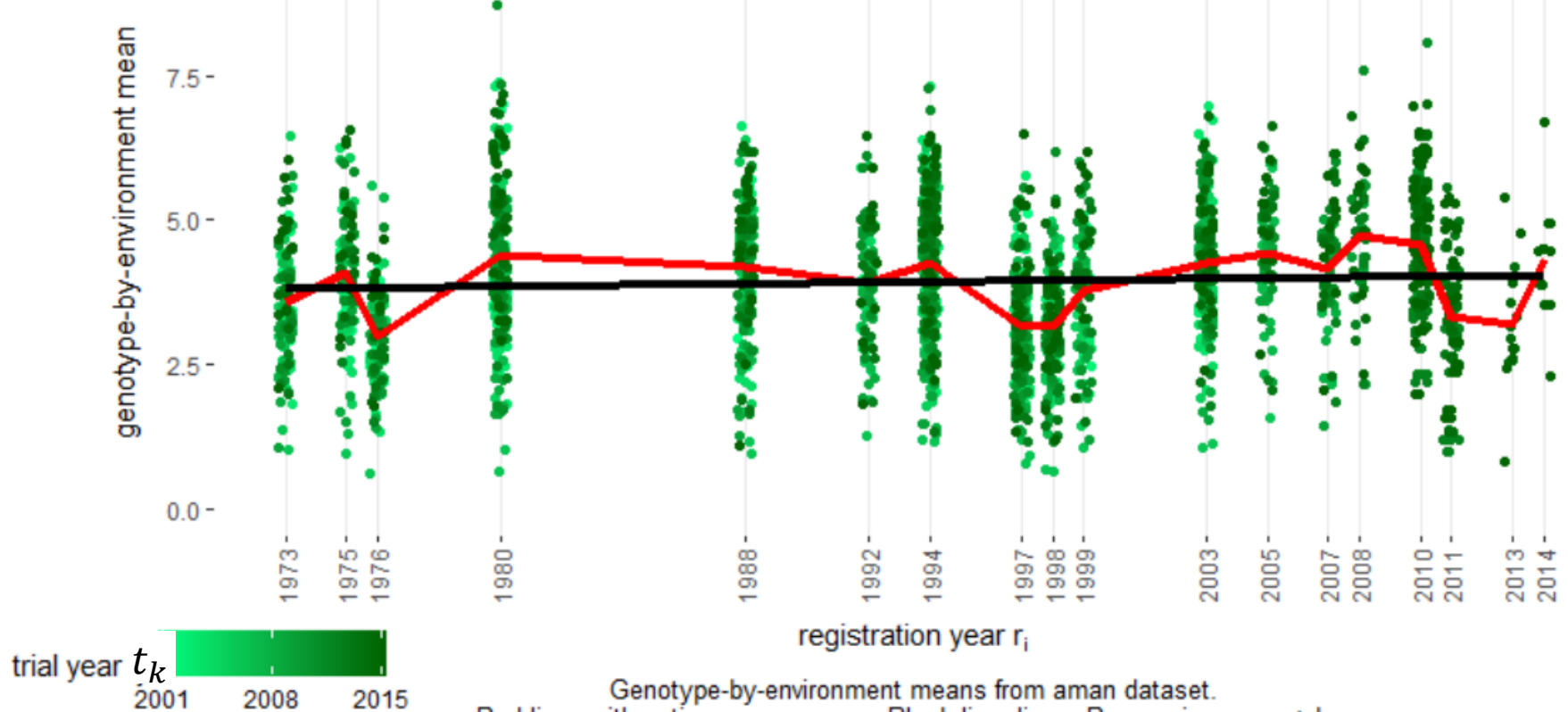


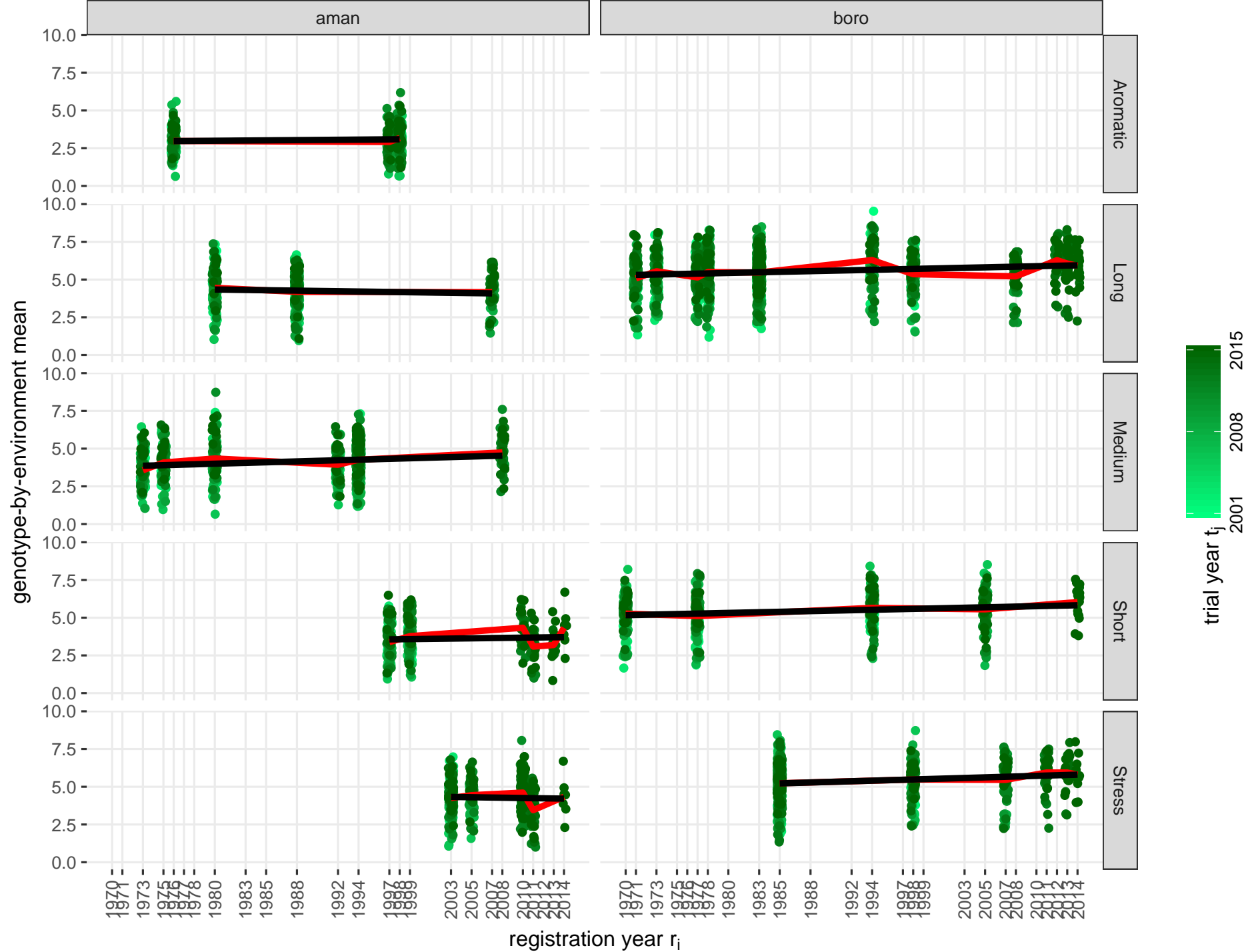
Genotype-by-environment means from aman dataset.

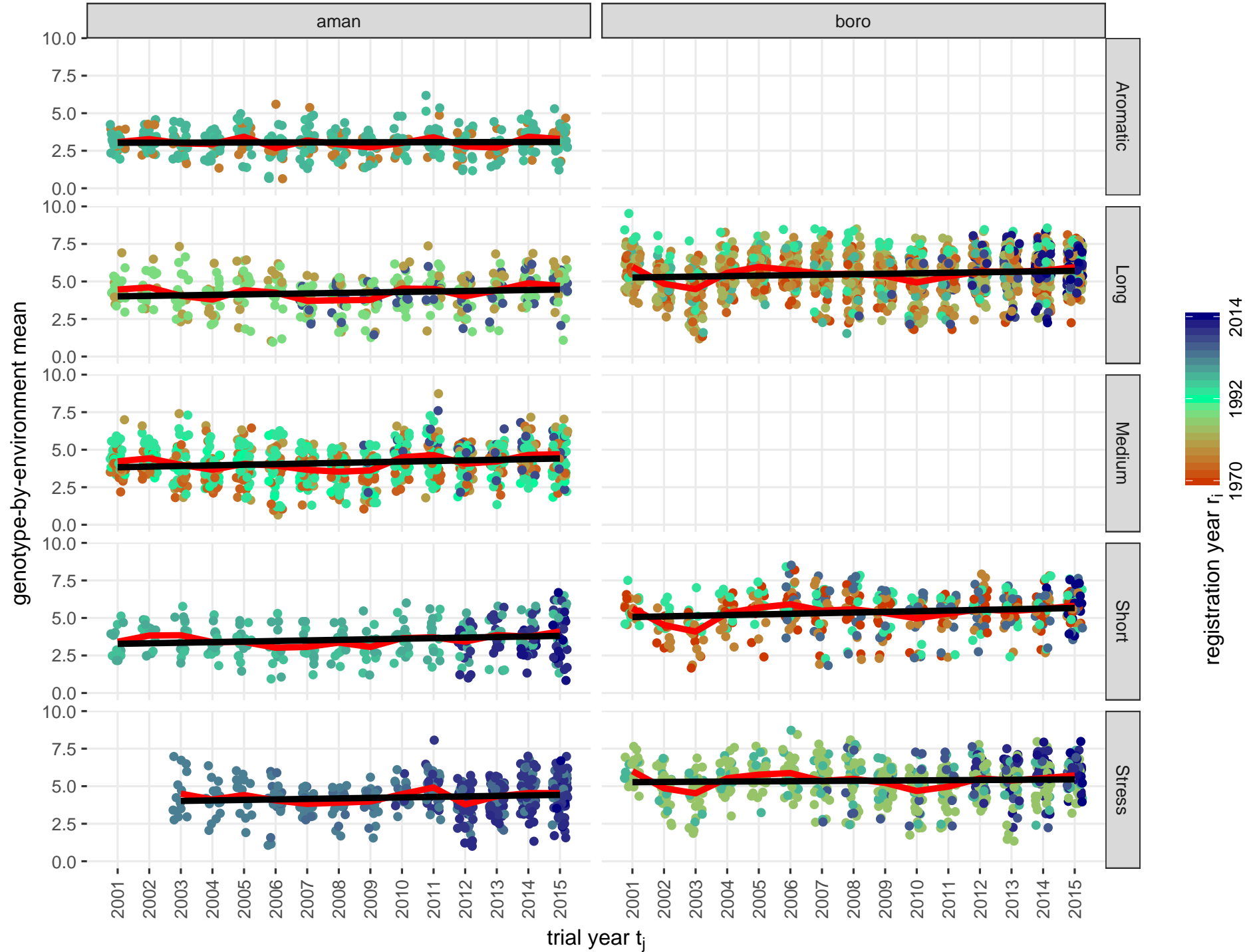
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Genetic gain assessment

1. Incorporating regression terms in basic MET mixed model

Genetic gain assessment

Genetic trend: βr_i
Agronomic trend: γt_k

```
lmer(formula = G.ari.mean ~ r.i + t.k +  
      (1|G) + (1|L) + (1|Y) + (1|Y:L) + (1|L:G) + (1|Y:G),  
      data = dat)
```

Basic model for long-term MET data

$$y_{ijk} = \mu + G_i + L_j + Y_k + (LY)_{jk} + (GL)_{ij} + (GY)_{ik} + (GLY)_{ijk} \quad (1)$$

y_{ijk} = mean yield of the i -th genotype in the j -th location and k -th year
 μ = overall mean
 G_i = main effect of the i -th genotype
 L_j = main effect of the j -th location
 Y_k = main effect of the k -th year
 $(LY)_{jk}$ = jk -th location \times year interaction
 $(GL)_{ij}$ = ij -th genotype \times location interaction
 $(GY)_{ik}$ = ik -th genotype \times year interaction
 $(GLY)_{ijk}$ = residual comprising both genotype \times location \times year interaction as well as the error of a mean

2. Incorporating regression terms

Genetic trend

$$G_i = \beta r_i + H_i \quad (2)$$

β = fixed regression coefficient for genetic trend

r_i = year of first trial for i -th variety

$$H_i \sim N(0, \sigma_H^2)$$

Non-genetic trend

$$Y_k = \gamma t_k + Z_k \quad (3)$$

γ = fixed regression coefficient for agronomic trend

t_k = calendar year

$$Z_k \sim N(0, \sigma_Z^2)$$

Genetic gain assessment

Genetic trend per group: βr_{il}
 Agronomic trend: γt_k

```
lmer(formula = G.ar1.mean ~ r.i:Group + t.k +  
      (1|G) + (1|L) + (1|Y) + (1|Y:L) + (1|L:G) + (1|Y:G),  
      data = dat)
```

Basic model for long-term MET data

$$y_{ijk} = \mu + G_i + L_j + Y_k + (LY)_{jk} + (GL)_{ij} + (GY)_{ik} + (GLY)_{ijk} \quad (1)$$

y_{ijk} = mean yield of the i -th genotype in the j -th location and k -th year
 μ = overall mean
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$$H_i \sim N(0, \sigma_H^2)$$

Non-genetic trend

$$Y_k = \gamma t_k + Z_k \quad (3)$$

γ = fixed regression coefficient for agronomic trend

t_k = calendar year

$$Z_k \sim N(0, \sigma_Z^2)$$

Summary: Genetic gain assessment

Dataset	Group	Genetic Trend	Agronomic Trend
aman	Aromatic	0.0053 (p=0.562)	0.0192 (p=0.353)
	Long	0.0059 (p=0.520)	
	Medium	0.0059 (p=0.523)	
	Short	0.0057 (p=0.527)	
	Stress	0.0057 (p=0.529)	
boro	Long	0.0124 (p<0.001)	0.0189 (p=0.779)
	Short	0.0123 (p<0.001)	
	Stress	0.0123 (p<0.001)	