Comparison of genomic selection approaches in Brown Swiss within Intergenomics

P. Croiseau, F. Guillaume and S. Fritz

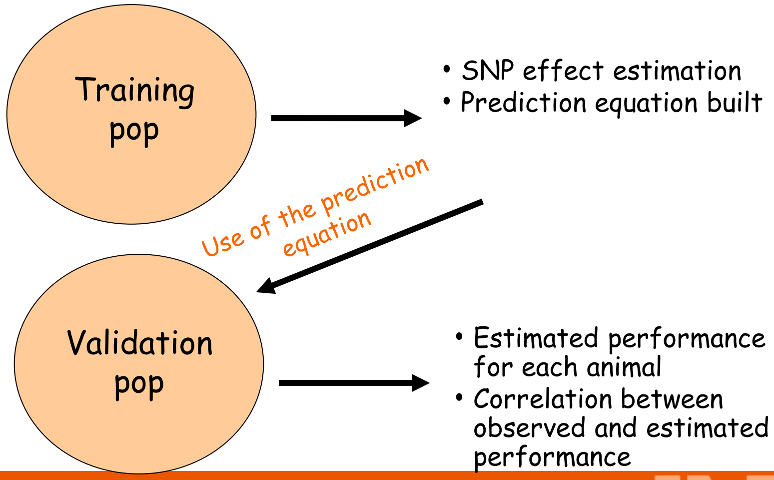
DATA

- 7041 animals genotyped on 50K chip
- 6 countries included: CHE, DEA, FRA, ITA, SVN, USA
- Between 3 and 15 traits by country

	CHE	DEA	FRA	ITA	SVN	USA
Nb of traits	15	15	13	12	3	15
production	3	3	3	3	3	3
type	9	9	8	7	0	9
functional	3	3	2	2	0	3

- In this study, we focus on
  - 5 countries: CHE, DEA, FRA, ITA and USA
  - 10 common traits (prod:3, func:1 and type:6)

DATA


Training pop

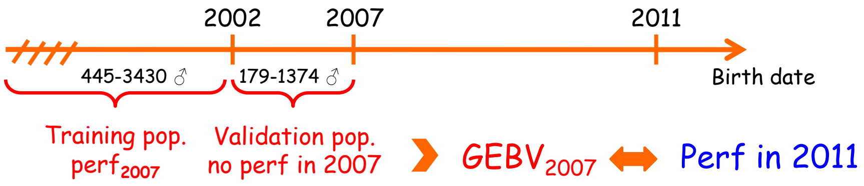
- SNP effect estimation
- Prediction equation built

Use of the prediction equation

Validation pop

- Estimated performance for each animal
- Correlation between observed and estimated performance

DATA



Training pop. perf_{2007}

Validation pop. no perf in 2007

❯ GEBV_{2007} ⟺ Perf in 2011

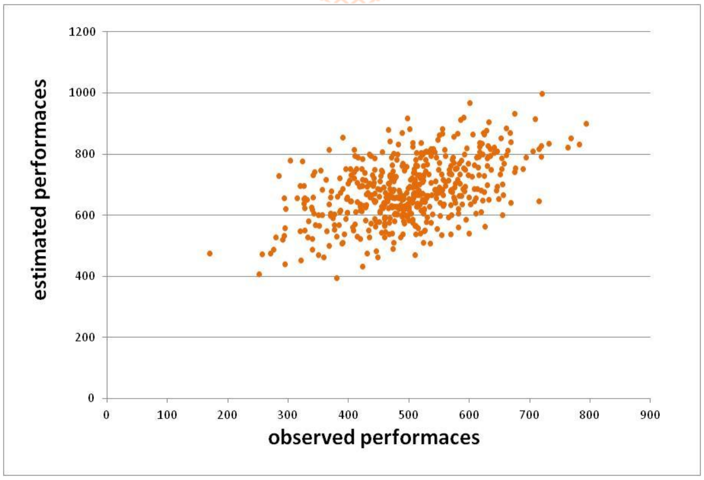
5 methods investigated

- gBLUP where a effect is estimated for each SNP
  - When the number of animal is drastically lower than the number of SNP, this method is not optimal
- Comparison with a set of methods of variable selection
  - The effect of a set of SNP will be shrinked toward 0 for a better estimation of the other SNP effect.
  - Bayesian LASSO
  - Bayes Cπ
  - EN
  - Genomics MAS (French approach)
- Comparison with a pedigree-based BLUP

Analysis

- 2 criteria to compare genomic selection approaches:
  - Correlation between observed and estimated performances
    - Included between 0 and 1

Analysis : corr=0.50



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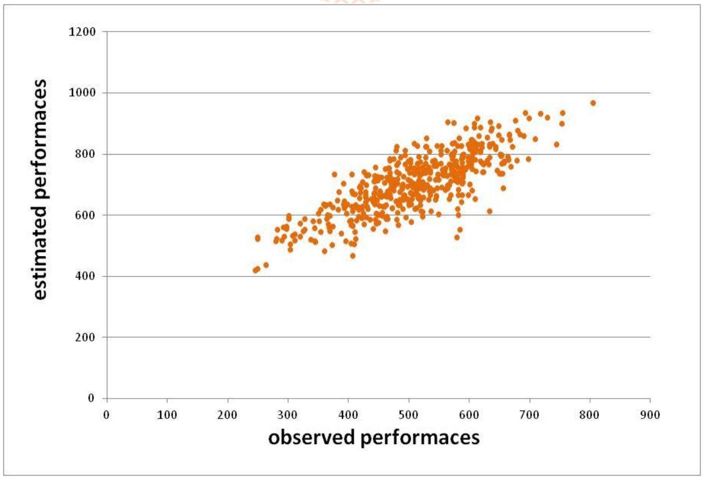
Analysis : corr=0.80



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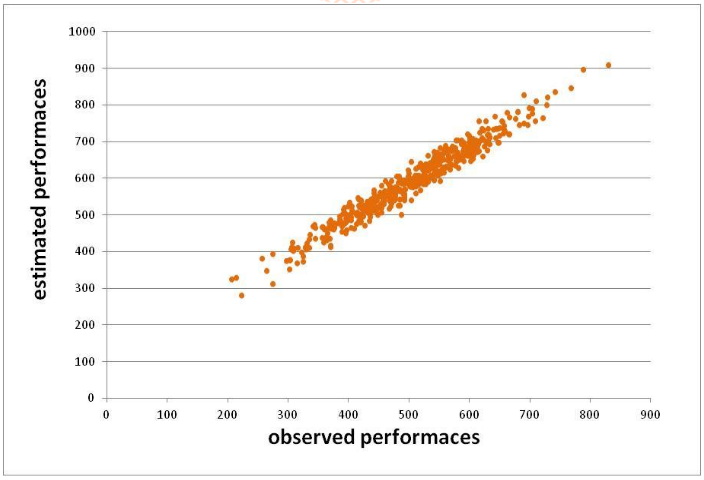
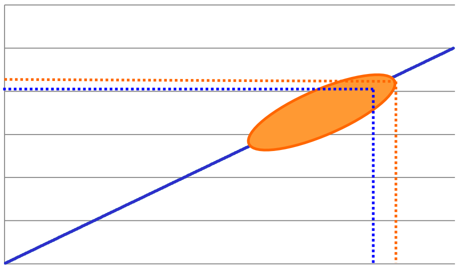
Analysis : corr=0.98



Analysis

- 2 criteria to compare genomic selection approaches:
  - Correlation between observed and estimated performances
    - Included between 0 and 1
  - Slope of regression
    - Expected to be close to 1

Analysis : corr=0.98



Same slope of regression
for the training pop and the validation pop

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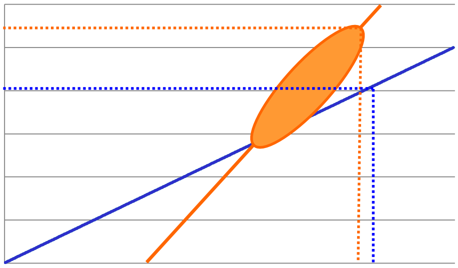
Analysis : corr=0.98



Different slope of regression
for the training pop (slope=1) and the validation pop (slope>1)

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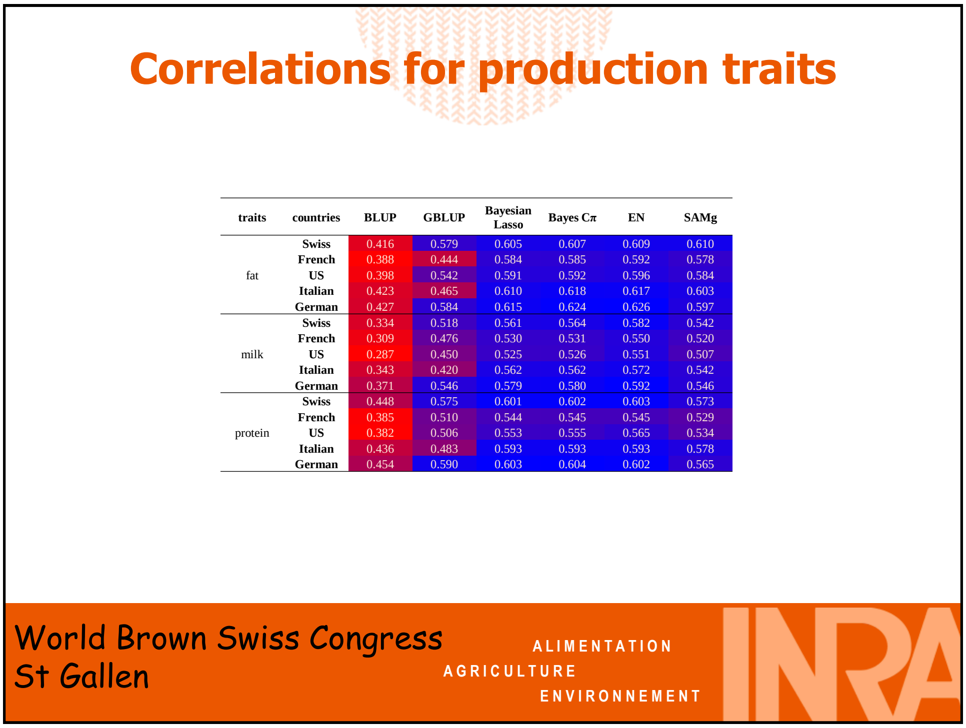
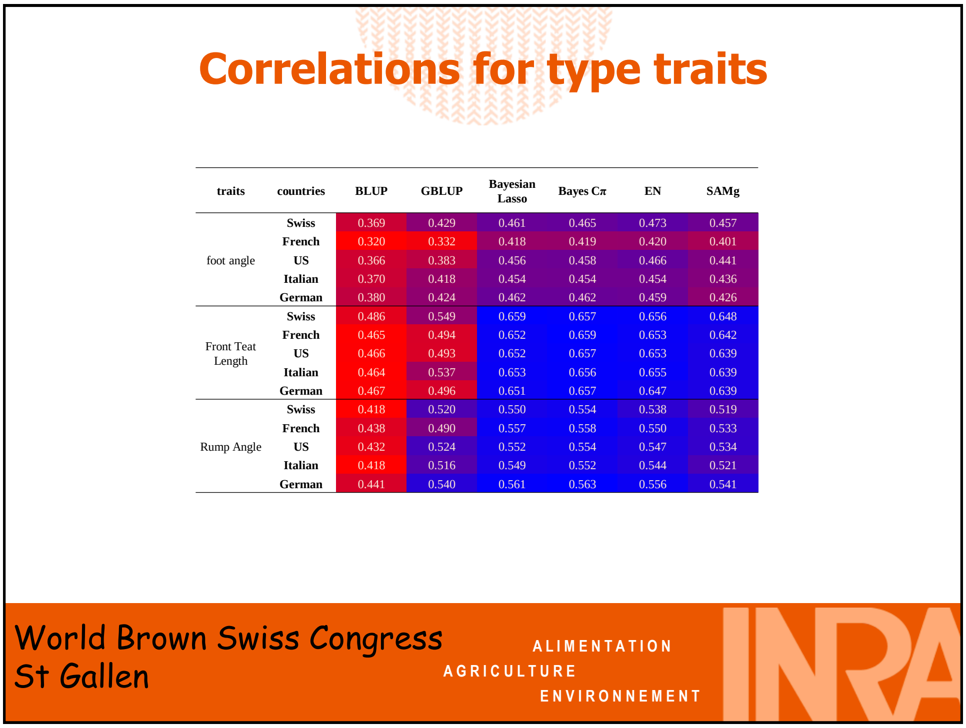


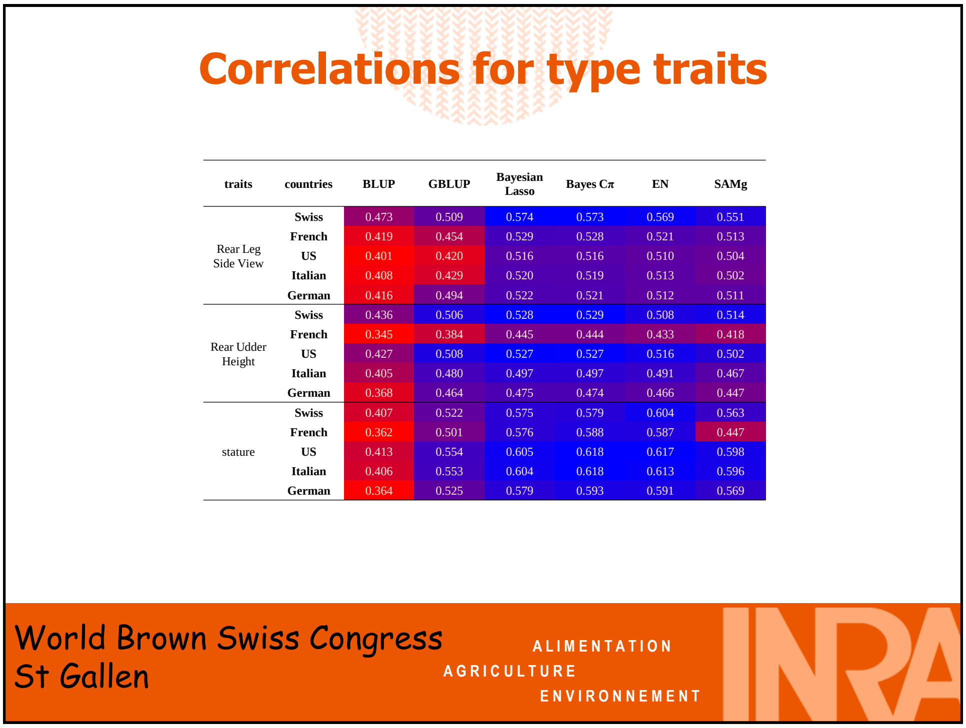
Correlations for production traits

traits	countries	BLUP	GBLUP	Bayesian Lasso	Bayes Cπ	EN	SAMg
fat	**Swiss**	0.416	0.579	0.605	0.607	0.609	0.610
	French	0.388	0.444	0.584	0.585	0.592	0.578
	US	0.398	0.542	0.591	0.592	0.596	0.584
	Italian	0.423	0.465	0.610	0.618	0.617	0.603
	German	0.427	0.584	0.615	0.624	0.626	0.597
milk	**Swiss**	0.334	0.518	0.561	0.564	0.582	0.542
	French	0.309	0.476	0.530	0.531	0.550	0.520
	US	0.287	0.450	0.525	0.526	0.551	0.507
	Italian	0.343	0.420	0.562	0.562	0.572	0.542
	German	0.371	0.546	0.579	0.580	0.592	0.546
protein	**Swiss**	0.448	0.575	0.601	0.602	0.603	0.573
	French	0.385	0.510	0.544	0.545	0.545	0.529
	US	0.382	0.506	0.553	0.555	0.565	0.534
	Italian	0.436	0.483	0.593	0.593	0.593	0.578
	German	0.454	0.590	0.603	0.604	0.602	0.565



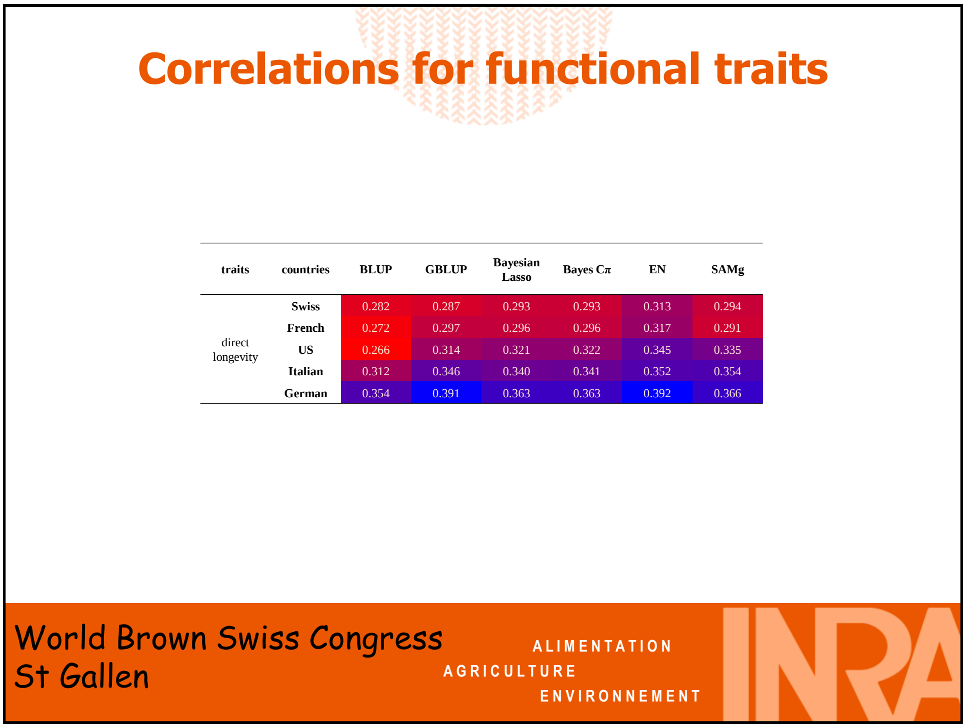
Correlations for type traits

traits	countries	BLUP	GBLUP	Bayesian Lasso	Bayes Cπ	EN	SAMg
foot angle	**Swiss**	0.369	0.429	0.461	0.465	0.473	0.457
	French	0.320	0.332	0.418	0.419	0.420	0.401
	US	0.366	0.383	0.456	0.458	0.466	0.441
	Italian	0.370	0.418	0.454	0.454	0.454	0.436
	German	0.380	0.424	0.462	0.462	0.459	0.426
Front Teat Length	**Swiss**	0.486	0.549	0.659	0.657	0.656	0.648
	French	0.465	0.494	0.652	0.659	0.653	0.642
	US	0.466	0.493	0.652	0.657	0.653	0.639
	Italian	0.464	0.537	0.653	0.656	0.655	0.639
	German	0.467	0.496	0.651	0.657	0.647	0.639
Rump Angle	**Swiss**	0.418	0.520	0.550	0.554	0.538	0.519
	French	0.438	0.490	0.557	0.558	0.550	0.533
	US	0.432	0.524	0.552	0.554	0.547	0.534
	Italian	0.418	0.516	0.549	0.552	0.544	0.521
	German	0.441	0.540	0.561	0.563	0.556	0.541



Correlations for type traits

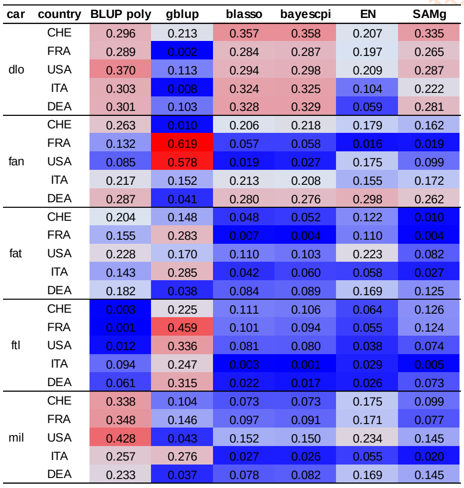
traits	countries	BLUP	GBLUP	Bayesian Lasso	Bayes Cπ	EN	SAMg
Rear Leg Side View	**Swiss**	0.473	0.509	0.574	0.573	0.569	0.551
	French	0.419	0.454	0.529	0.528	0.521	0.513
	US	0.401	0.420	0.516	0.516	0.510	0.504
	Italian	0.408	0.429	0.520	0.519	0.513	0.502
	German	0.416	0.494	0.522	0.521	0.512	0.511
Rear Udder Height	**Swiss**	0.436	0.506	0.528	0.529	0.508	0.514
	French	0.345	0.384	0.445	0.444	0.433	0.418
	US	0.427	0.508	0.527	0.527	0.516	0.502
	Italian	0.405	0.480	0.497	0.497	0.491	0.467
	German	0.368	0.464	0.475	0.474	0.466	0.447
stature	**Swiss**	0.407	0.522	0.575	0.579	0.604	0.563
	French	0.362	0.501	0.576	0.588	0.587	0.447
	US	0.413	0.554	0.605	0.618	0.617	0.598
	Italian	0.406	0.553	0.604	0.618	0.613	0.596
	German	0.364	0.525	0.579	0.593	0.591	0.569



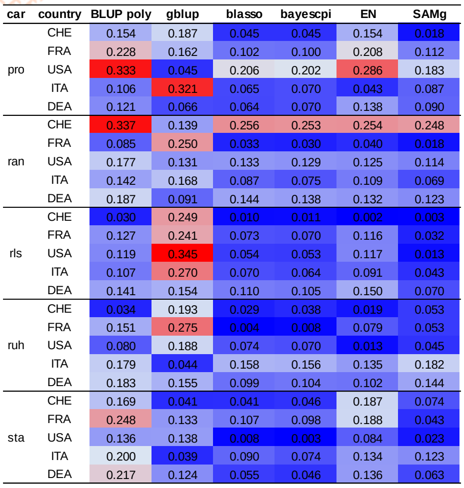
Correlations for functional traits

traits	countries	BLUP	GBLUP	Bayesian Lasso	Bayes Cπ	EN	SAMg
direct longevity	**Swiss**	0.282	0.287	0.293	0.293	0.313	0.294
	French	0.272	0.297	0.296	0.296	0.317	0.291
	US	0.266	0.314	0.321	0.322	0.345	0.335
	Italian	0.312	0.346	0.340	0.341	0.352	0.354
	German	0.354	0.391	0.363	0.363	0.392	0.366

Slope of regression



car	country	BLUP poly	gblup	blasso	bayescpi	EN	SAMg
dlo	CHE	0.296	0.213	0.357	0.358	0.207	0.335
	FRA	0.289	0.002	0.284	0.287	0.197	0.265
	USA	0.370	0.113	0.294	0.298	0.209	0.287
	ITA	0.303	0.008	0.324	0.325	0.104	0.222
	DEA	0.301	0.103	0.328	0.329	0.059	0.281
fan	CHE	0.263	0.010	0.206	0.218	0.179	0.162
	FRA	0.132	0.619	0.057	0.058	0.016	0.019
	USA	0.085	0.578	0.019	0.027	0.175	0.099
	ITA	0.217	0.152	0.213	0.208	0.155	0.172
	DEA	0.287	0.041	0.280	0.276	0.298	0.262
fat	CHE	0.204	0.148	0.048	0.052	0.122	0.010
	FRA	0.155	0.283	0.007	0.004	0.110	0.004
	USA	0.228	0.170	0.110	0.103	0.223	0.082
	ITA	0.143	0.285	0.042	0.060	0.058	0.027
	DEA	0.182	0.038	0.084	0.089	0.169	0.125
ftl	CHE	0.003	0.225	0.111	0.106	0.064	0.126
	FRA	0.001	0.459	0.101	0.094	0.055	0.124
	USA	0.012	0.336	0.081	0.080	0.038	0.074
	ITA	0.094	0.247	0.003	0.001	0.029	0.005
	DEA	0.061	0.315	0.022	0.017	0.026	0.073
mil	CHE	0.338	0.104	0.073	0.073	0.175	0.099
	FRA	0.348	0.146	0.097	0.091	0.171	0.077
	USA	0.428	0.043	0.152	0.150	0.234	0.145
	ITA	0.257	0.276	0.027	0.026	0.055	0.020
	DEA	0.233	0.037	0.078	0.082	0.169	0.145



car	country	BLUP poly	gblup	blasso	bayescpi	EN	SAMg
pro	CHE	0.154	0.187	0.045	0.045	0.154	0.018
	FRA	0.228	0.162	0.102	0.100	0.208	0.112
	USA	0.333	0.045	0.206	0.202	0.286	0.183
	ITA	0.106	0.321	0.065	0.070	0.043	0.087
	DEA	0.121	0.066	0.064	0.070	0.138	0.090
ran	CHE	0.337	0.139	0.256	0.253	0.254	0.248
	FRA	0.085	0.250	0.033	0.030	0.040	0.018
	USA	0.177	0.131	0.133	0.129	0.125	0.114
	ITA	0.142	0.168	0.087	0.075	0.109	0.069
	DEA	0.187	0.091	0.144	0.138	0.132	0.123
rls	CHE	0.030	0.249	0.010	0.011	0.002	0.003
	FRA	0.127	0.241	0.073	0.070	0.116	0.032
	USA	0.119	0.345	0.054	0.053	0.117	0.013
	ITA	0.107	0.270	0.070	0.064	0.091	0.043
	DEA	0.141	0.154	0.110	0.105	0.150	0.070
ruh	CHE	0.034	0.193	0.029	0.038	0.019	0.053
	FRA	0.151	0.275	0.004	0.008	0.079	0.053
	USA	0.080	0.188	0.074	0.070	0.013	0.045
	ITA	0.179	0.044	0.158	0.156	0.135	0.182
	DEA	0.183	0.155	0.099	0.104	0.102	0.144
sta	CHE	0.169	0.041	0.041	0.046	0.187	0.074
	FRA	0.248	0.133	0.107	0.098	0.188	0.043
	USA	0.136	0.138	0.008	0.003	0.084	0.023
	ITA	0.200	0.039	0.090	0.074	0.134	0.123
	DEA	0.217	0.124	0.055	0.046	0.136	0.063

Mean correlation per country

- In Brown Swiss, the contribution of each country to the reference population is very different
  - Mean correlation over the common traits are consequently different according to the country scale
  - Country with a high contribution will convert CD of abroad bulls with a higher accuracy

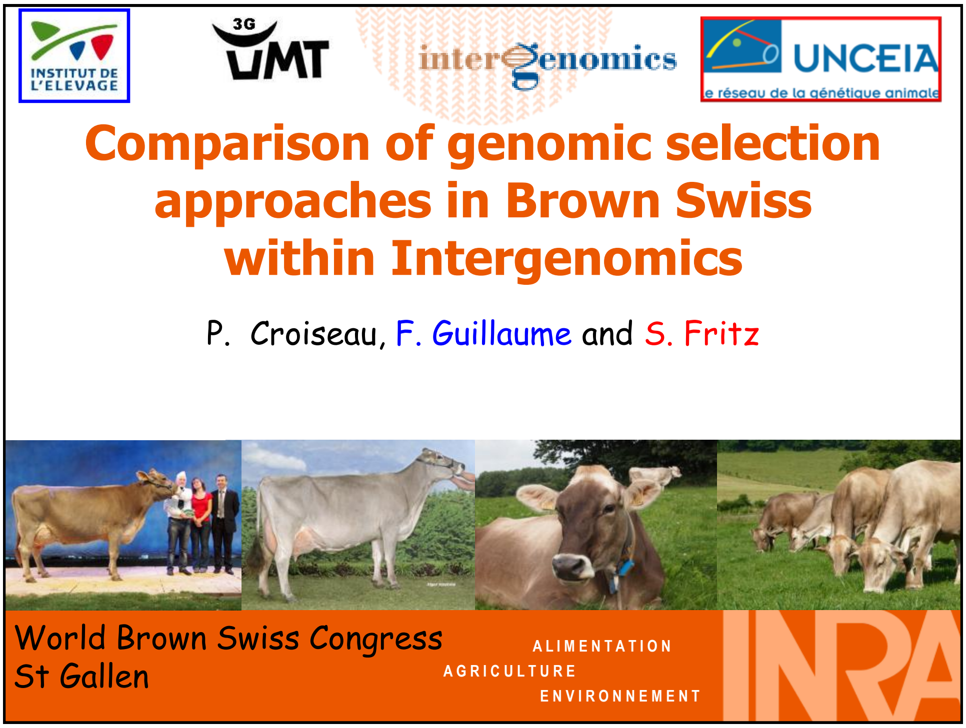
country scale	mean correlations
Swiss	0.527
French	0.487
US	0.518
Italian	0.524
German	0.521

Results

	correlations	Deviation to 1 of the slope	Traits which validate Interbull test
BLUP poly	0.393	0.184	6
gblup	0.475	0.138	9
blasso	0.533	0.110	8.2
bayescpi	0.535	0.108	8.4
EN	**0.537**	0.124	9.2
SAMg	0.515	**0.097**	**9.6**

Conclusions

- Compared to a traditional BLUP, genomic selection allows a gain in correlation between 6.5 and 20.9%
- Among the set of genomic selection approaches
  - There is some variability!
  - Bayesian Lasso, Bayes Cπ and EN give the best results with a gain in correlation near 3% compared to GBLUP
  - The slope of the regression
    - is closer to 1 with the French approach
    - More traits validate Interbull test with this approach.



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