Effect of genomic preselection on the stability of EBV's from traditional BLUP procedure for production traits – a practical illustration

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Current status for genomic selection

- One out of ten bulls selected for total merit (selection intensity 1.8 and selection differential 1.4)

- Selection intensity for the single traits in total merit is lower (Protein: selection intensity 1.0 selection differential 0.8)

- Second batch bulls are now used less intensively

- First year batch of genomic preselected bulls get milking daughters

- Progeny test by traditional BLUP procedure is done per trait or trait group

Traditional BLUP evaluation

Unbiased, if all data on which selection is based is included

- Ignoring genomic selection

In theory:

- – Evaluations are biased because in BLUP progenies are assumed to be average of their parents, i.e. E[MS-term]=0

- – Leads into problems of separating environmental and genetic levels, i.e. genetic trend is underestimated and environmental trend is overestimated

- – as a result: young bulls in progeny test are underestimated

Question: how robust is our evaluation model against unaccounted selection?

- Phenotypic trend = Environmental + genetic trends

- Genetic trend estimation in BLUP:
  - Selection of parents (and now Mendelian term)
- Environmental trend estimation in BLUP:
  - Animals from different generations/birth years are producing in same environment classes
  1. First crop vs. second crop daughters
  2. Same bulls having daughters in consecutive years
  3. Same cows having records in consecutive years

Objective

- Test the effect of bull second crop daughters for the robustness

- Try to test the effect of genomic selection on accuracy of evaluations

- Mimic the effect of bias from preselection on real data for a strongly selected trait. Protein is chosen

Material

- Nordic Test Day model for production trait (Multi trait, multi lactation, single breed model. Test day records since 1988)

- Protein Holstein investigated
  - P-index, relative index
    - Base = 100, cows born in 1990 and 1991
    - STD = 10, genetic std. app. 10.5

Scenarios

- Routine evaluation: All animals included (Rout)

- Preselection of young bulls born 1990-2003. AI bulls with progeny test above average selected(Selection intensity 0.8, selection differential 0.75) . Records from daughters of discarded bulls were set to missing (no progeny test) (Y_1990-2003)

- Same as in previous scenario for young bulls born 2000 and onwards (Y_2000-)

- No preselection for young bulls, but second crop daughters born in 1995 and onwards have their records set to missing (Sec_1995-)

- Year 2000 and onwards. No second crop daughters with records. Preselection of young bulls above average. Daughter records from not selected bulls were set to missing (Y_Sec_2000-)

All scenarios: No changes for private or foreign bulls.

No of progeny tested bulls

Birth year	Rout	Y_1990-03	Y_2000-	Sec_1995-	Y_Sec_2000-
1990	412	**201**	412	412	412
1992	537	**269**	537	537	537
1994	469	**238**	469	469	469
1996	475	**236**	475	475	475
1998	450	**225**	450	450	**227**
2000	392	**182**	**182**	392	**182**
2002	398	**200**	**200**	398	**200**
2004	357	357	**181**	357	**181**
2006	393	393	**186**	393	**186**

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Largest progeny group size

Birth year	Rout	Y_1900-03	Y_2000-	Sec_1995-	Y_Sec_2000-
1990	23654	23654	23654	**312**	**20477**
1992	54491	54491	54491	**350**	**25842**
1994	22013	22013	22013	**297**	**1644**
1996	53705	53705	53705	**244**	**244**
1998	37655	37655	37655	**396**	**396**
2000	21794	21794	21794	**216**	**214**
2002	20251	20251	20251	**227**	**212**
2004	552	552	552	**275**	**275**
2006	405	405	316	**405**	**316**
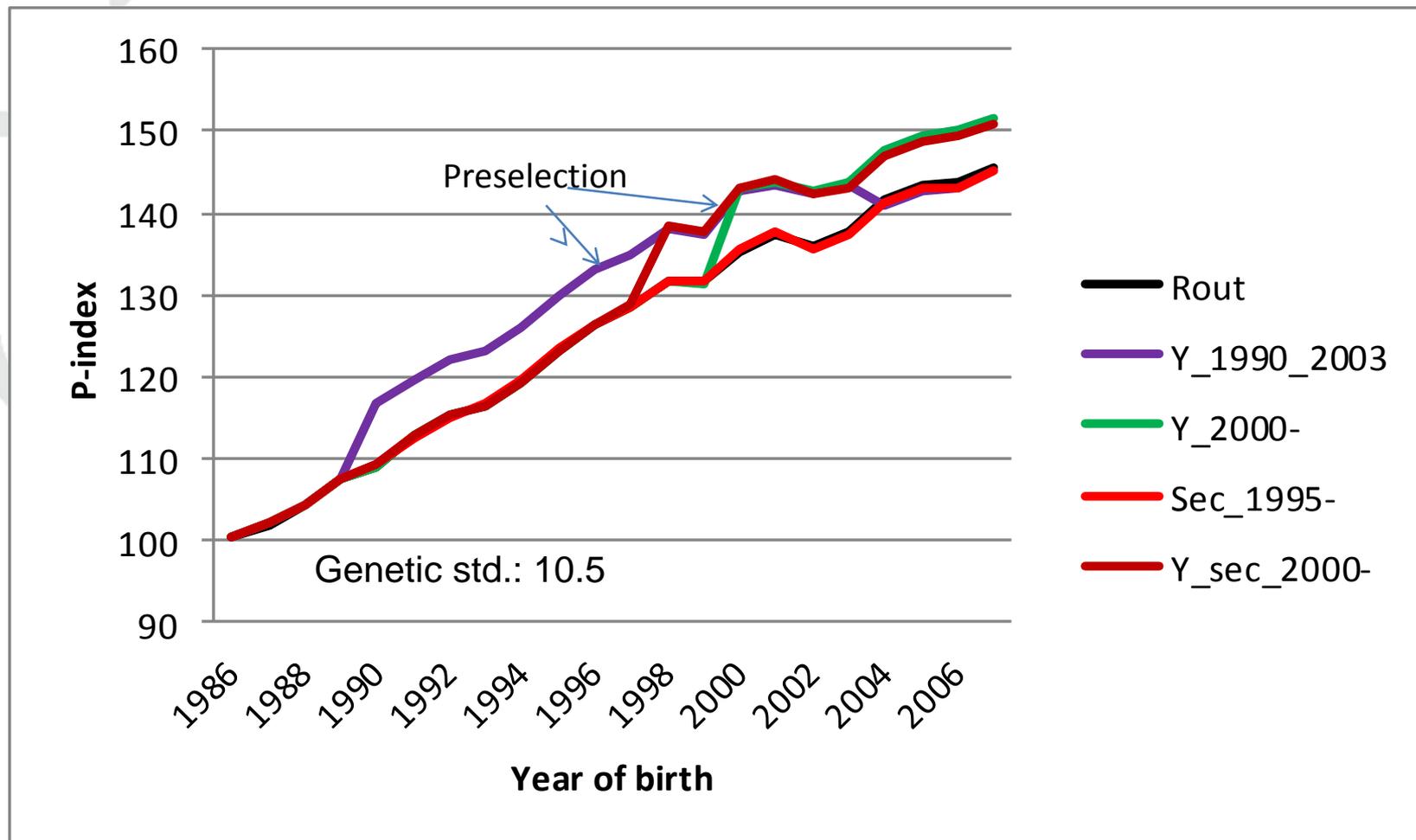
Difference to routine run, protein
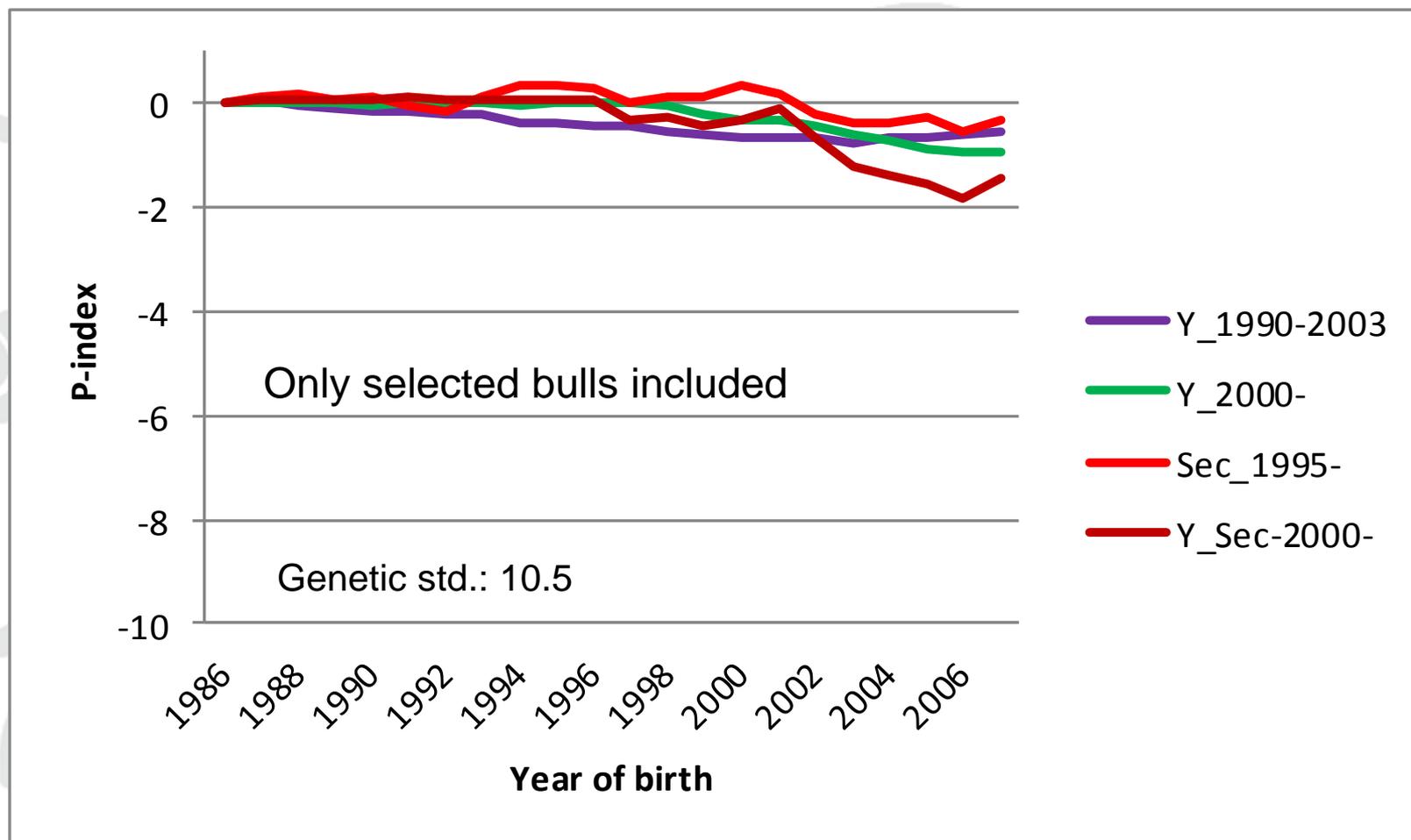
Correlation with routine run

Y_1990-2003
Y_2000-
Sec_1995-
Y_Sec-2000-

P-indeks

Year of birth

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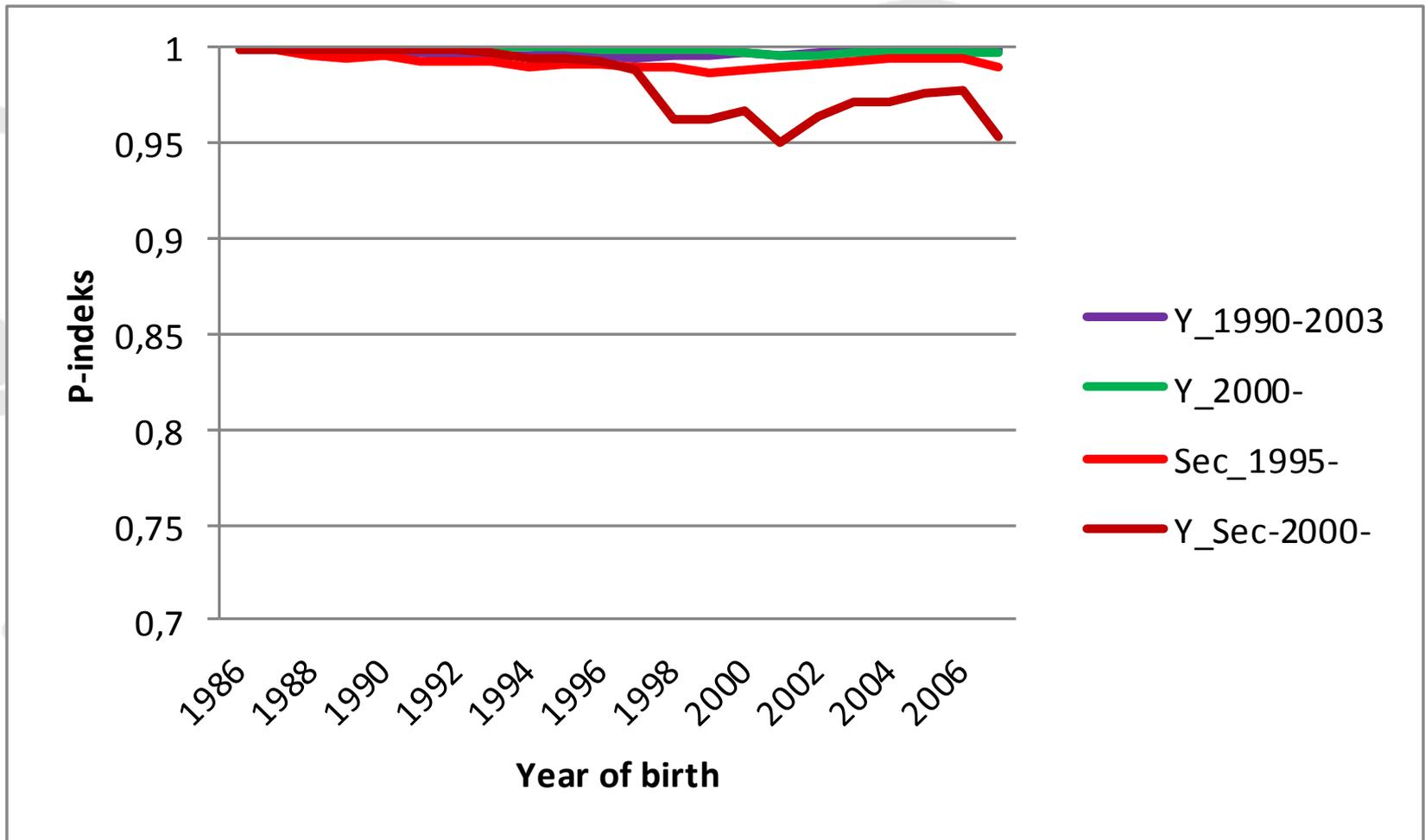
Difference in P-index in scenario (Y_Sec_2000-) compared to routine run for bulls born after 2000 with no second batch daughters. No correction for differences in trend

Difference	Frequency	Percent
-6	5	0.4
-5	5	0.4
-4	21	1.8
-3	155	12.9
-2	298	24.9
-1	348	29.1
0	223	18.6
1	104	8.7
2	33	2.8
3	6	0.5

Conclusion

- Preselection of young bulls with a reliability of 0.90 and a selection intensity of 0.8 has negative effect on the genetic trend
  - Bias in expected direction, i.e. trend is underestimated
  - Effect less than was expected
- Omitting second crop daughters has less effect on trend.
- Preselection of young bulls **in combination with omitting second crop daughters** has bigger but still minor effect.
- Likely: When genomic selection will take place, genomic selected bulls will be used over a longer time span and some even as proven bulls.
- Genomic selection will not ruin traditional estimation of breeding values in the first years after start