Effect of genomic pre-selection on the stability of EBVs from traditional BLUP procedure for production traits – a practical illustration

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Current status for genomic selection
HOL, (DNK,FIN,SWE)

- 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 used less intensively. Only 10-20% of inseminations is done with second batch bulls.

- Genomic selected bulls are used intensively as bull sires

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

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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 pre-selection 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 yield for Holstein is investigated
  - P-index, relative index
    - Base = 100, cows born in 1990 and 1991
    - STD = 10, genetic std. app. 10.5

Material

- Data is from February 2012

- Results has been presented at Interbull meeting in Cork 2012

Senarios

- Rout: Routine evaluation with all animals included

- Y_1990-2003: Pre-selection 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_2000-: Same as in previous scenario but for young bulls born 2000 and onwards

Senarios (continued)

• Sec_1995-: No pre-selection for young bulls, but second crop daughters born in 1995 and onwards have their records set to missing

• Y_Sec_2000-: Daughters born year 2000 and onwards :

    No second crop daughters with records

    Pre-selection of young bulls above average

    Daughter records were set to missing but pedigree information kept

All senarious: No changes for private and 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	**225**
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**

Genetic trend protein Nordic A.I. bulls
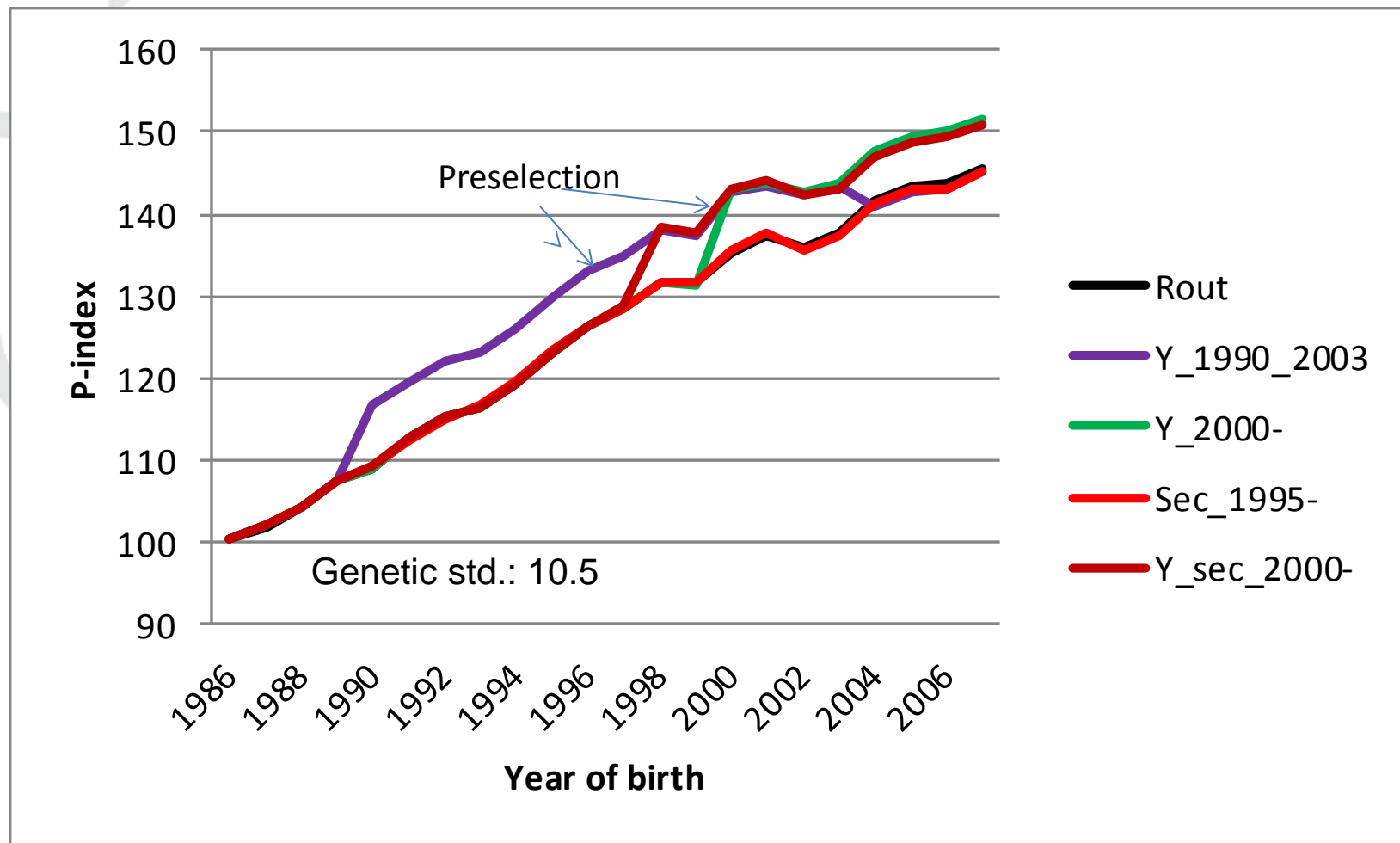
Difference to routine run, protein

P-index

Only selected bulls included

Genetic std.: 10.5

Year of birth

Legend:
- Y_1990-2003
- Y_2000-
- Sec_1995-
- Y_Sec-2000-

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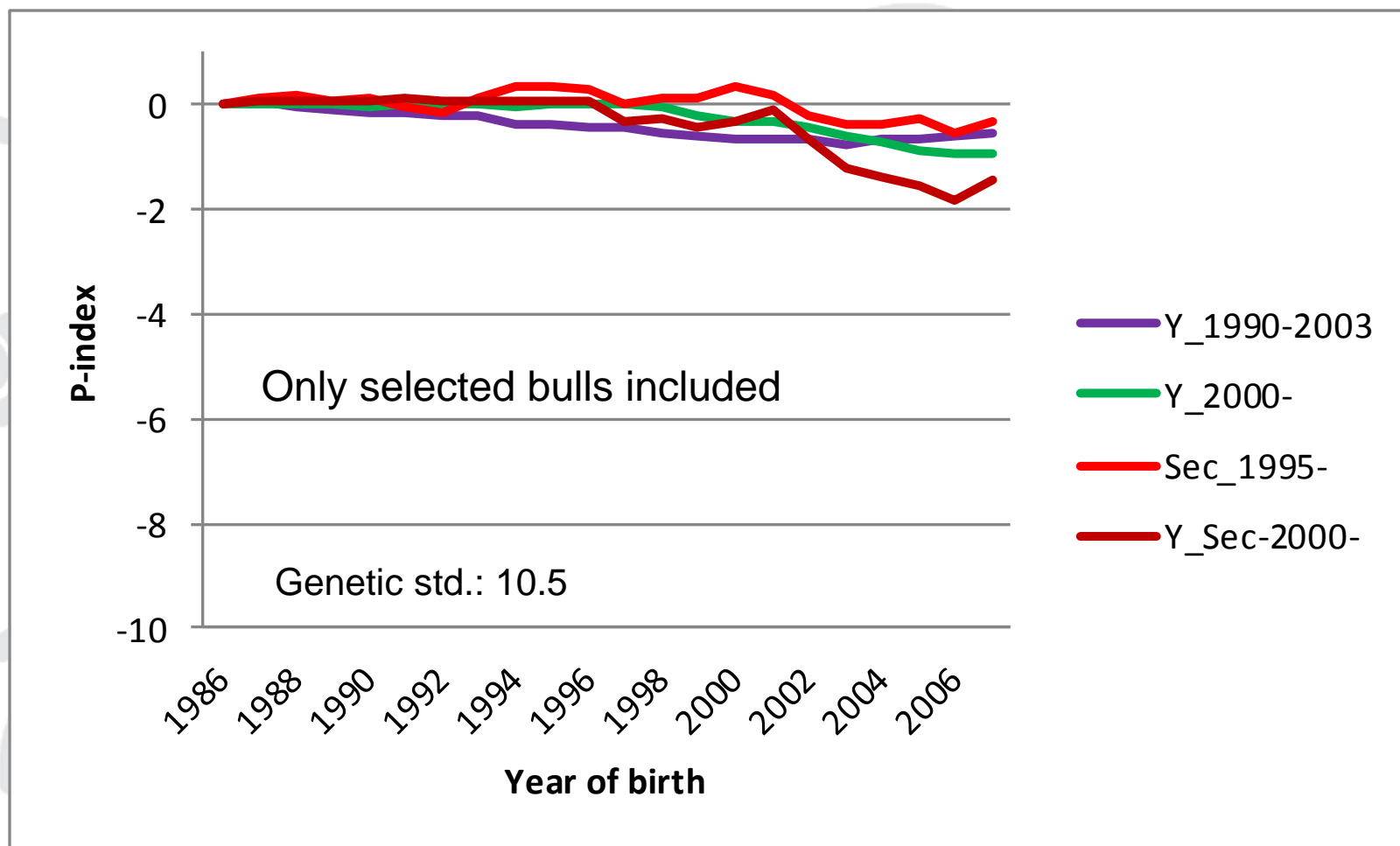
Correlation with routine run
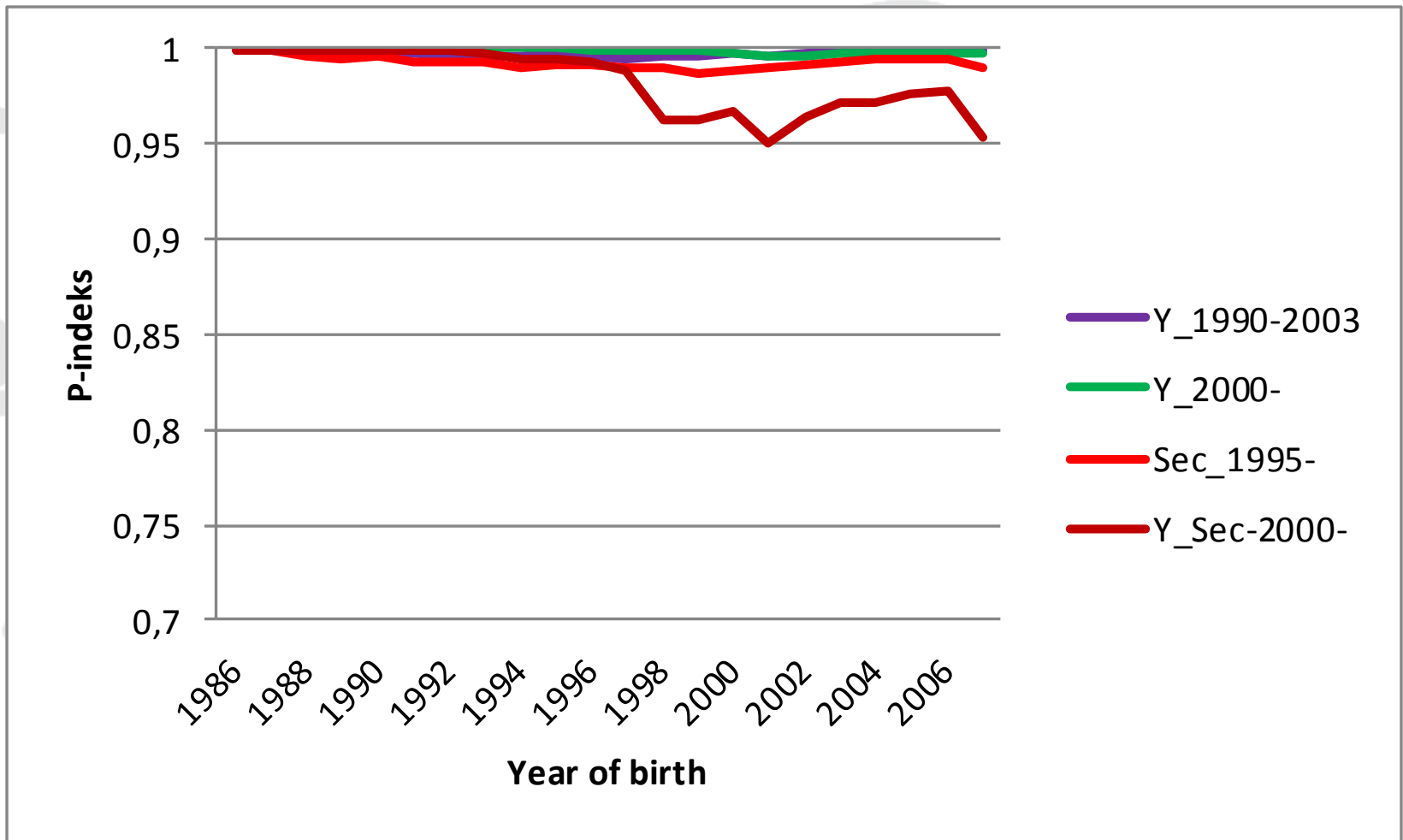
Difference in P-index in scenario Y_Sec_2000- compared to routine run for bulls born after 2000. No correction for differences in trend

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

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Conclusion

- Pre-selection 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.
- Pre-selection of young bulls **in combination with omitting second crop daughters** has bigger but still minor effect
- Likely: Genomic selected bulls will be used over a longer time span than young bulls in the old young bull system, and some genomic tested bulls are used for nearly a year
- Selection intensity for a single trait is lower than for the Total Merit Index
- Genomic selection will not ruin traditional estimation of breeding values in the first years