Finding the optimal #of testers for the EA-Maize program

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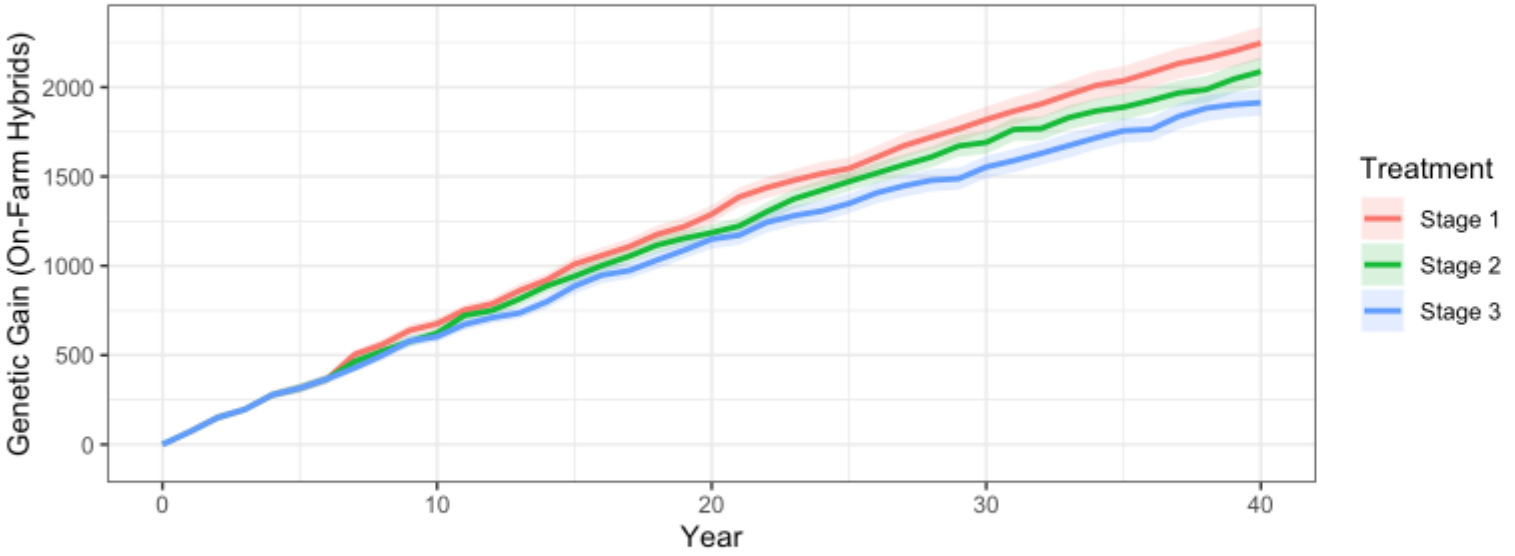
Treatment	Description
Stage 3	Current scheme, recycling after three testcross stages. Crossing block consists of 48 lines, the 16 best lines from each of the last three stage 3 evaluations.
	16 best stage 3 from 2020 -- 16 best stage 3 from 2019 -- 16 best stage 3 from 2018
Stage 2	Recycling one year earlier. Crossing block consists of 48 lines, the 16 best lines from the last stage 2 evaluation and the 16 best lines from each of the last two stage 3 evaluations.
	16 best stage 3 from 2020 -- 16 best stage 3 from 2019 -- 16 best stage 2 from 2020
Stage 1	Recycling two years earlier. Crossing block consists of 48 lines, the 16 best lines from the last stage 1, stage 2 and stage 3 evaluations.
	16 best stage 3 from 2020 -- 16 best stage 2 from 2020 -- 16 best stage 1 from 2020

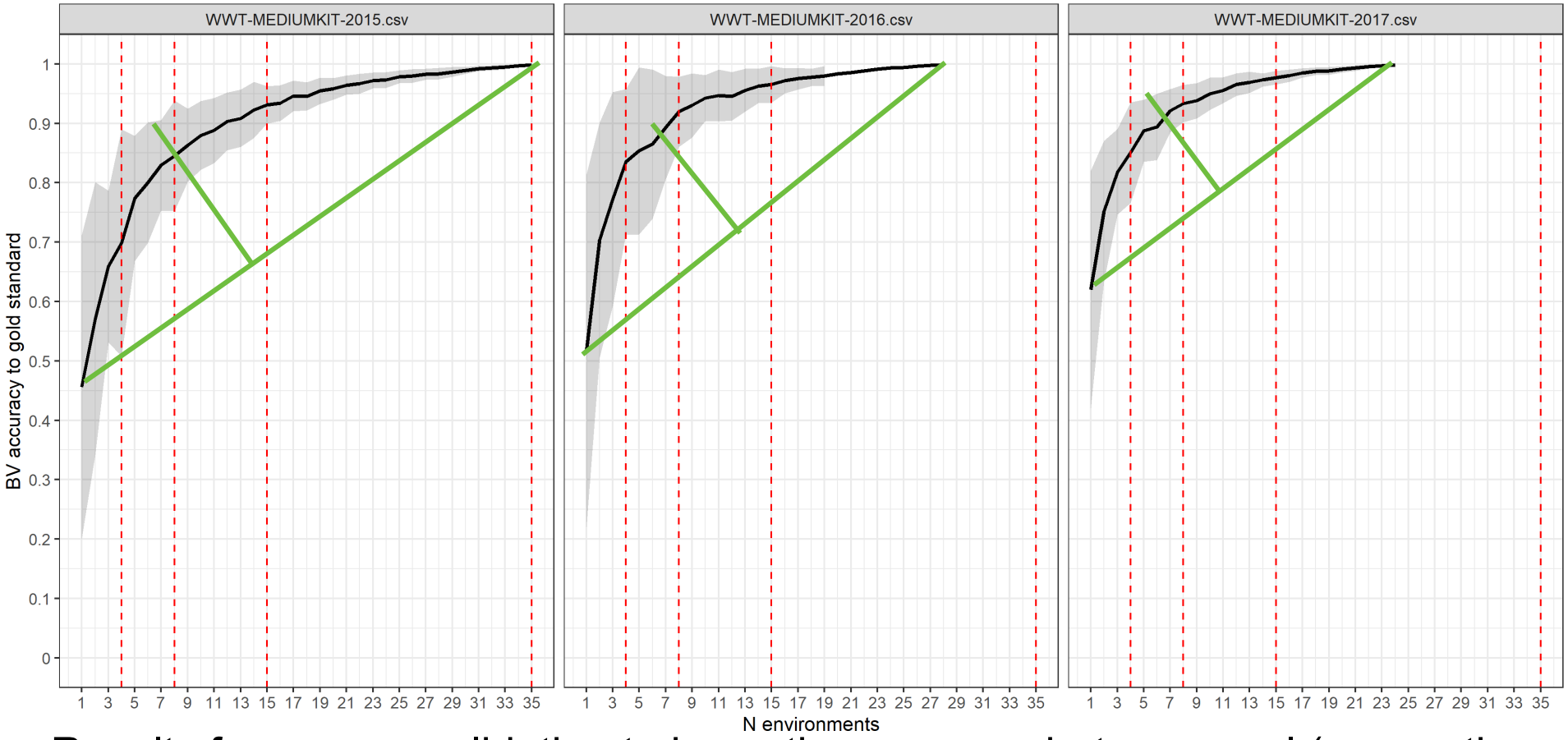
Recommendation was to start using parent from other stages without any additional change. In the discussion donors suggested to don't wait for Stage 3 material and focus only in Stage 1 and 2 to get parents. In response EiB suggested that if the programs wanted to do that, they should have good levels of accuracy for which is critical to know how many environments and how many tester are needed at recycling.



By year 40, all reduced cycle time treatments generated more genetic gain than the baseline Stage 3 treatment. The Stage 2 and Stage 1 treatments generated 1.09 (95% CI: 1.06,1.13) and 1.17 (95% CI: 1.14,1.2) times more gain, respectively.

Only necessary if parents will come mainly from Stage 1 and Stage 2 (forgetting recycling at Stage 3).
Although these learnings can be used to optimize the approach form improvement 1.

We identified 5-7 environments to be enough to reach great accuracy for safe recycling



Results from cross validation to know the accuracy between real (across the entire TPE) and estimated BV when selecting a given number of environments (we assume the max #of environments represent the real BV).

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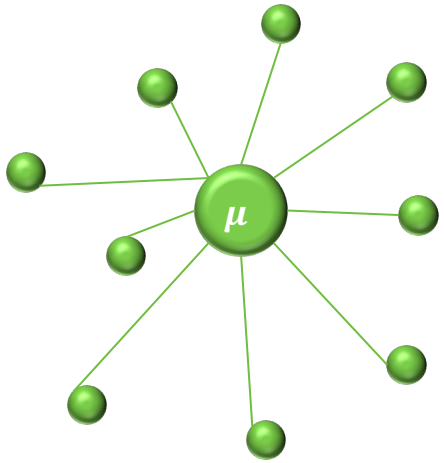
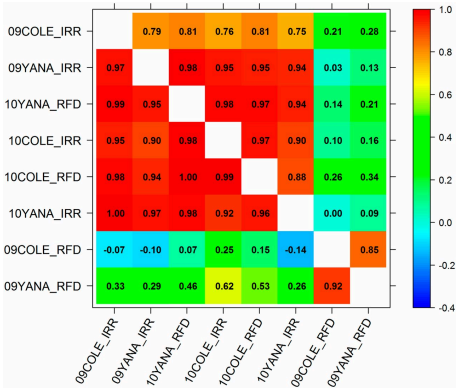
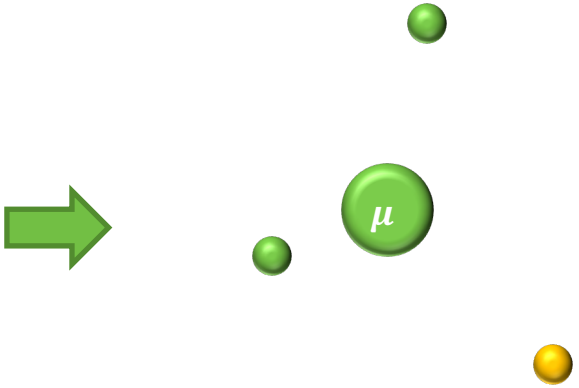
Approach

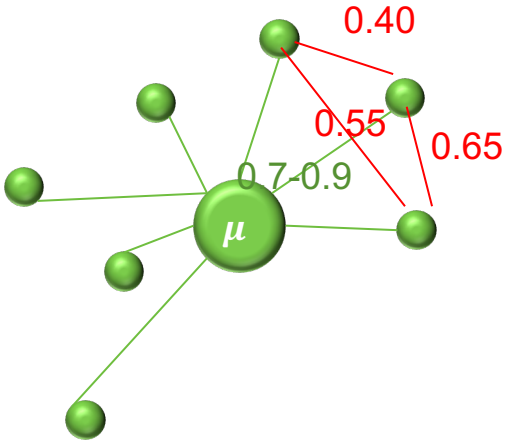
1. Identify the optimal number of testers to accurately select across testers
2. Identify tester with high correlation with across-tester GCA.

The logic behind the analysis









If $\mu_{r_G} = 0.6$ and $\sigma_{r_G} = 0.2$ it means that by selecting individuals using across-tester GCA have rg=0.9 with tester-specific GCA, so selecting using across-tester GCA we will have genetic gain as if we were interested in a specific tester, and the other way around.

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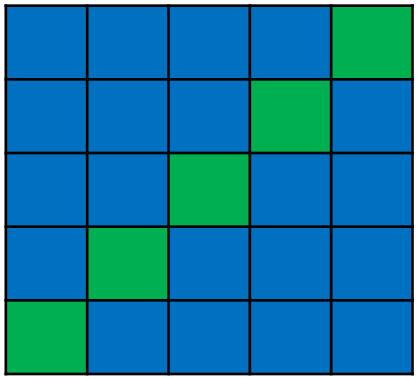
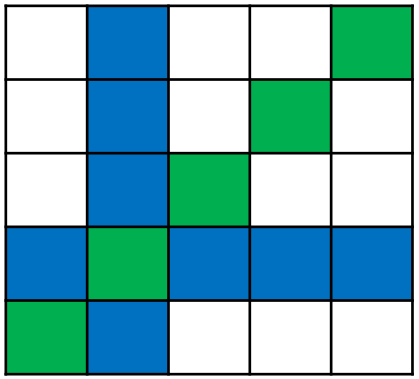
The number of testers used has a big impact in programs



Program tests across the opposite pool (several testers)



Programs tests using some tester of the opposite pool

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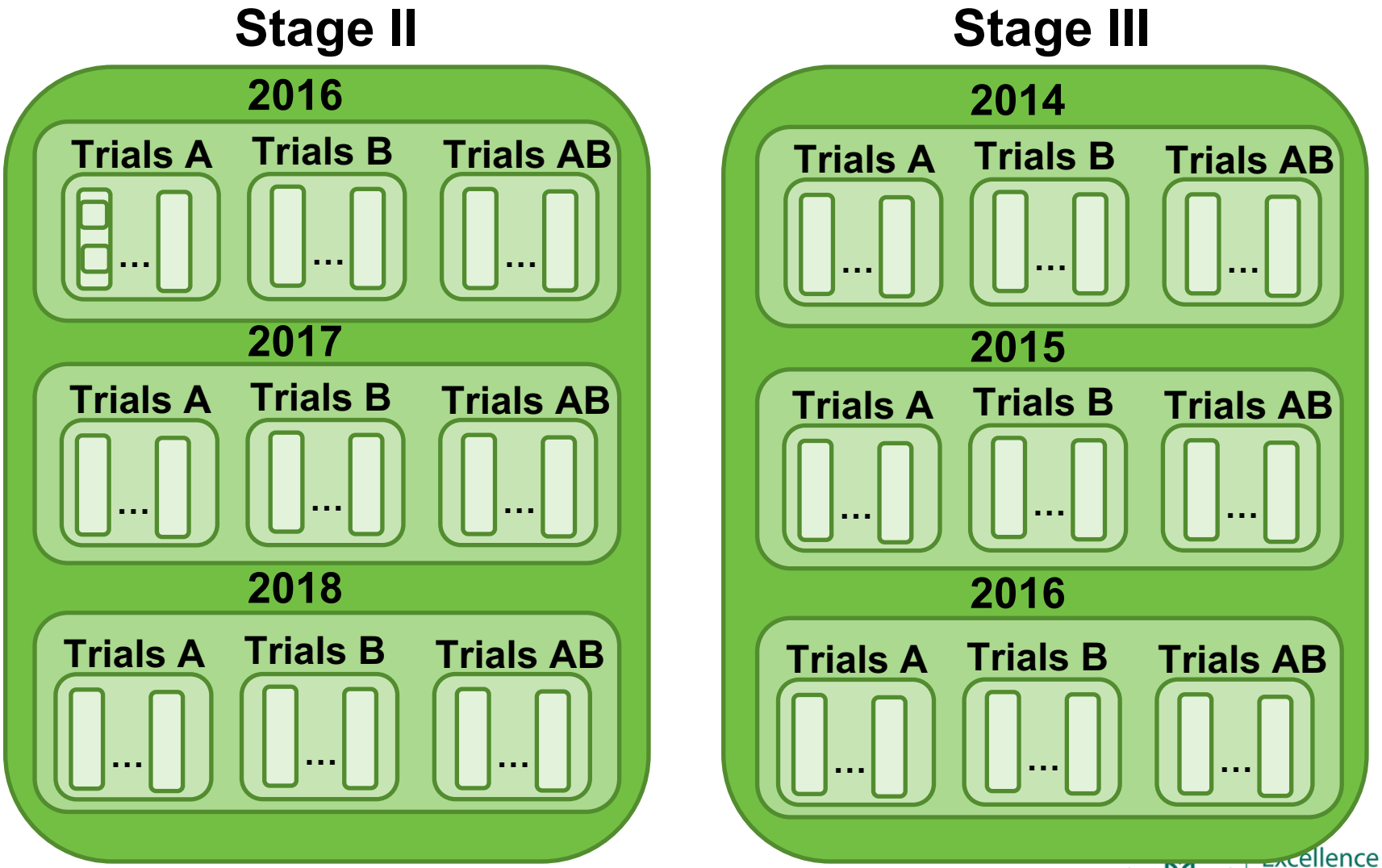
Data structure



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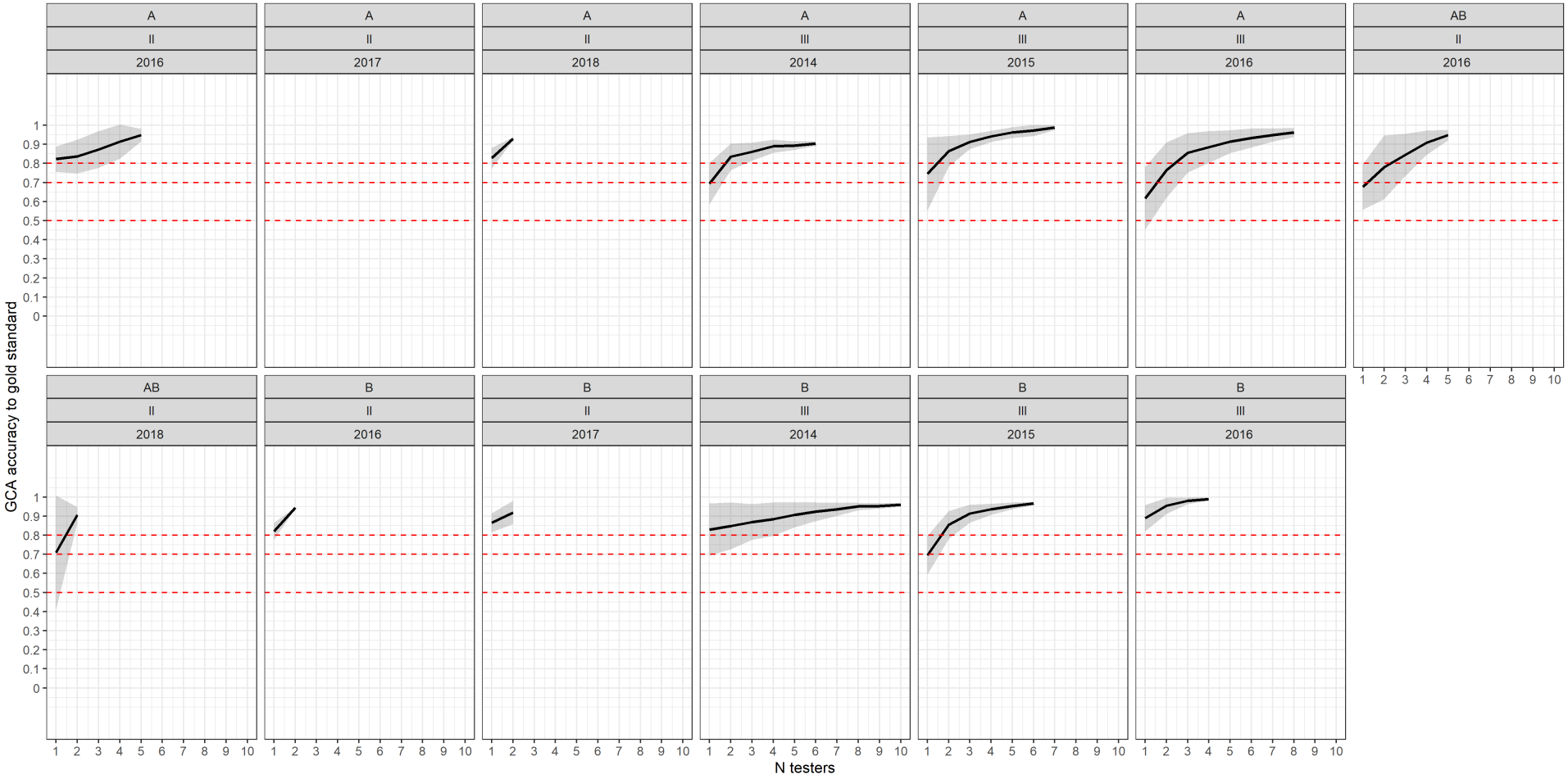
Identify the optimal number of testers to accurately select

Results from cross validation to know the accuracy between real (across tester GCA) and estimated GCA when using a given number of testers (we assume the max #of testers represent the real GCA).



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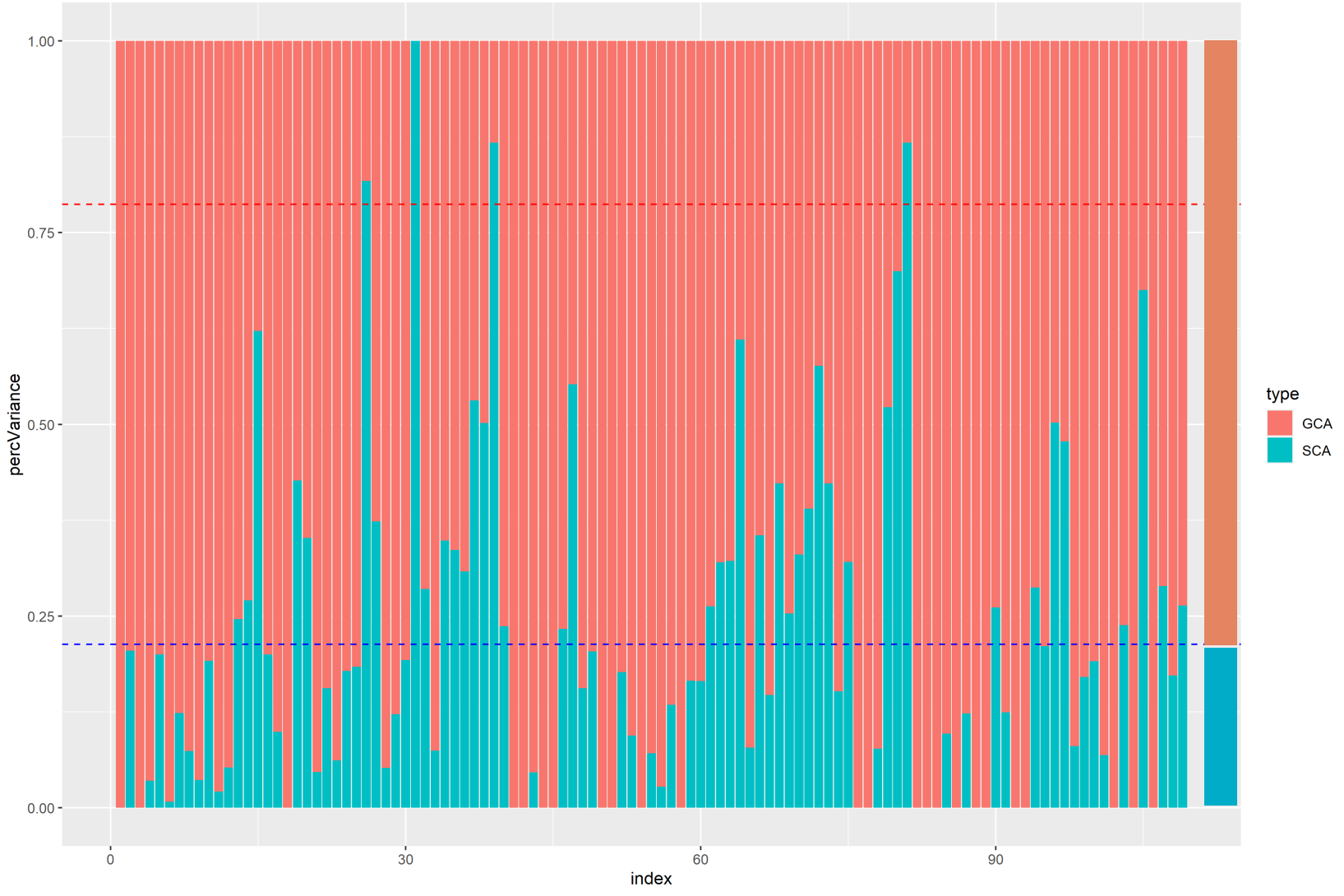
Variance components for GCA and SCA



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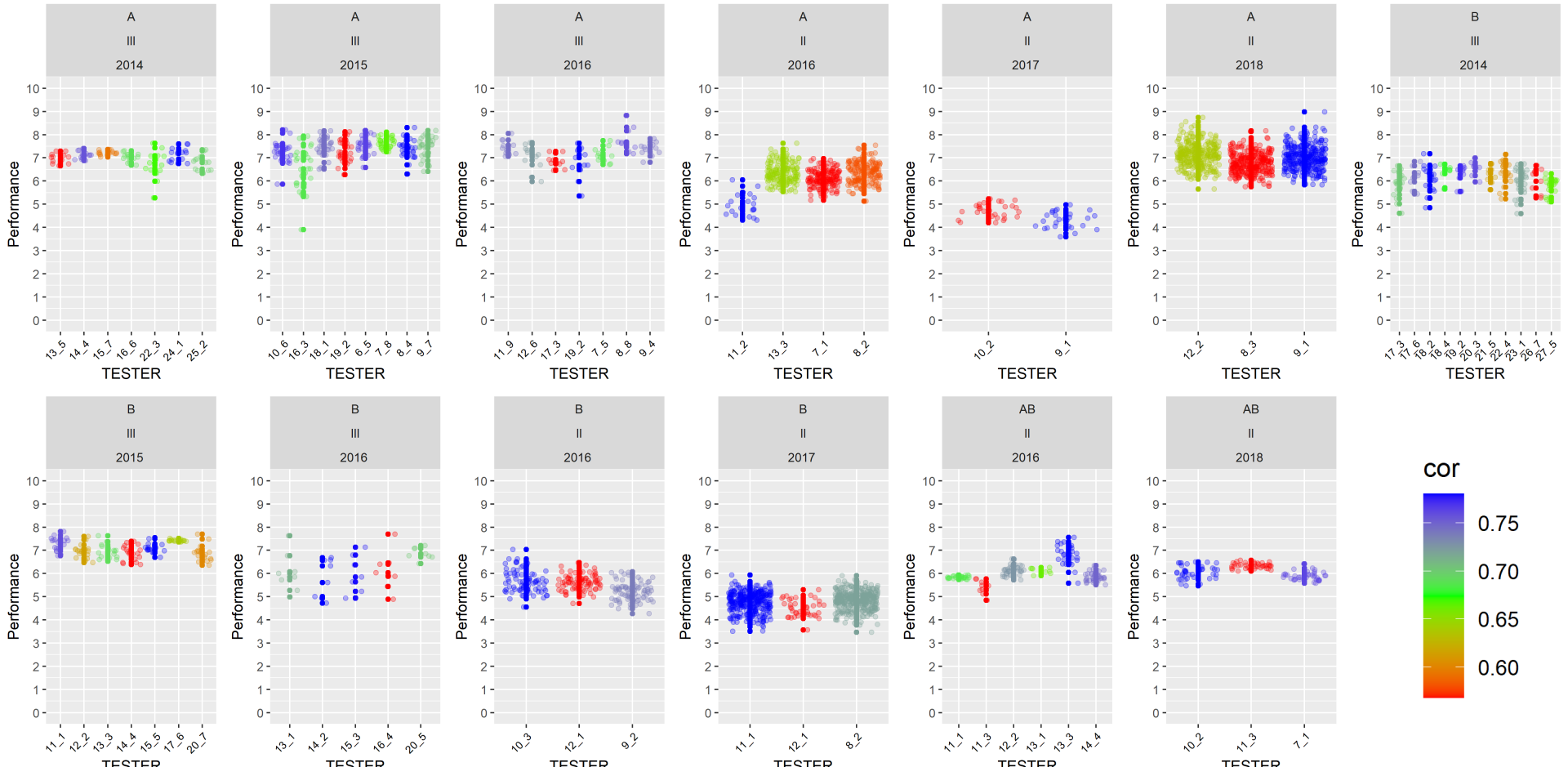
	filePool	nlineTrial
2016	Stage III Data.xlsx-B	13
2016	Stage III Data.xlsx-A	17
2014	Stage III Data.xlsx-A	21
2015	Stage III Data.xlsx-B	23
2015	Stage III Data.xlsx-A	32
2014	Stage III Data.xlsx-B	41
2017	Stage II Data.xlsx-A	32
2016	Stage II Data.xlsx-AB	40
2018	Stage II Data.xlsx-AB	43
2016	Stage II Data.xlsx-B	86
2016	Stage II Data.xlsx-A	190
2018	Stage II Data.xlsx-A	313
2017	Stage II Data.xlsx-B	360

Some of the best testers

There’s some testers that provide higher correlation than others.



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Thank you for your interest!

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