

3D Point clouds for high throughput Phenotyping in canola

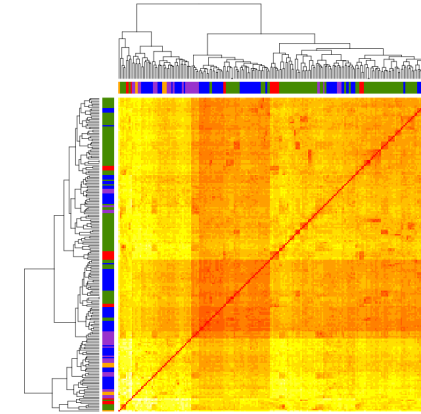
Part of: Increase of N-efficiency through extension of genetic diversity

Sven Weber
Brisbane
15.11.2022

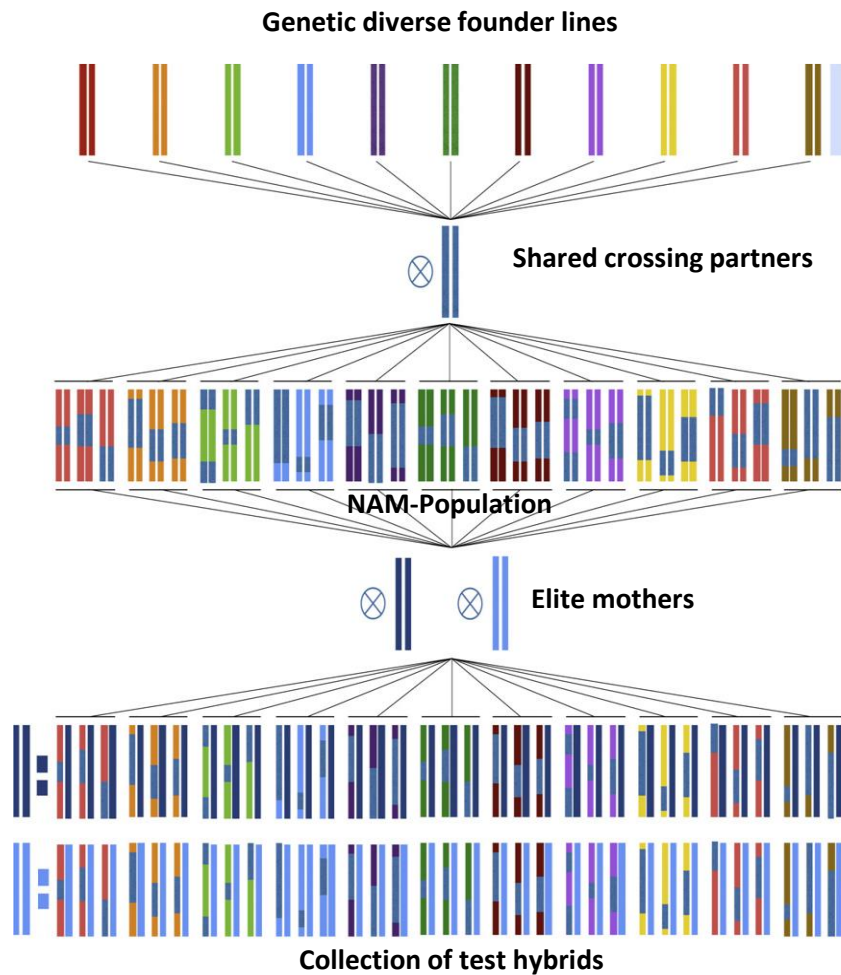


Hypothesis in the project

- 1) The **extension of genetic diversity** could be useful to enrich variation for NUE in breeding pools.
- 2) Incorporation of **plant architectural traits** that are in an relationship with **NUE and Seed yield** and have a **higher heritability** than the primary traits could **help in the selection** process.
- 3) The **digital assessment of plant architecture** can be a useful tool in research and industry for high throughput phenotyping.



Selection of test hybrid fathers



Screening of first test hybrids
with one mother at 12 sites

n=968

>48,9 dt/ha of DH-Populations (2014)
>46,2 dt/ha of SSD-Populations (2015)

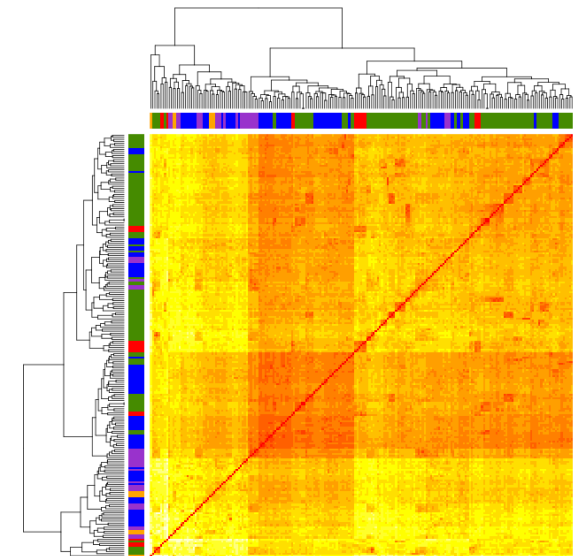
n=262

28 409 SNP-marker based genetic
distance
(Rodger's Distances)

n=207

n=ca. 160

Test hybrids with two mothers



Field trials



7 locations in 2 years (2020 & 2021)

one level of N-fertilization: 125 kg N ha⁻¹

400 plots in p-rep design:

350 genotypes:

50 plots for repetitions

Mixed linear model for entry mean adjustment

- fixed: Genotype
- random: Env, Env:Row, Env:Col, Env:Rep

Assessment of plant architecture



Parzelle: Genotyp: Pflanze: Barcode:

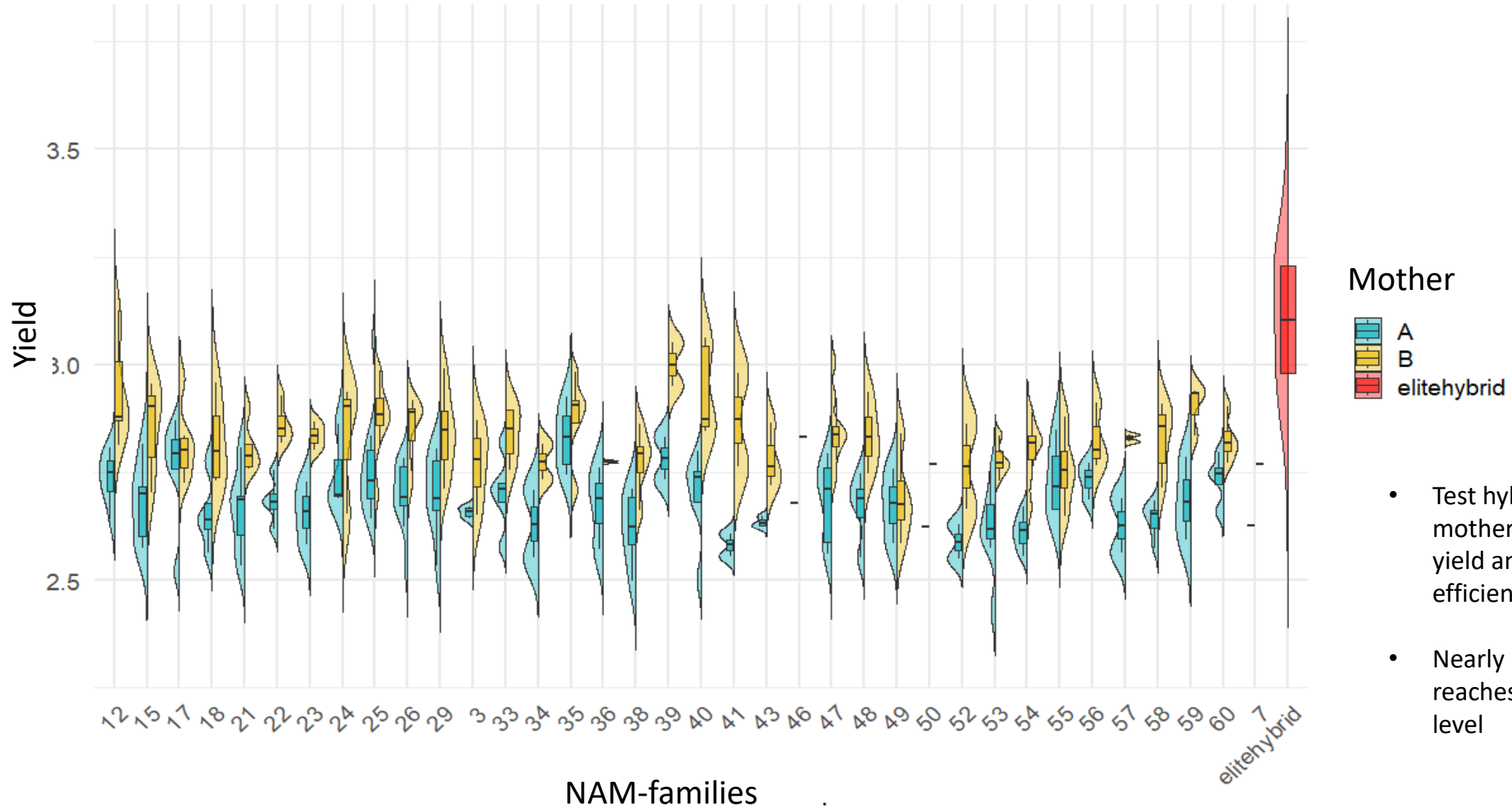
Höhe 1.NT: cm
Höhe 2.NT: cm
Höhe 3.NT: cm
Gesamt-Höhe: cm

Winkel 1.NT: Grad
Winkel 2.NT: Grad
Winkel 3.NT: Grad

Schoten: ☐ Seite 2

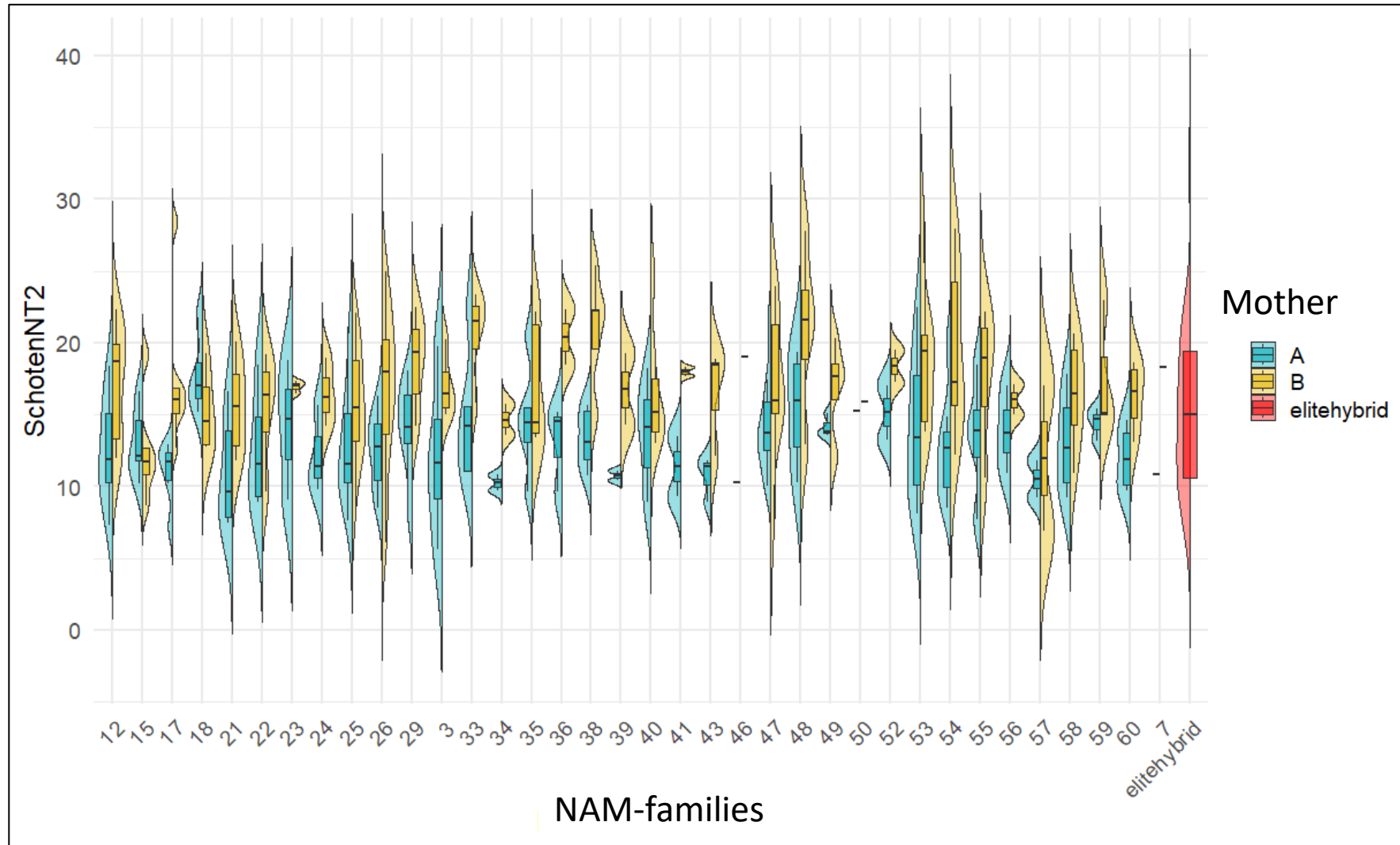
	Schoten	Verzweigungen		Schoten	Verzweigungen
1. NT	<input type="text"/>	<input type="text"/>	11. NT	<input type="text"/>	<input type="text"/>
2. NT	<input type="text"/>	<input type="text"/>	12. NT	<input type="text"/>	<input type="text"/>
3. NT	<input type="text"/>	<input type="text"/>	13. NT	<input type="text"/>	<input type="text"/>
4. NT	<input type="text"/>	<input type="text"/>	14. NT	<input type="text"/>	<input type="text"/>
5. NT	<input type="text"/>	<input type="text"/>	15. NT	<input type="text"/>	<input type="text"/>
6. NT	<input type="text"/>	<input type="text"/>	16. NT	<input type="text"/>	<input type="text"/>
7. NT	<input type="text"/>	<input type="text"/>	17. NT	<input type="text"/>	<input type="text"/>
8. NT	<input type="text"/>	<input type="text"/>	18. NT	<input type="text"/>	<input type="text"/>
9. NT	<input type="text"/>	<input type="text"/>	19. NT	<input type="text"/>	<input type="text"/>
10. NT	<input type="text"/>	<input type="text"/>	20. NT	<input type="text"/>	<input type="text"/>
HT	<input type="text"/>				

Adj. means for yield from 14 environments



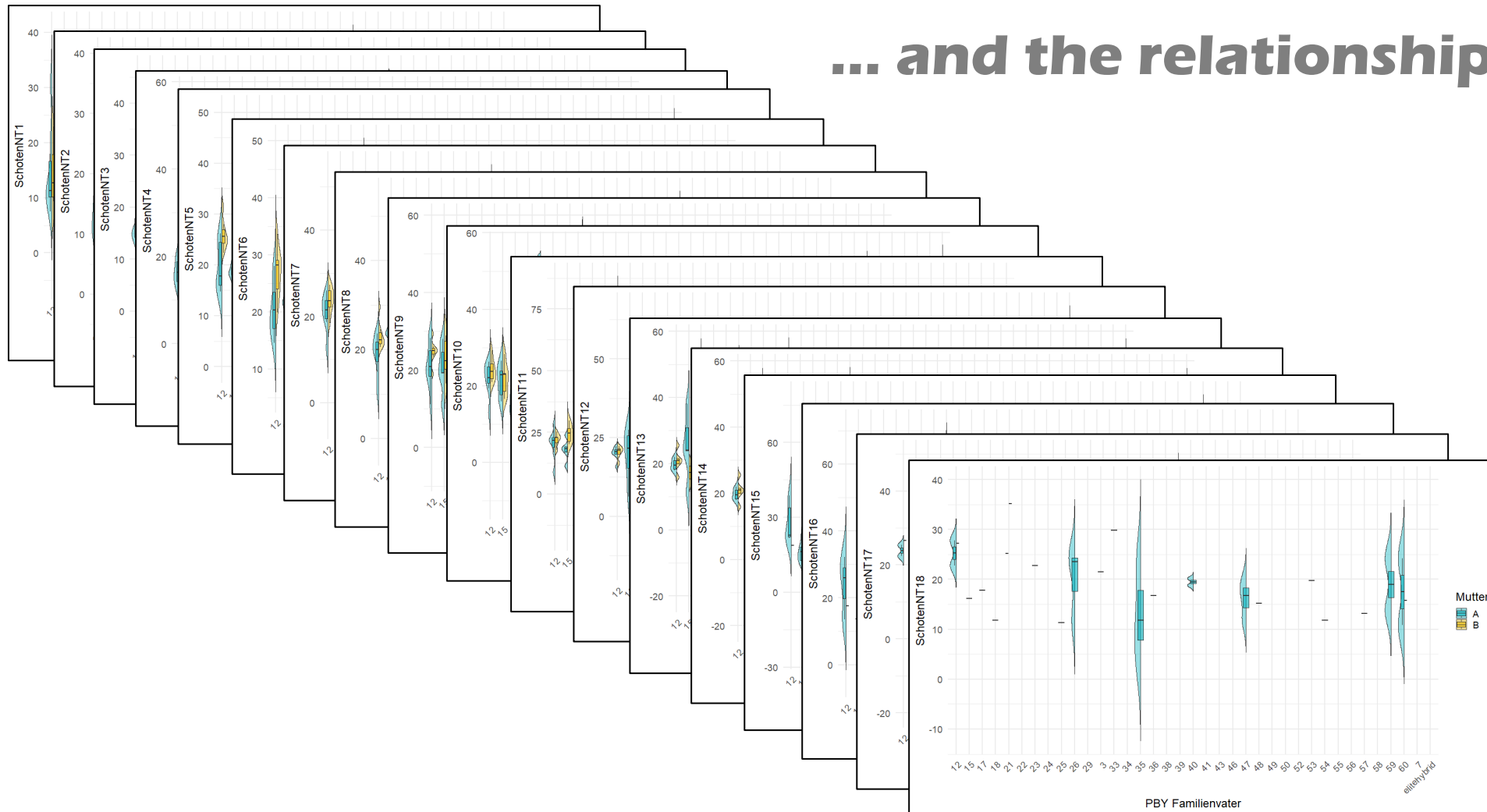
- Test hybrids from mother B have a higher yield and hence more efficient
- Nearly non family reaches elite material level

Pods per side branch



Pods per side branch

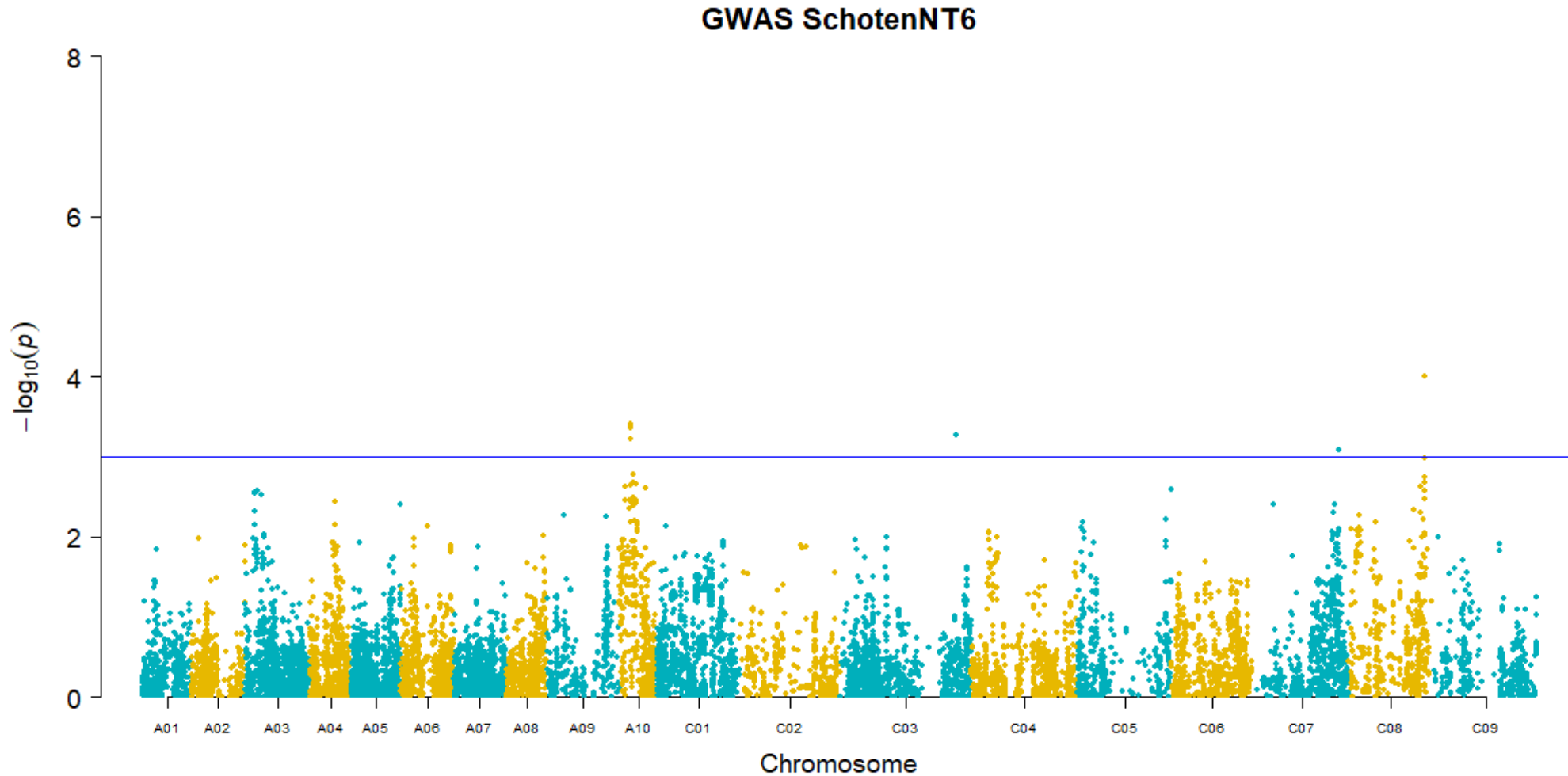
... and the relationship to seed yield



r (to yield)

SchotenNT1	0.084
SchotenNT2	0.123
SchotenNT3	0.221
SchotenNT4	0.297
SchotenNT5	0.307
SchotenNT6	0.377
SchotenNT7	0.317
SchotenNT8	0.260
SchotenNT9	0.218
SchotenNT10	0.212
SchotenNT11	0.247
SchotenNT12	0.178
SchotenNT13	0.242
SchotenNT14	0.242
SchotenNT15	0.223
SchotenNT16	0.047
SchotenNT17	0.173
SchotenNT18	0.069

GWAS pods on 6th side branch



Assessment of plant architecture



Parzelle: Genotyp: Pflanze: Barcode:

Höhe 1.NT: cm
Höhe 2.NT: cm
Höhe 3.NT: cm
Gesamt-Höhe: cm

Winkel 1.NT: Grad
Winkel 2.NT: Grad
Winkel 3.NT: Grad

The diagram illustrates the measurement of plant architecture. It shows a central vertical stem with three horizontal arrows indicating the height of the first, second, and third nodes (NT). To the right, three angles are shown, each measured from the vertical stem to a branch at the first, second, and third nodes. The angles are labeled 'Winkel 1.NT', 'Winkel 2.NT', and 'Winkel 3.NT'.

Schoten: ☐ Seite 2

	Schoten	Verzweigungen		Schoten	Verzweigungen
1. NT	<input type="text"/>	<input type="text"/>	11. NT	<input type="text"/>	<input type="text"/>
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10. NT	<input type="text"/>	<input type="text"/>	20. NT	<input type="text"/>	<input type="text"/>
HT	<input type="text"/>				

Digital assessment of plant architecture



PHenOSPEx
Smart Plant Analysis

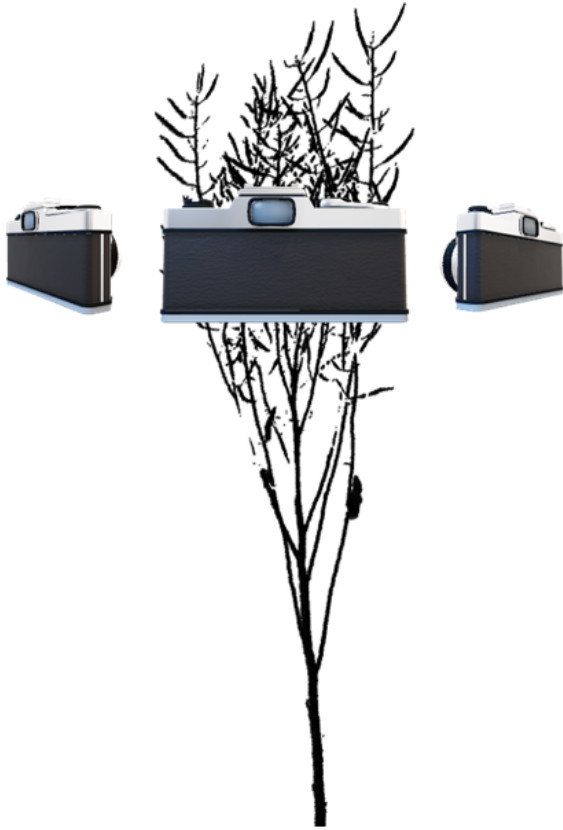


From point cloud to phenotype

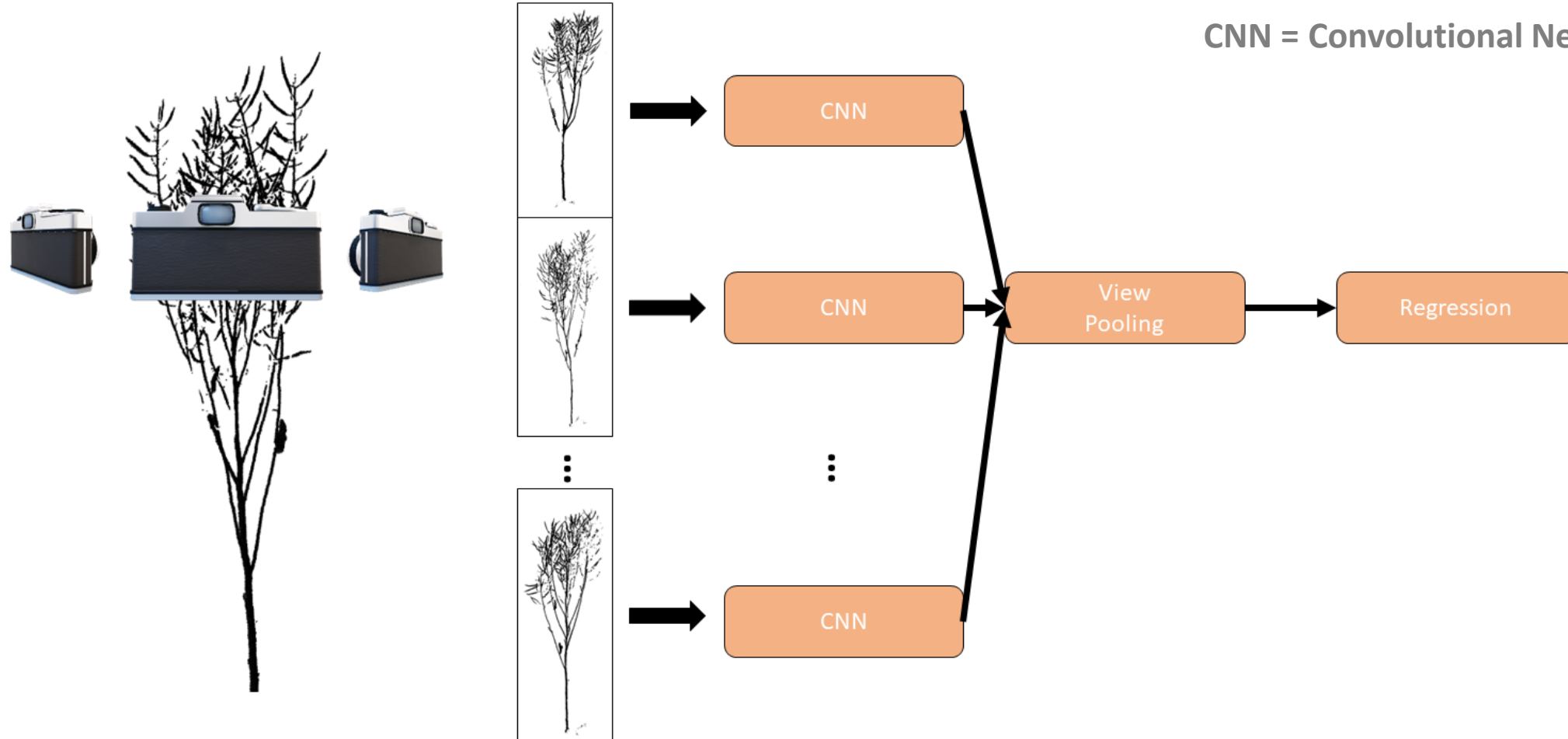


	X	Y	Z
P1	10	5	6
P5	23	17	8
P3	12	22	9
P4	4	1	3
P2	66	55	18

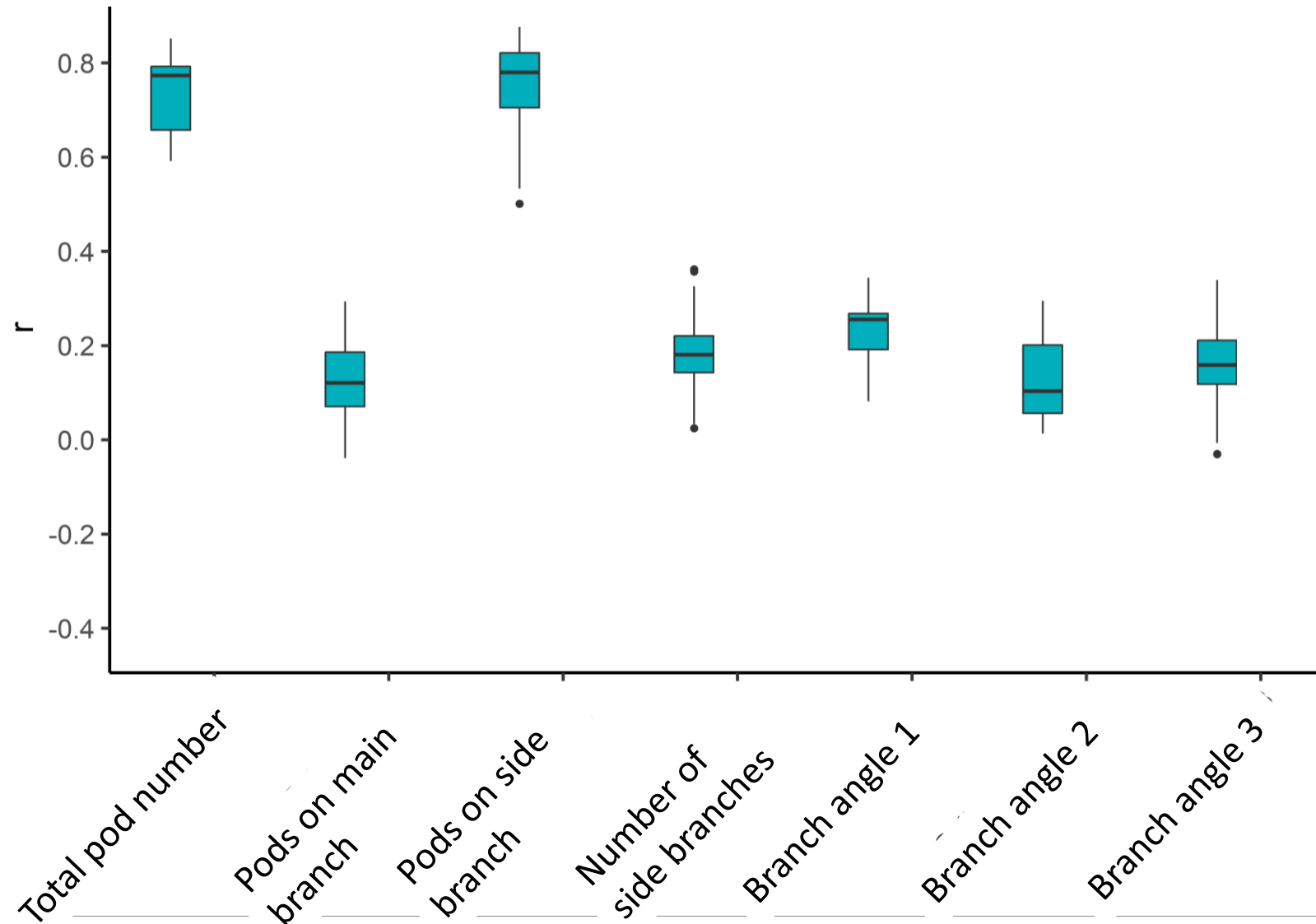
CNN to predict architecture based on point clouds



CNN to predict architecture based on point clouds



CNN to predict architecture based on point clouds



CNN = Convolutional Neural Network

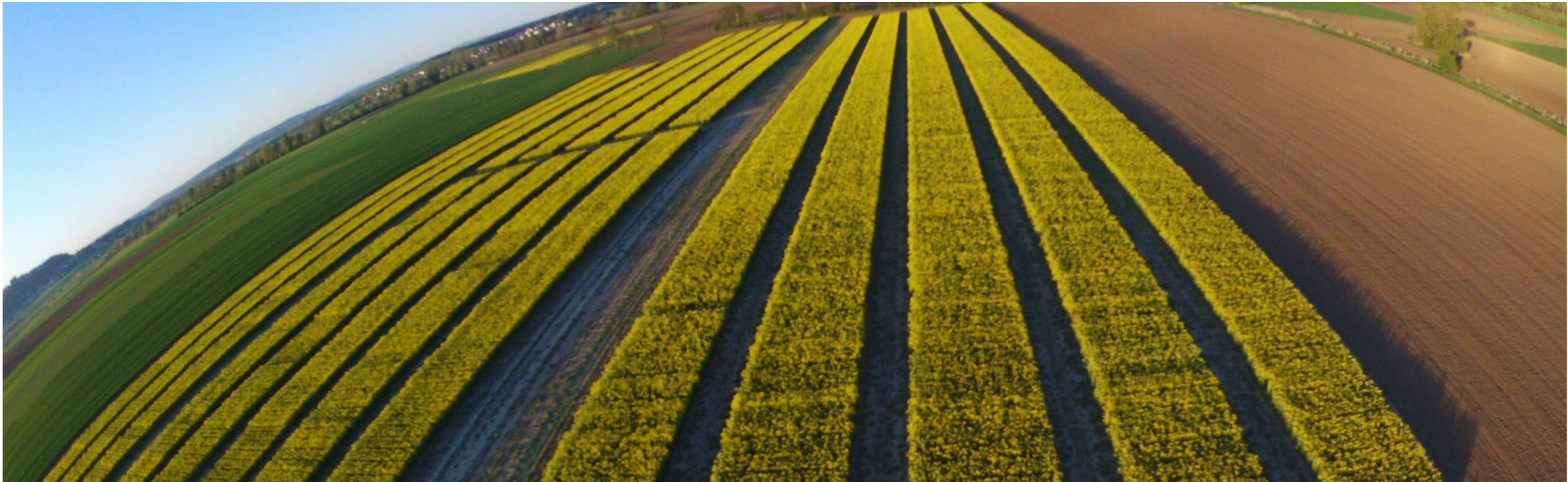
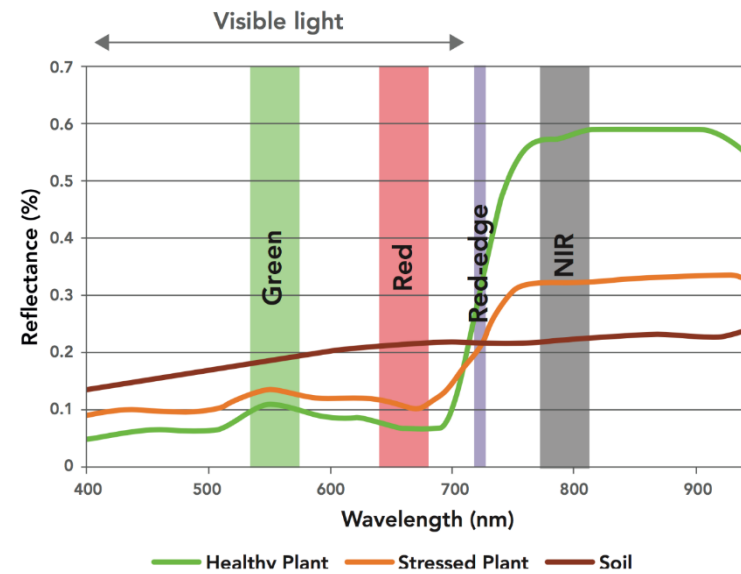
Pointcloud

Vegetation indices

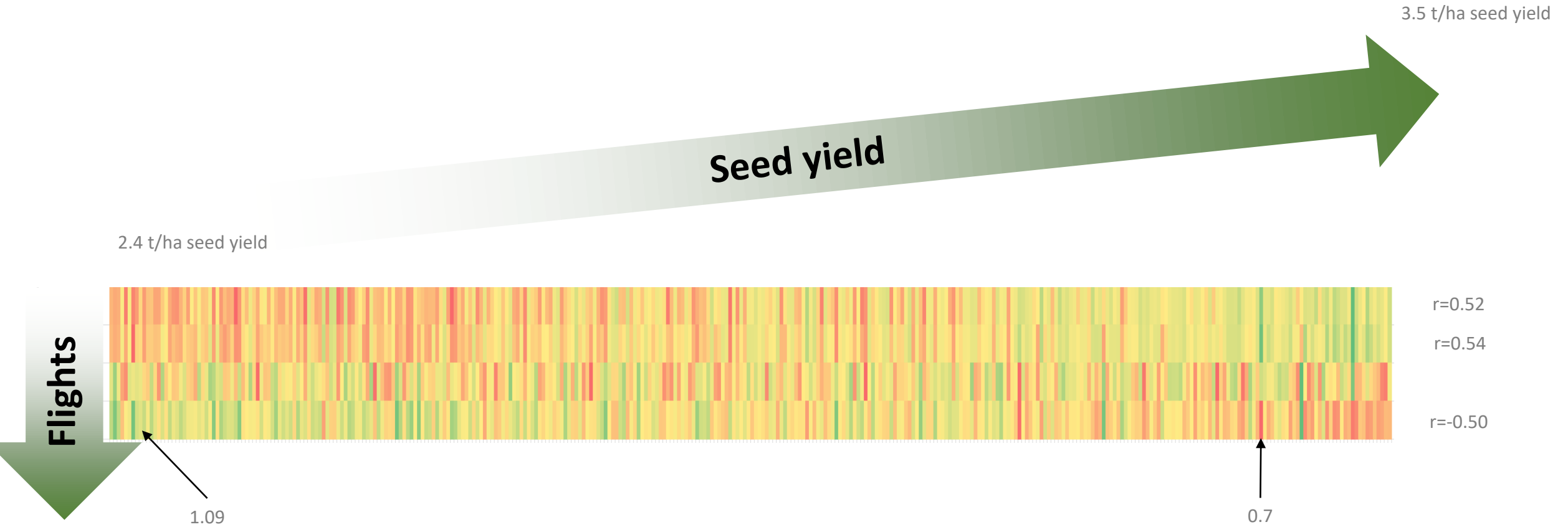
$$\text{NDVI} = (\text{NIR} - \text{red}) / (\text{NIR} + \text{red})$$

$$\text{GNDVI} = (\text{NIR} - \text{GREEN}) / (\text{NDVI} + \text{GREEN})$$

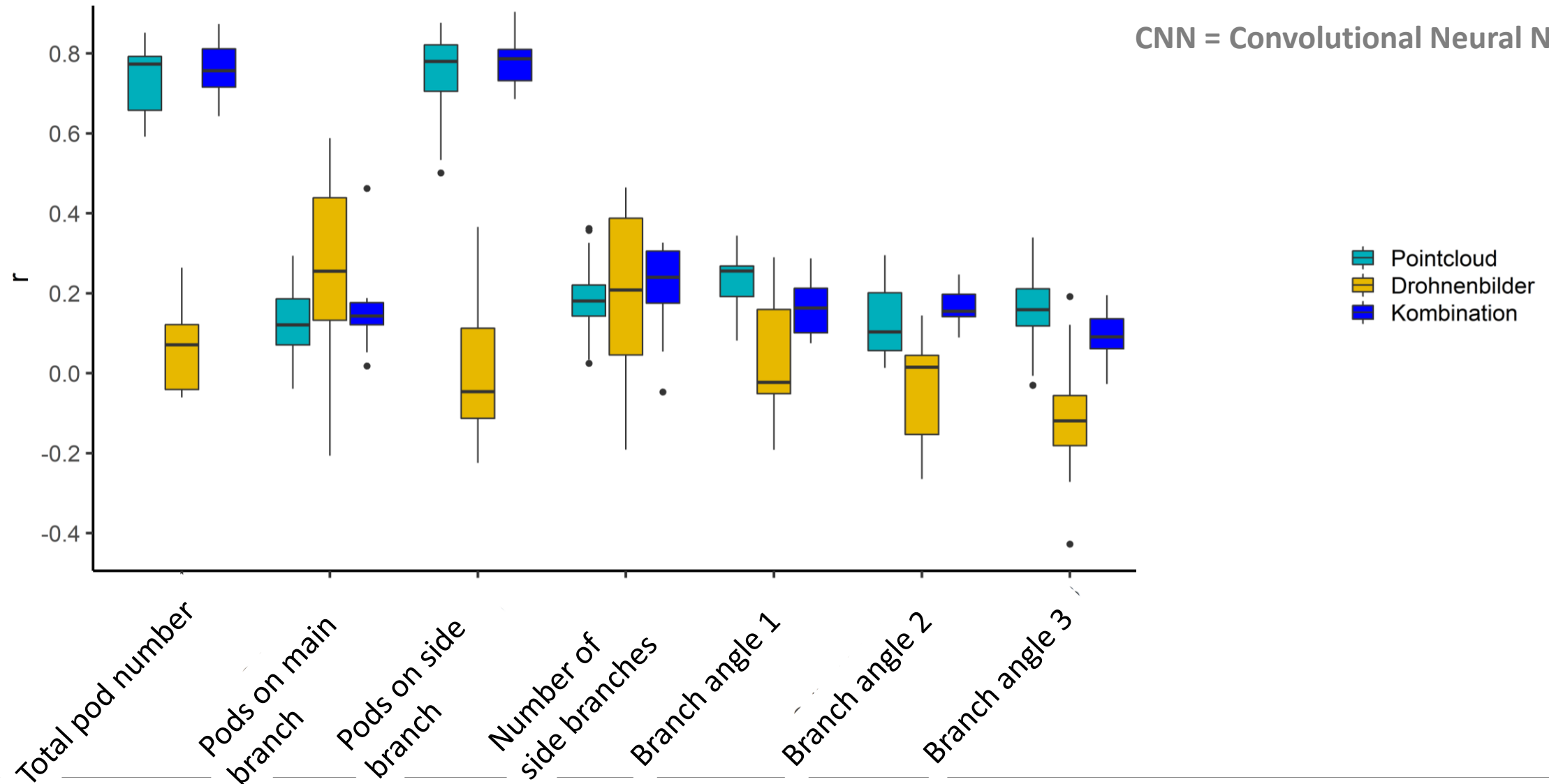
$$\text{NDRE} = (\text{NIR} - \text{RED EDGE}) / (\text{NIR} + \text{RED EDGE})$$



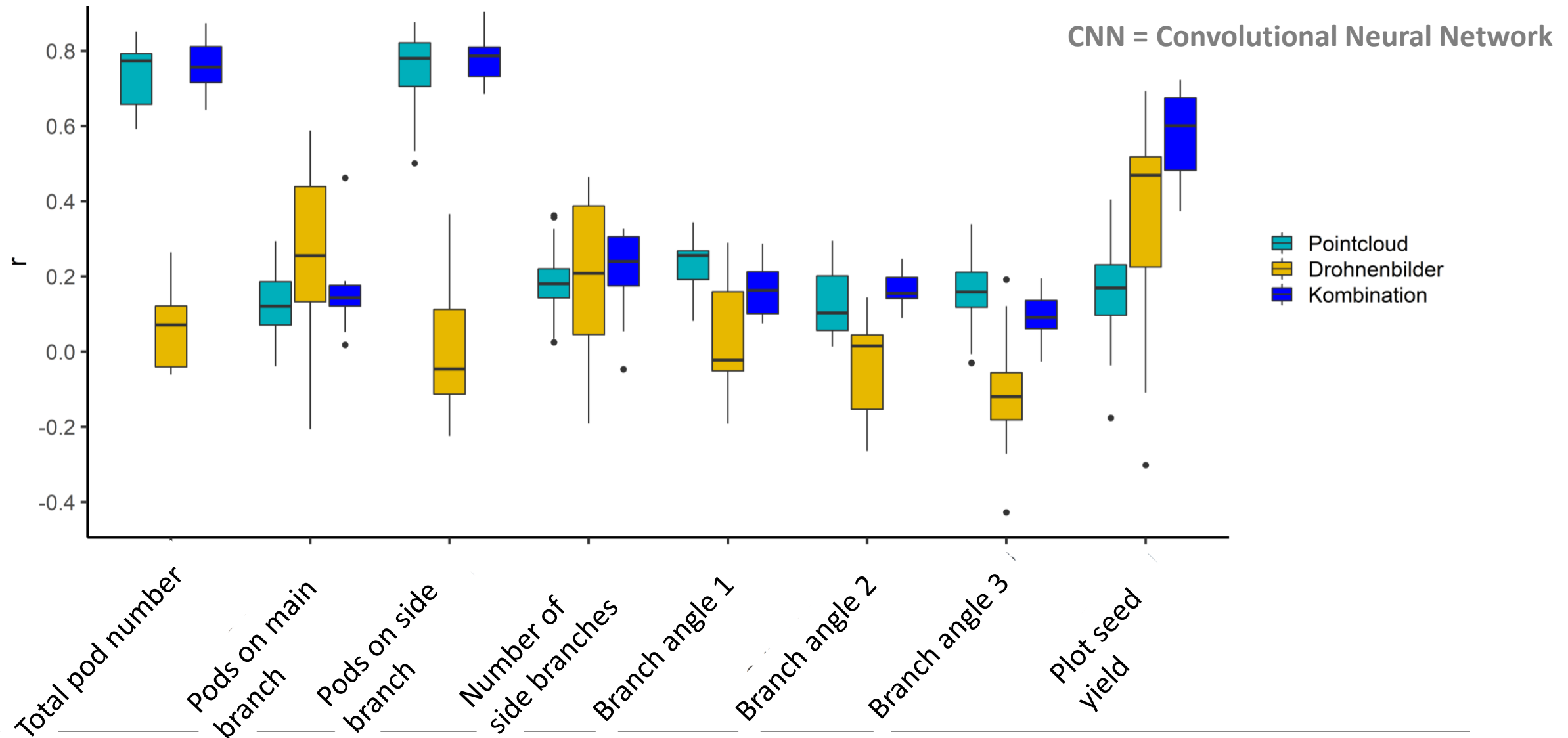
Normalized Difference Red Edge



CNN to predict architecture based on point clouds and UAV pictures



CNN to predict architecture based on point clouds and UAV pictures



Thanks for your attention!

Any questions?

- **Prof. Dr. Andreas Stahl (JKI)**
- **Andreas Eckert (PhD-student)**
- **Prof. Dr. Rod Snowdon**
- **Dr. Benjamin Wittkop**
- **Stjepan Vukasovic**
- **Anna Langstroff**
- **Lennard Ehrig**
- **Lennart Scheer**
- **Lukas Förter (Master)**



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