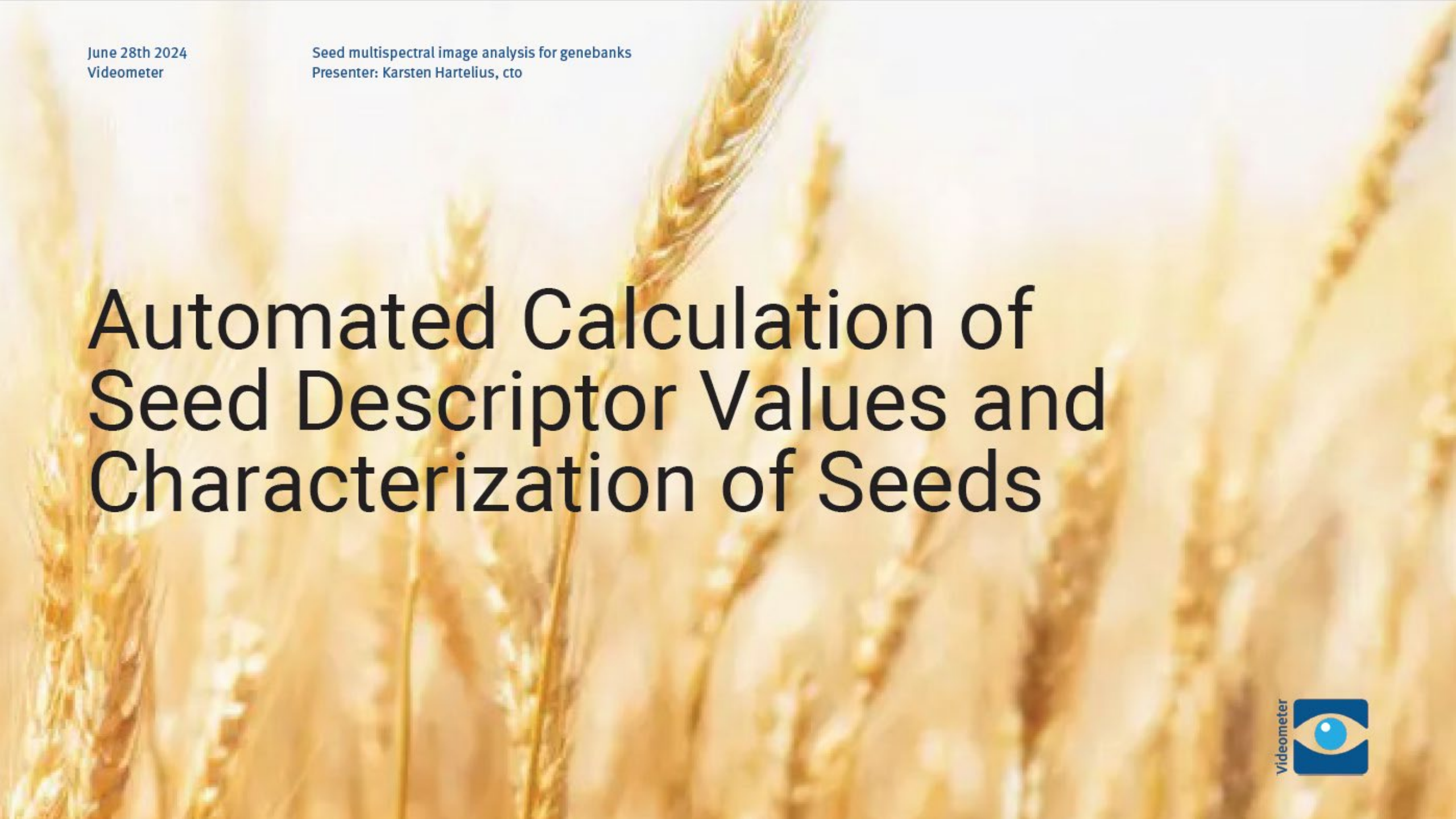
June 28th 2024
Videometer

Seed multispectral image analysis for genebanks
Presenter: Karsten Hartelius, cto

Automated Calculation of Seed Descriptor Values and Characterization of Seeds



The One CGIAR Genebanks' SQM CoP

- SQM CoP = Seed Quality Management Community of Practice

- **Scope: Improving the efficiency and effectiveness in how we manage genebank seed collections through research and capacity building to assure the availability and quality of seeds to users**

- **Research areas**
  - Optimizing dormancy breaking / germination protocols for viability monitoring
  - Improving regeneration and post-harvest handling procedures (e.g. drying) for better seed quality
  - Understanding the longevity of seeds in genebank storage to customize monitoring intervals
  - Introducing technologies to improve seed genebank management, for example, multispectral image analysis for seed phenotyping

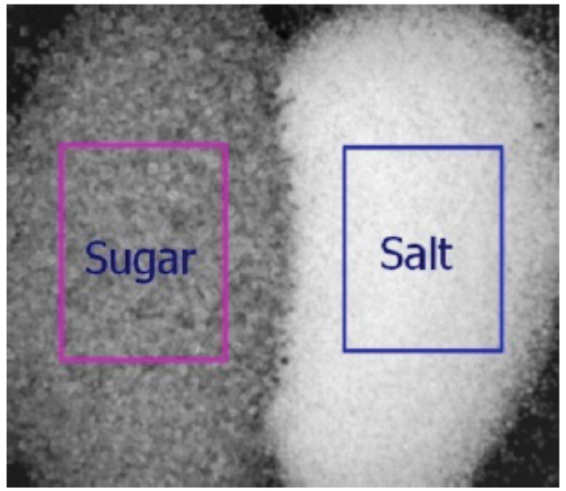
Contact: fiona.hay@agro.au.dk

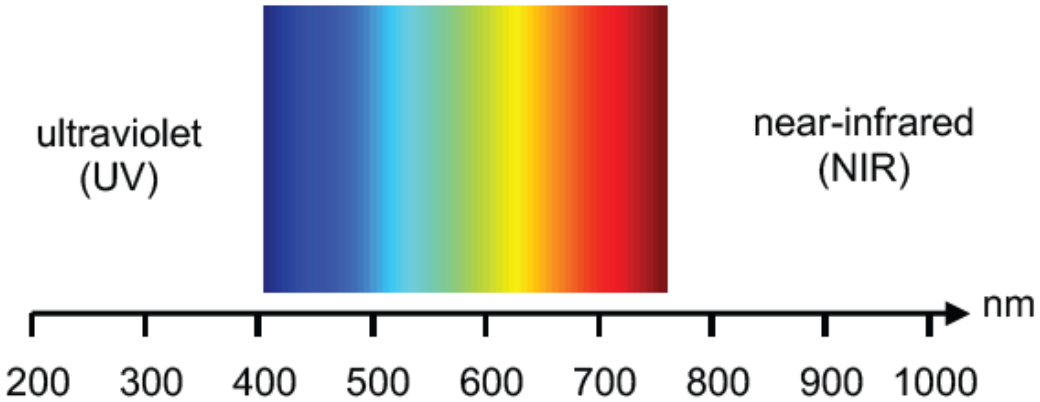
VideometerLab4

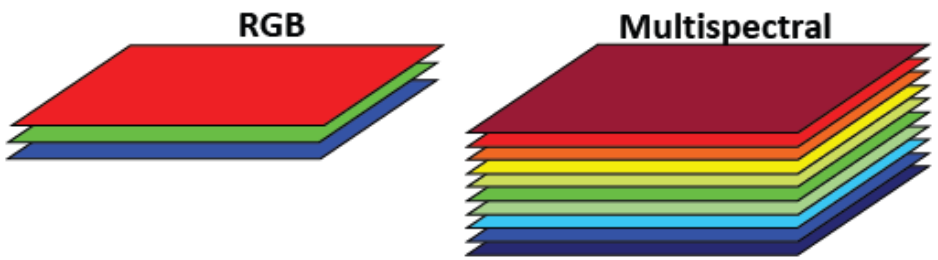
Flexible lab and at-line instrument for spectral imaging

- 19-20 spectral bands in the range 365 nm to 970 nm
- 2192 × 2192 pixels per band = 40 µm pixel-resolution
- Highly homogeneous and diffuse illumination
- NIST referenced calibration ensures reproducebility and transferability between instruments.
- 10 seconds per sample including handling
- Powerfull image analysis toolbox
- Optional backlight
- Optional fluorescense bands

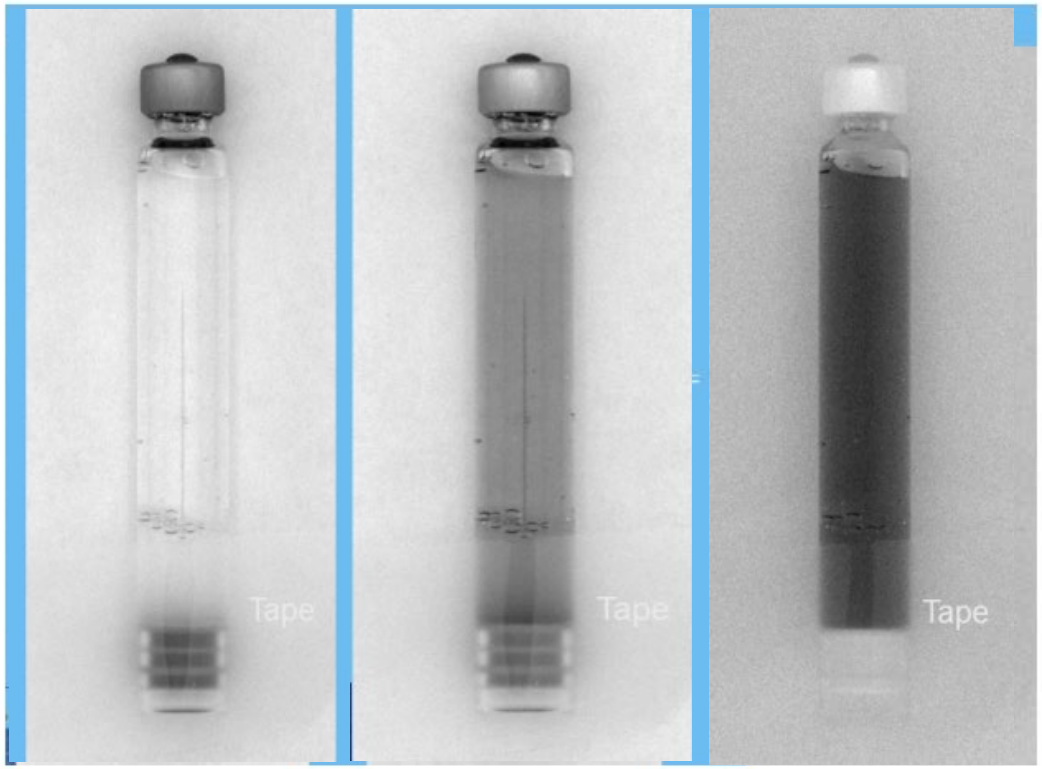
Multispectral imaging

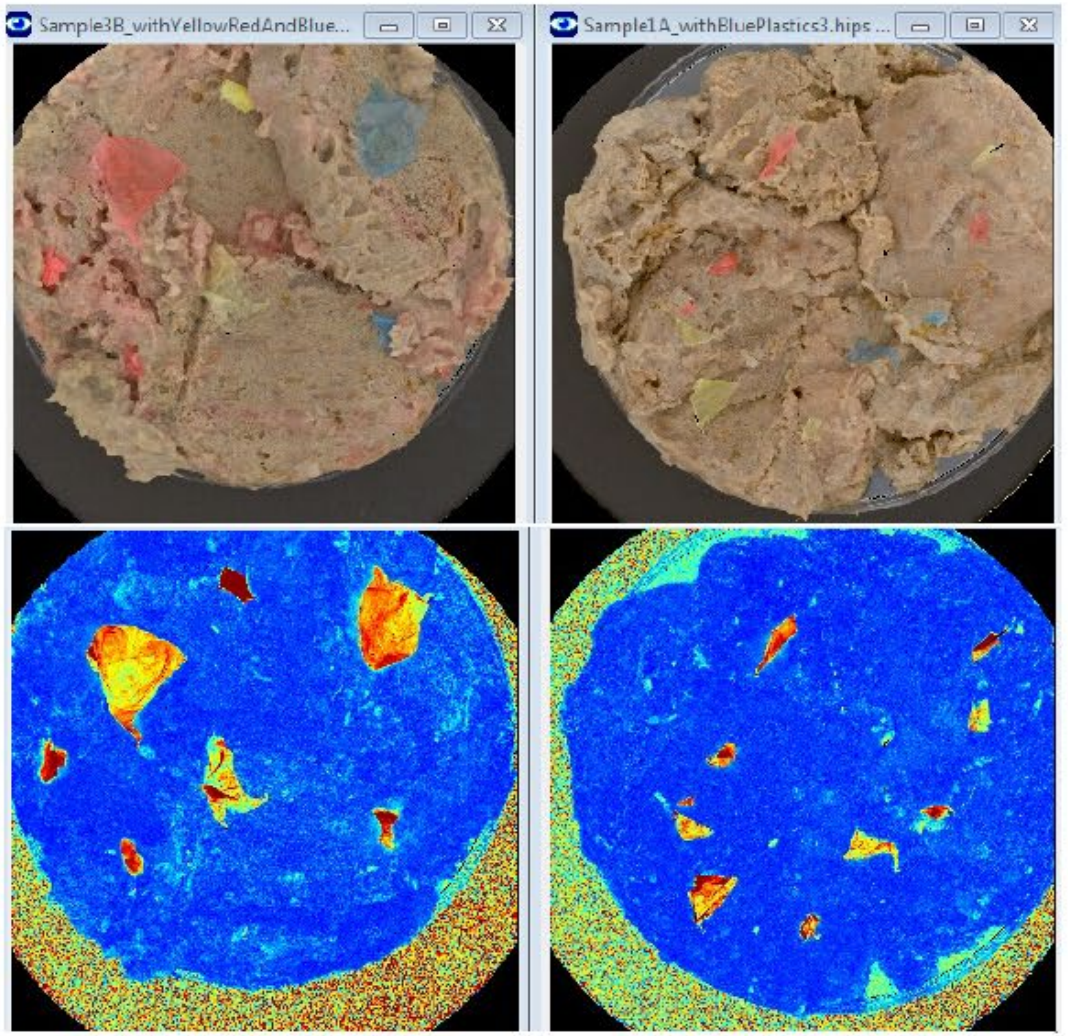






Spectral imaging examples



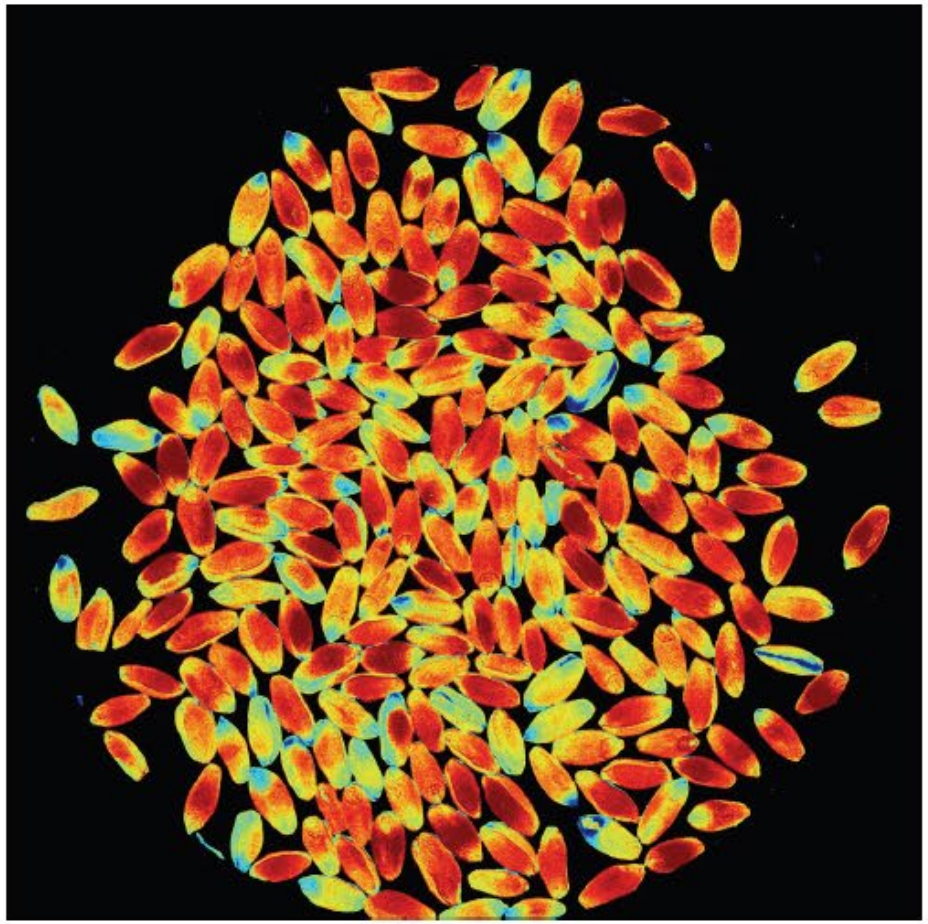


Separation of durum and common wheat via multispectral transformation

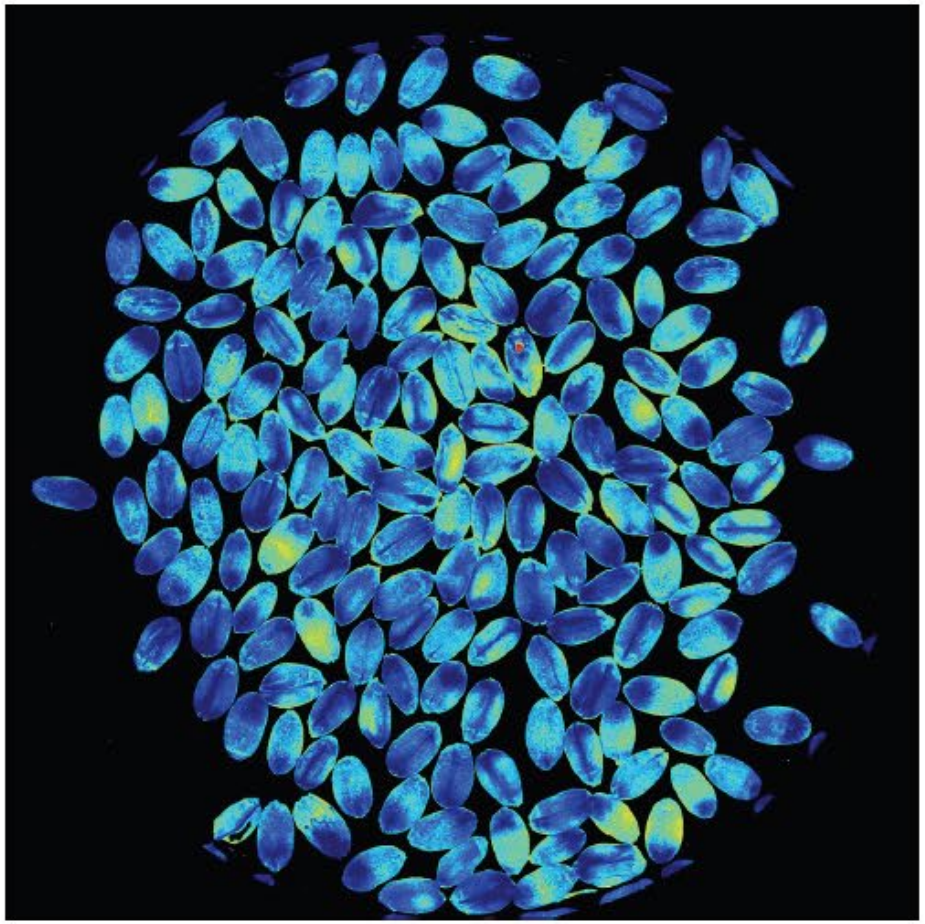
Durum

Common wheat

Energy image of multispectral transformation



Durum acts as positive



Common wheat acts as negative

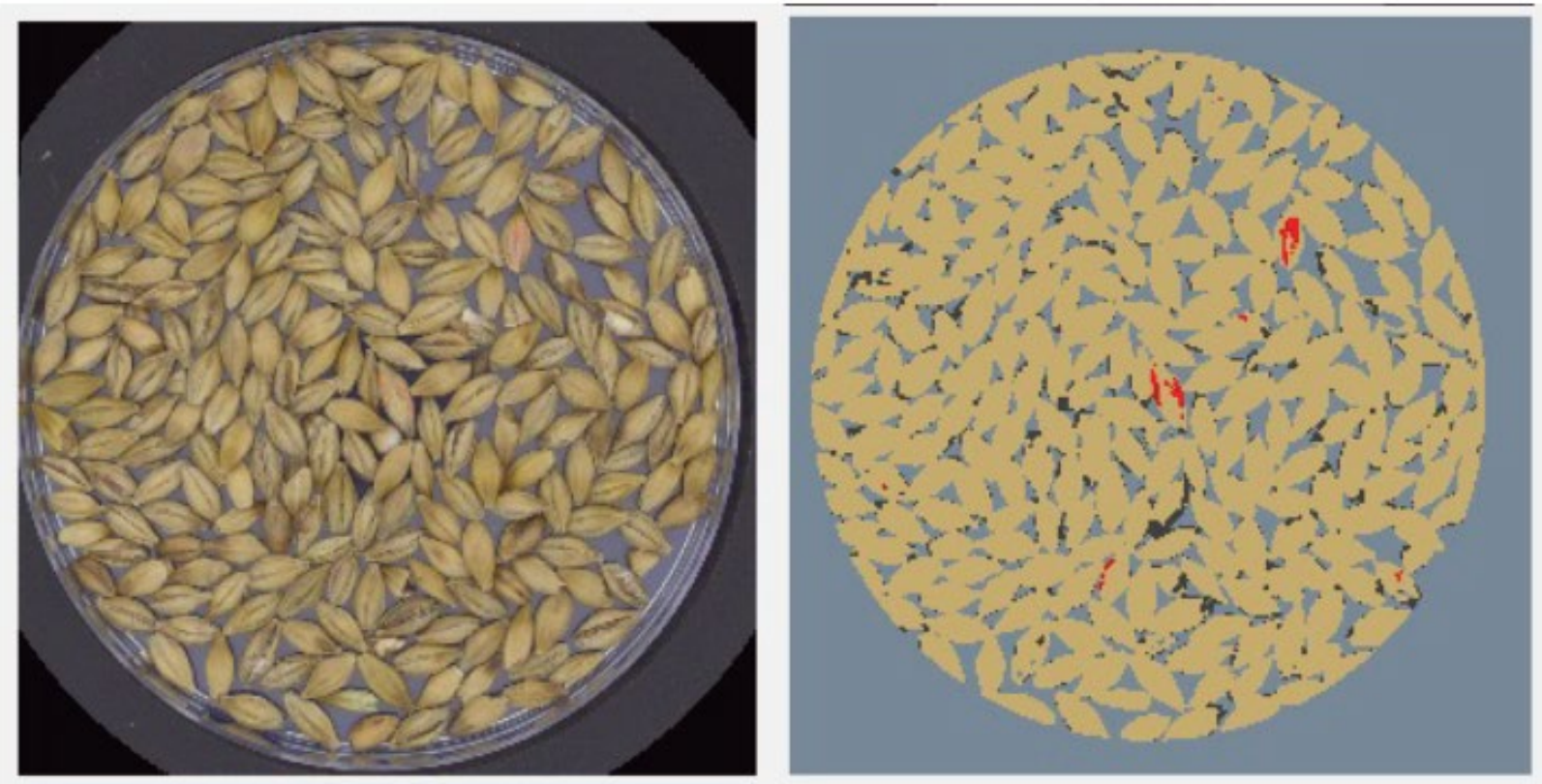
Fusarium and grey mold detection

2 Step test

1. Present the barley in a 90 mm petri dish (single layer)
2. Press F12

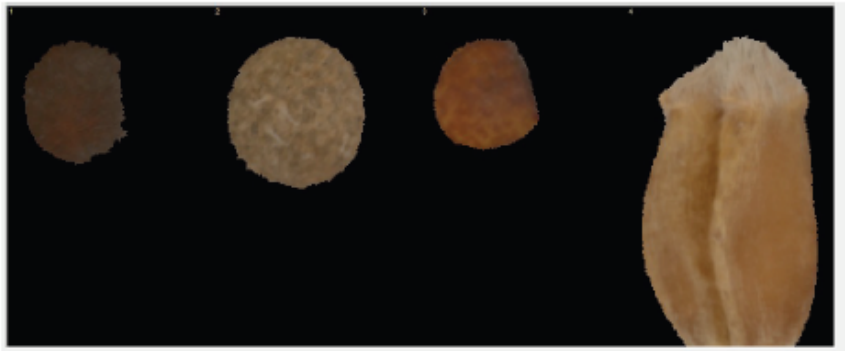
Output will show

1. a **color image** of the sample
2. a **segmented image** with red type Fusarium marked with red color and gray type molds with black color
3. an **area fraction** of red type Fusarium and of gray type molds

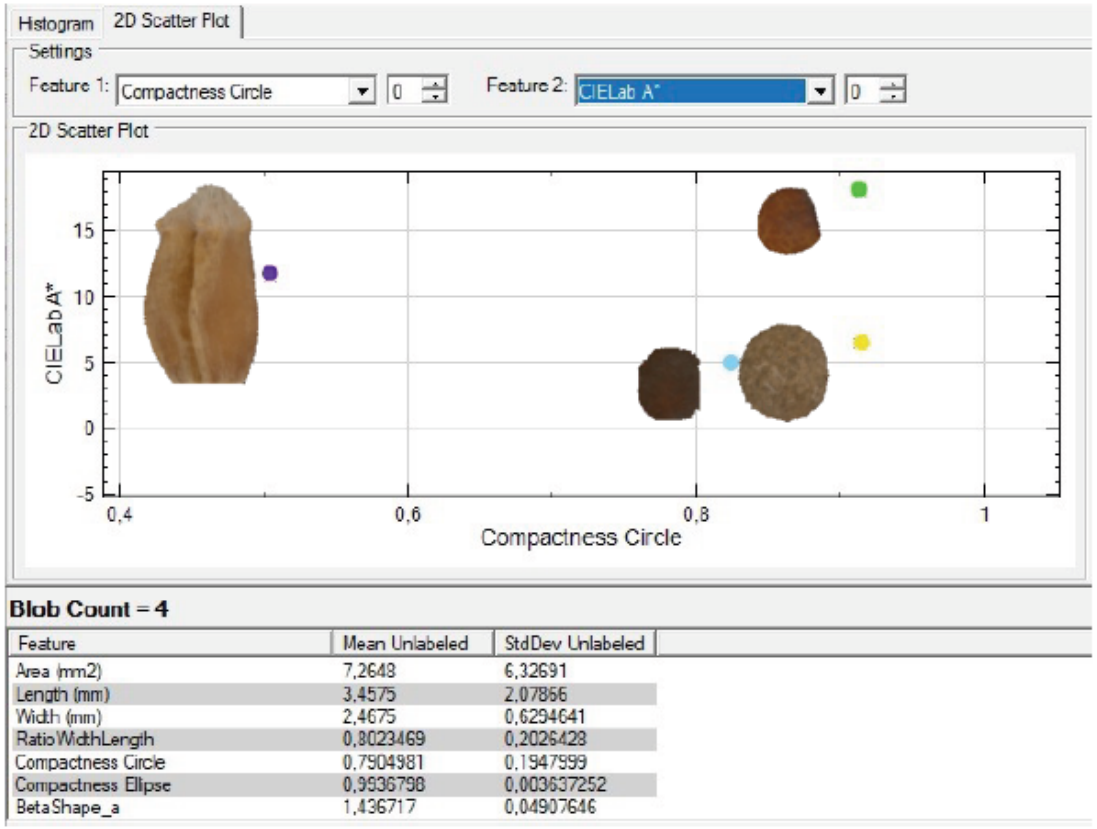


Attributes for characterizing seeds

- Color
- Spectral components
- Shape
- Texture
- Size
- Contour



Oilseed rape Clever Oilseed rape Wheat



Blob Count = 4

Feature	Mean Unlabeled	StdDev Unlabeled
Area (mm2)	7,2648	6,32691
Length (mm)	3,4575	2,07856
Width (mm)	2,4675	0,6294641
RatioWidthLength	0,8023469	0,2026428
Compactness Circle	0,7904981	0,1947999
Compactness Ellipse	0,9936798	0,003637252
BetaShape_a	1,436717	0,04907646

Descriptors for Rice seed characterization

- **Implement blob features that identifies landmarks on rice seeds and utilizes this information to calculate seed descriptors in the form of color, shape and texture parameters**

Descriptors for wild and cultivated

Rice

(*Oryza* spp.)

7.5.3 Awn colour (late observation)

	(IRRI)	
0	0	Absent (awnless)
1	020	Straw
2	040	Gold
3	052	Brown (tawny)
4	070	Red
5	080	Purple
6	100	Black

7.5.4 Lemma and palea pubescence

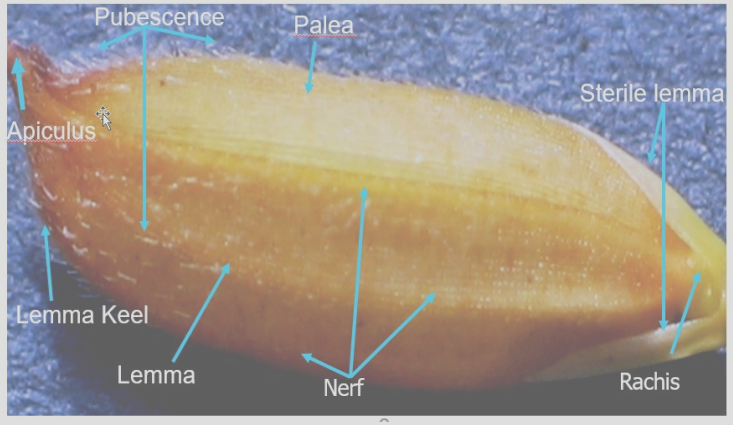
Visual assessment of the presence and distribution of matu
lens.

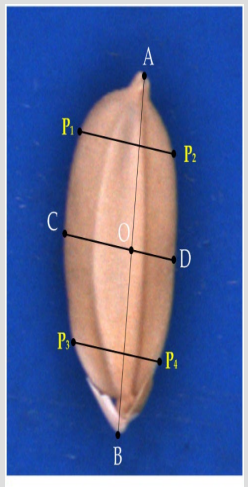
1	Glabrous
2	Hairs on lemma keel
3	Hairs on upper portion
4	Short hairs
5	Long hairs (velvety)

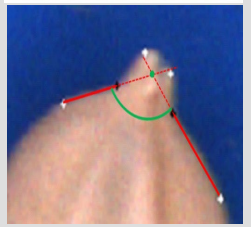
7.5.5 Lemma and palea colour (late observation)

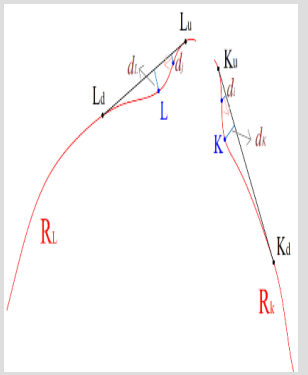
	(IRRI)	
1	010	White
2	020	Straw
3	042	Gold and gold furrows
4	052	Brown (tawny)
5	053	Brown spots
6	054	Brown furrows
7	080	Purple
8	082	Reddish to light purple
9	090	Purple spots
10	091	Purple furrows
11	100	Black

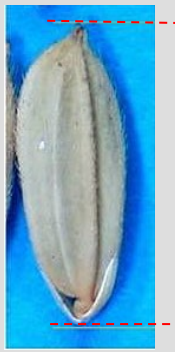
Example: Rice seeds





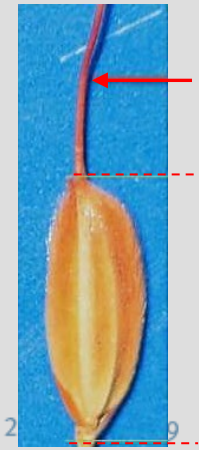






Top of ap

Base of sterile lemma

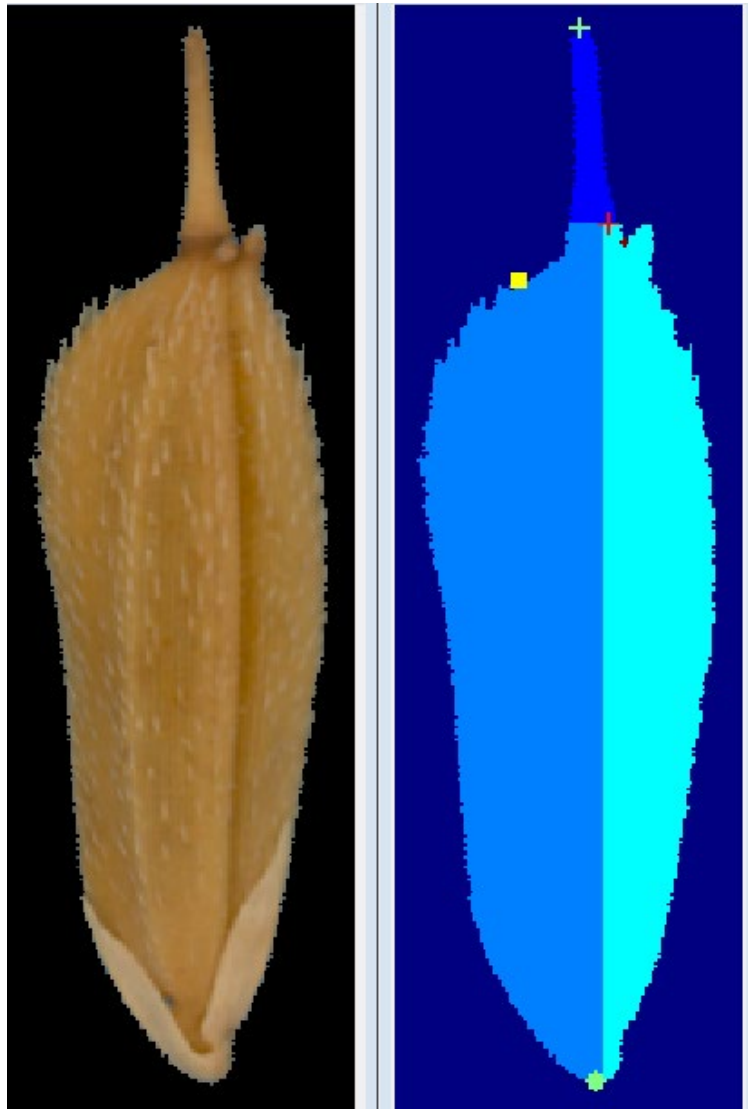


Awn

Top of ap Excluding

Base of sterile lemma

Rice seed landmark detection



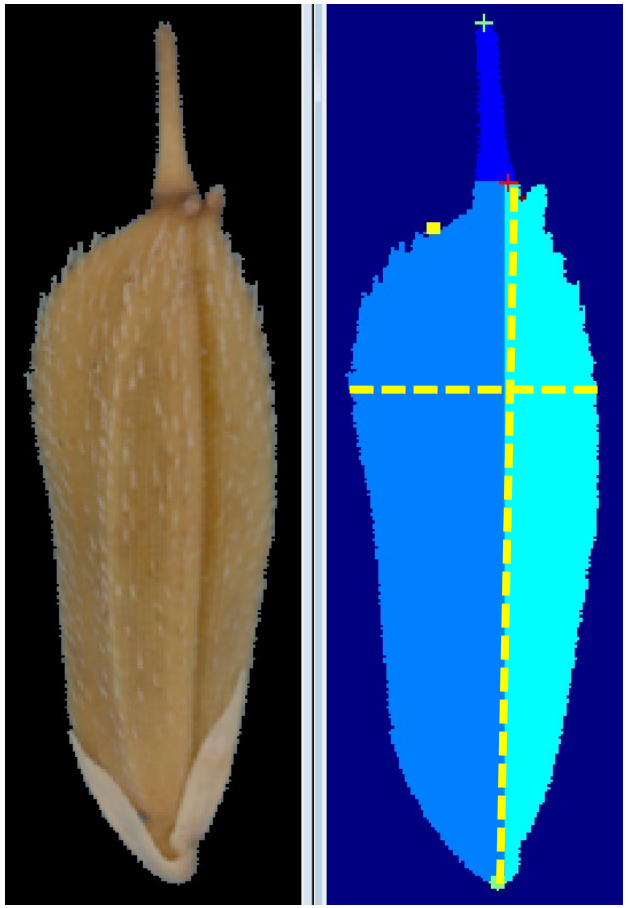
Landmarks detected:

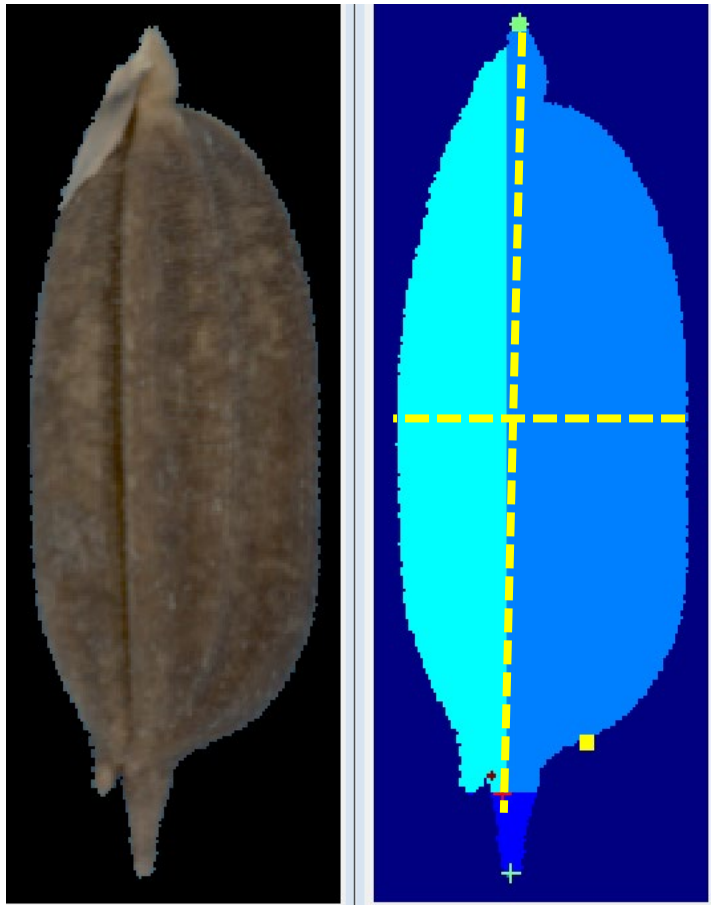
- Sterile lemma base point
- Lemma keel point
- Apiculus tip point (lemma apiculus)
- Tip of awn
- Lemma region
- Palea region

Rice Seed Length & Width

Measurement of the length and width of the rice seed:

1. Length of seed is measured between sterile lemma base and palea tip point
2. Width of seed is measured at the widest point on the seed perpendicular to the length-axis

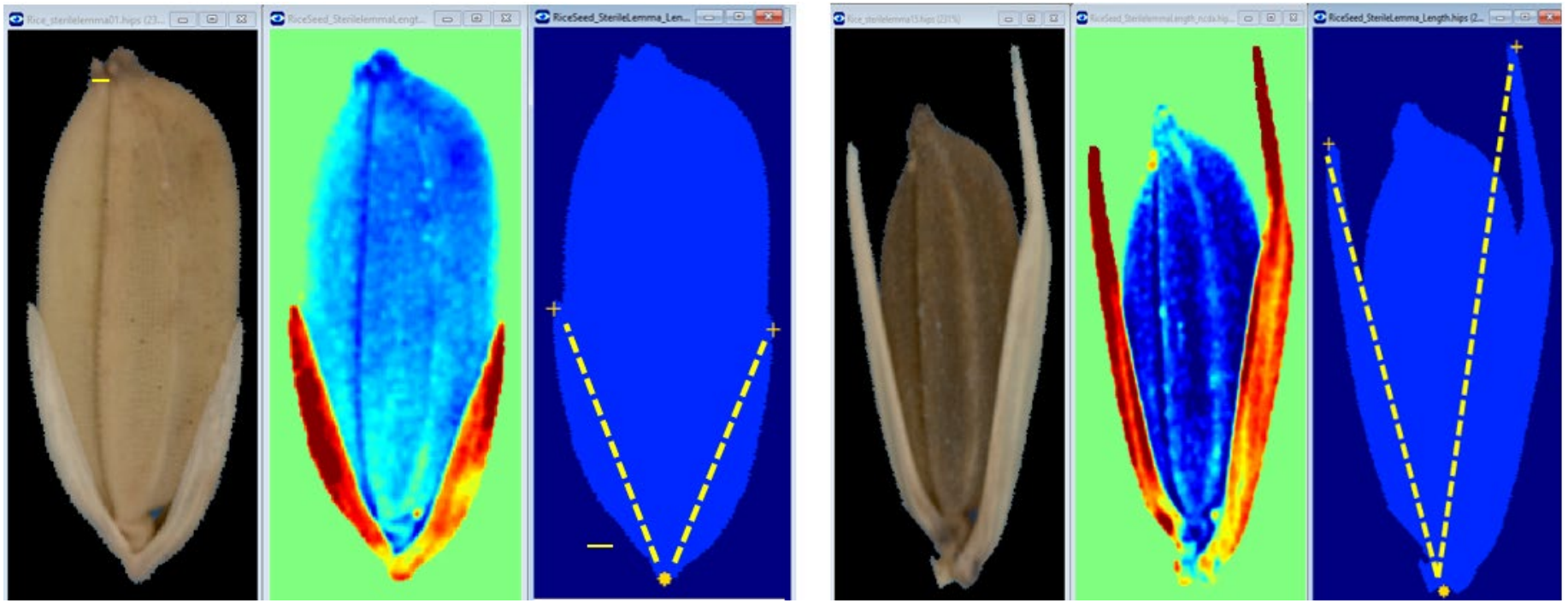




Rice seed Sterile lemma length

Measure length of shorter sterile lemma (index 1) and longer sterile lemma (index 2)

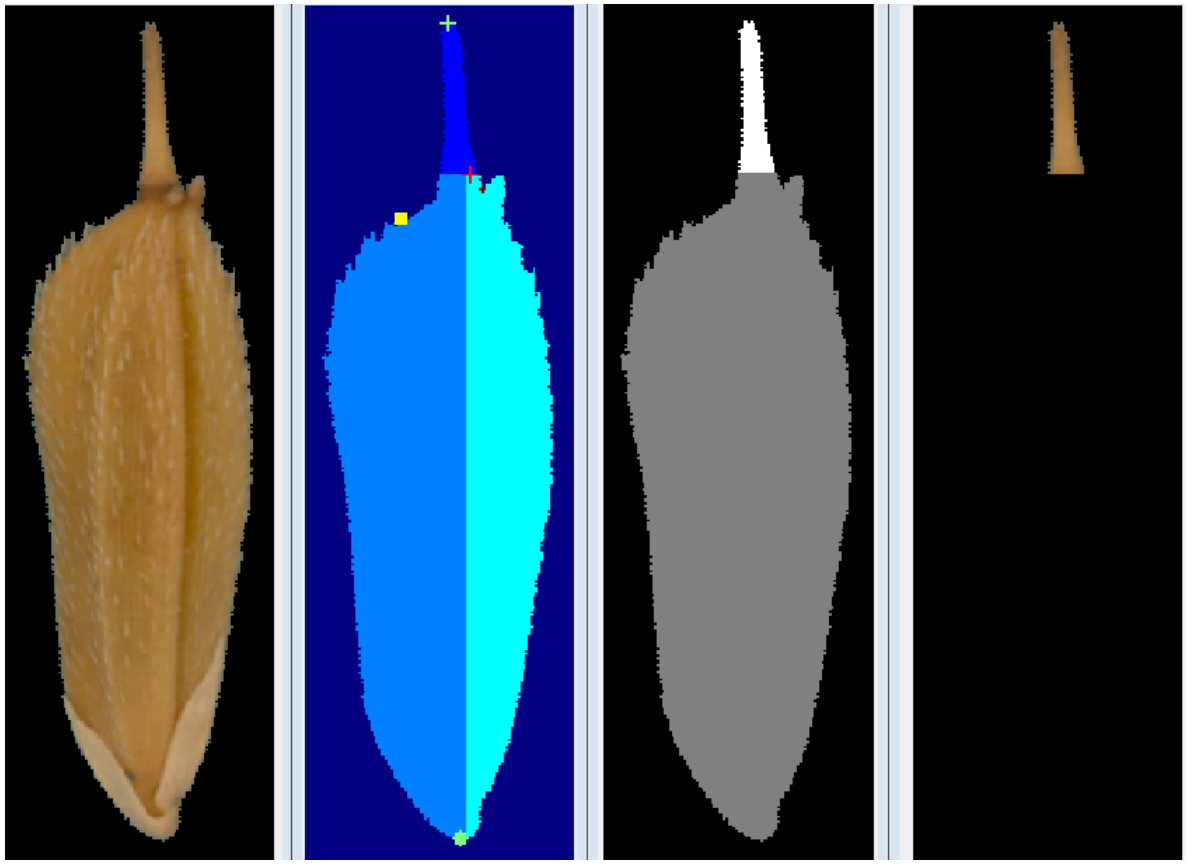
1. Multispectral transformation enhancing sterile lemma is calculated first (image 2)
2. Landmarks on seed detected (image 3).
3. Sterile lemma length detected on both sides and measured from sterile lemma base (image 4).



Rice seed Awn color

Procedure for calculation of descriptor:

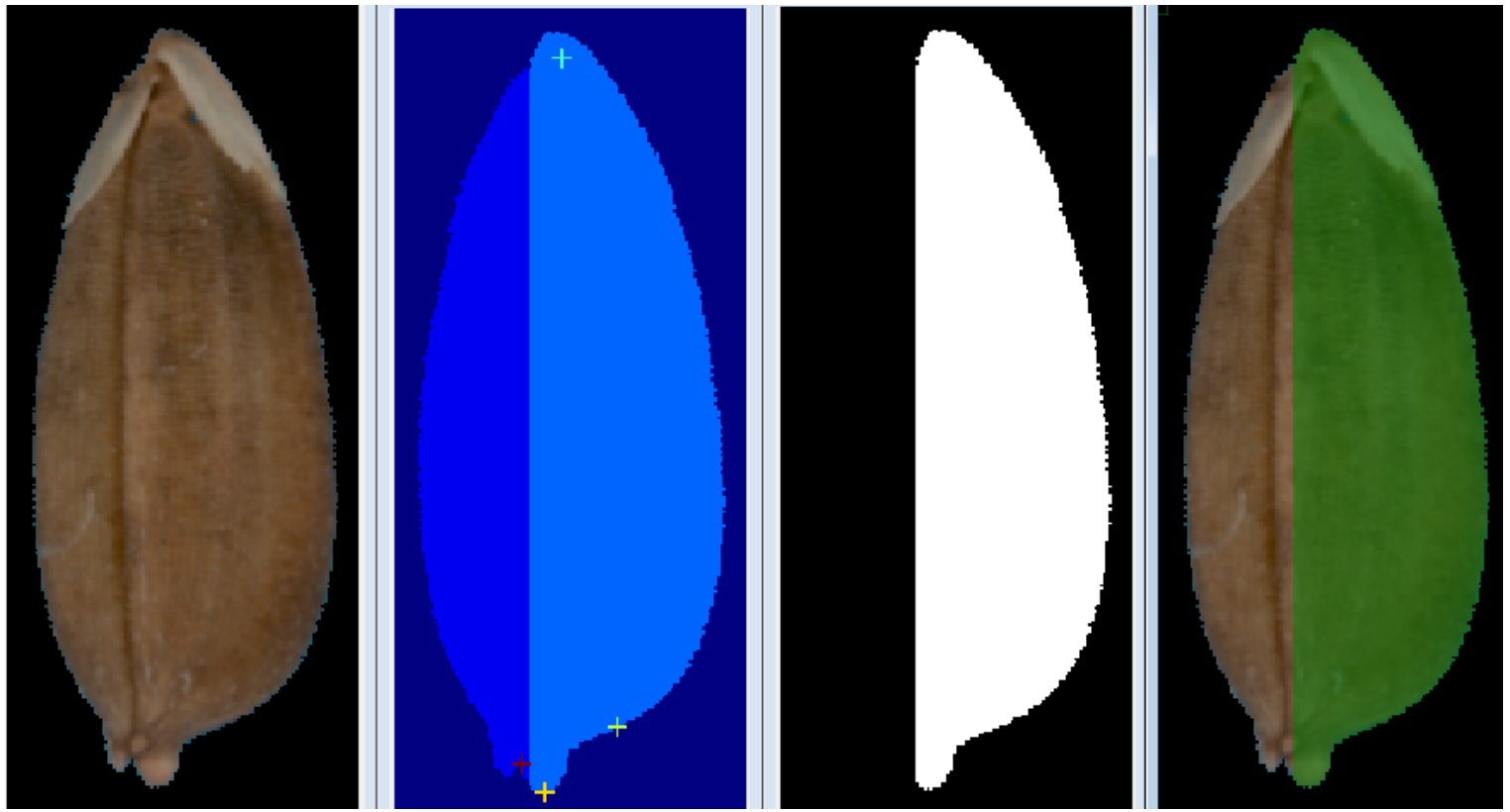
1. Locate awn (image 3)
2. Calculate color distribution in awn mask (image 4)



Rice seed Lemma and palea color

Procedure for calculation of descriptor:

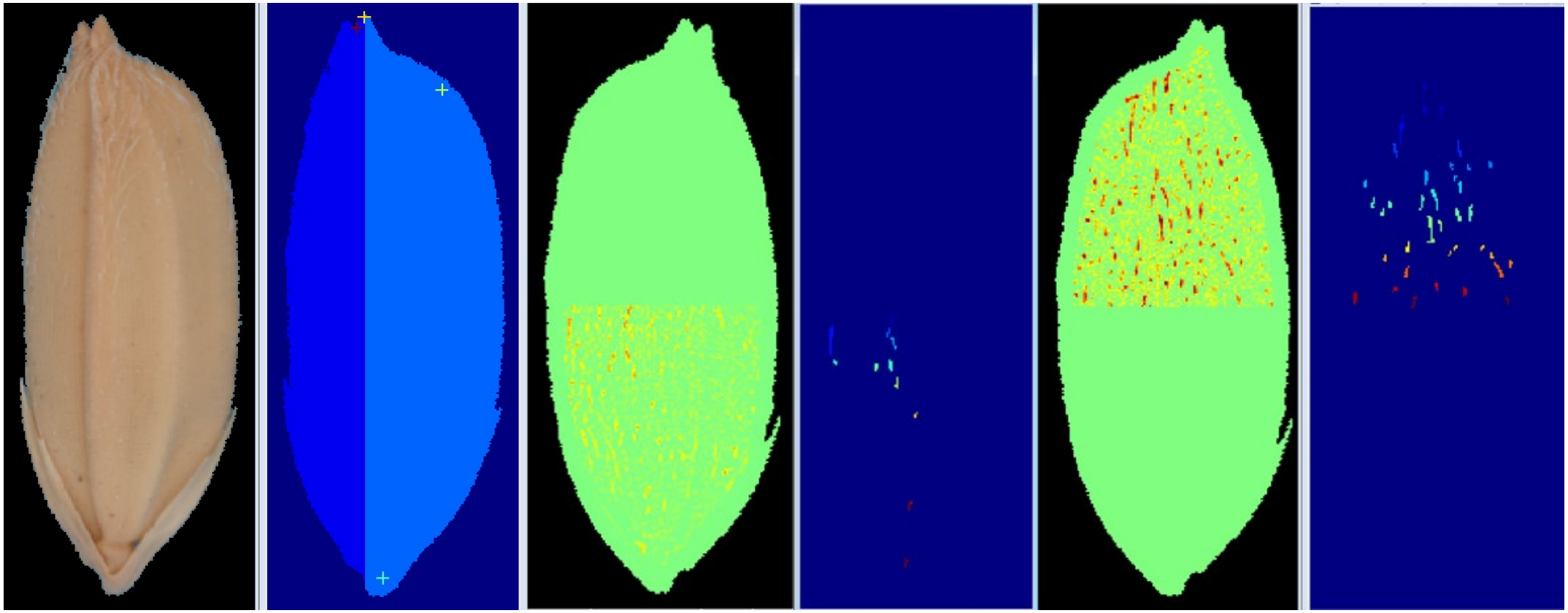
1. Locate landmarks (image 2)
2. Locate lemma region without nerf separating lemma and palea regions (image 3)
3. Calculate color-transformations in lemma region on grain (image 4)



Rice seed Pubescence

Procedure for calculation of descriptor:

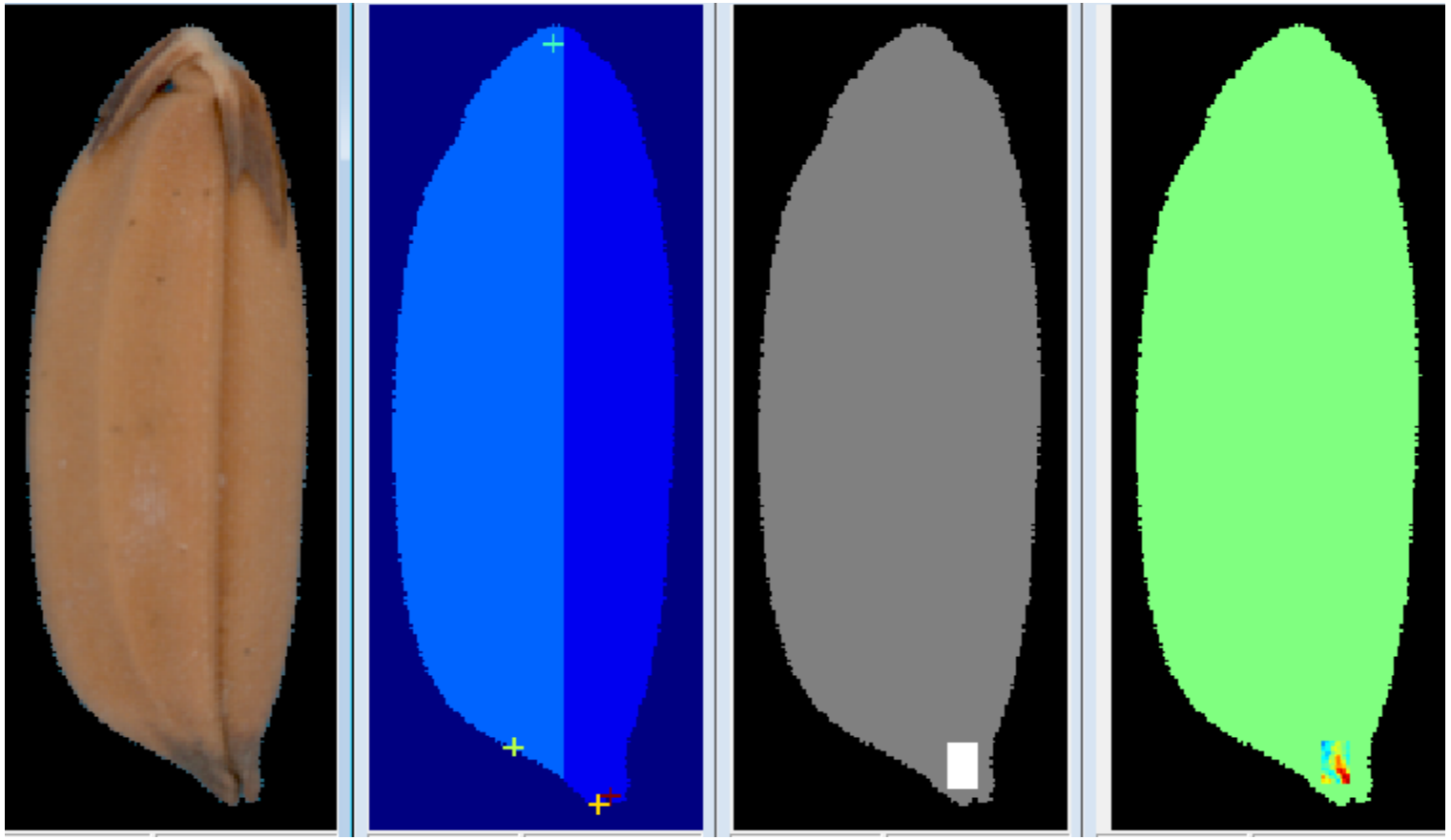
1. Locate landmarks (image 2)
2. Detect hairs in upper and lower half of grain (image 3 & 5)
3. Calculate amount of long and short hairs in the two portions (image 4 & 6)



Anthocyanin level below apiculus

Procedure for calculation of descriptor:

1. Locate landmarks (image 2)
2. Locate area below apiculus (image 3)
3. Calculate anthocyanin specific color-transformation in area below apiculus(image 4)

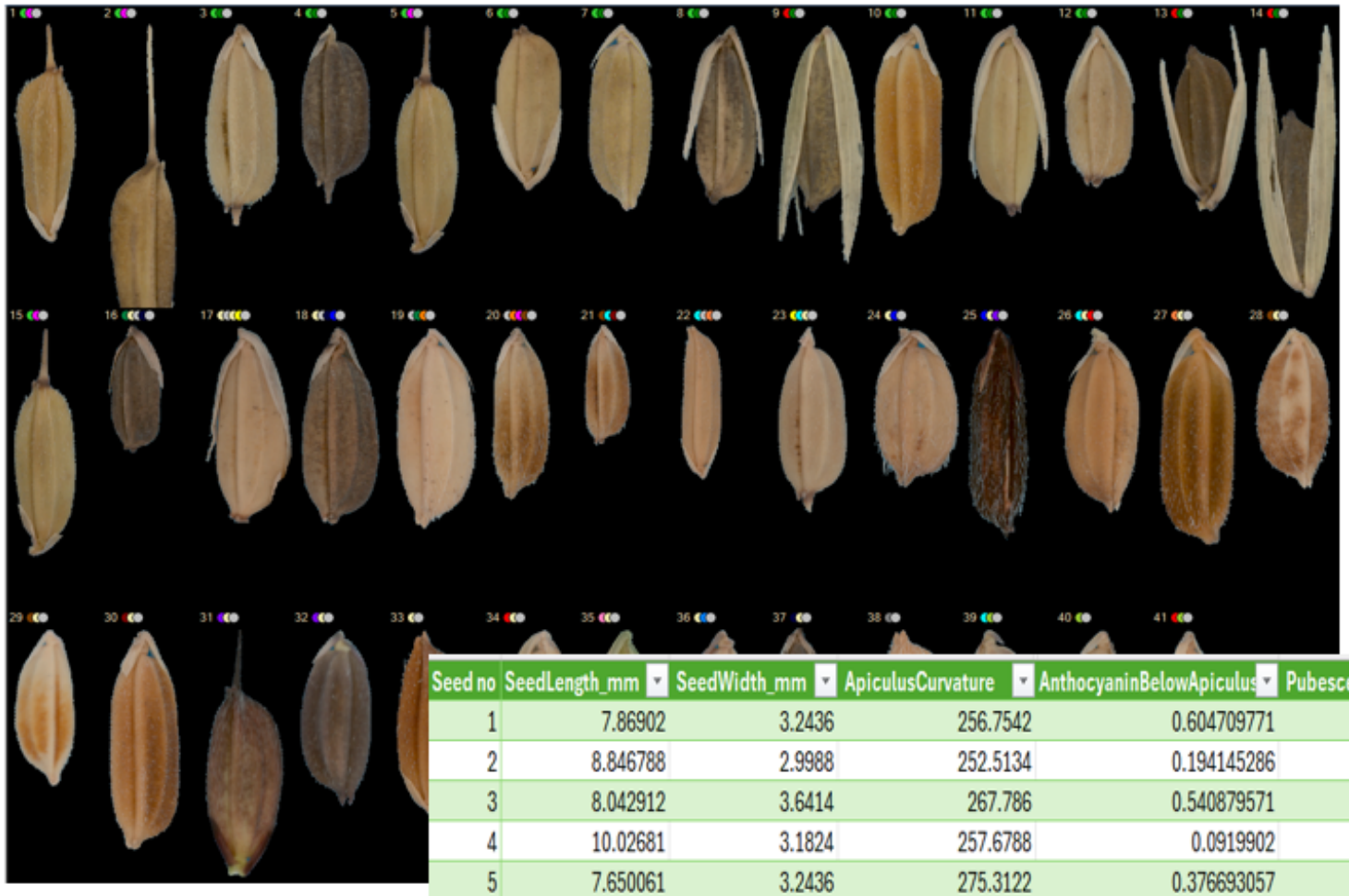


Blob features for rice seed descriptors

A list of blob features has been developed that uses the above described landmark detection as basis for calculation of traits needed for the rice seed descriptors:

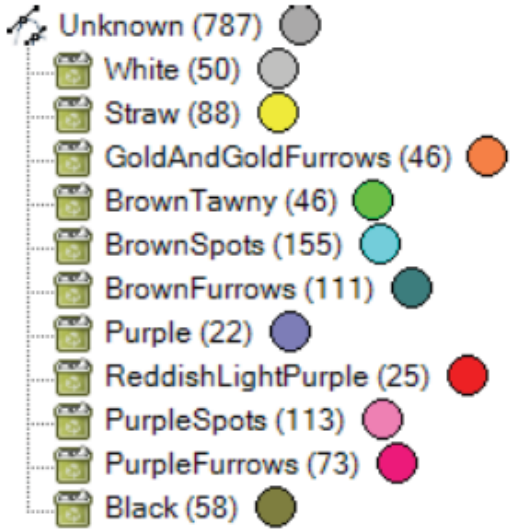
1. Awn color: 7.5.3
2. Lemma and palea pubescence: 7.5.4
3. Lemma and palea color: 7.5.5
4. Anthocyanin coloration of keel: 7.5.6
5. Anthocyanin coloration of area below apiculus: 7.5.7
6. Color of apiculus: 7.5.8
7. Shape of apiculus: 7.5.9
8. Sterile lemma length: 7.5.10
9. Sterile lemma color: 7.5.13
10. Length of grain between sterile lemma base and apiculus tip point: 7.5.15
11. Width of grain at widest point: 7.5.16

Characterization of rice varieties at Africa Rice



Seed no	SeedLength_mm	SeedWidth_mm	ApiculusCurvature	AnthocyaninBelowApiculus	Pubescence_upper	Pubescence_lower	SterilelemmaLength_short	SterilelemmaLength_long
1	7.86902	3.2436	256.7542	0.604709771	0.001543364	0.002240367	0.5126747	0.5502909
2	8.846788	2.9988	252.5134	0.194145286	0.02099977	0.02214106	0.2271242	0.2562114
3	8.042912	3.6414	267.786	0.540879571	0.000326691	0.000145655	0.6091626	0.6537814
4	10.02681	3.1824	257.6788	0.0919902	0.005396492	0.005996102	0.2227827	0.2565887
5	7.650061	3.2436	275.3122	0.376693057	0.003344654	0.002469898	0.5277879	0.9245886
6	8.945725	3.7332	272.1993	0.657752857	0.005981378	0.003946476	1.353852	1.450092
7	8.198299	3.564	251.1614	0.753728571	0.000003456	0.000897586	0.410494	0.5496623
8	8.317047	3.432	256.7621	0.867398	0.000357462	0.000893655	0.5043925	0.5885887
9	9.272255	3.9168	193.1323	0.5101524	0.000602909	0.000866682	0.6467602	0.7030284

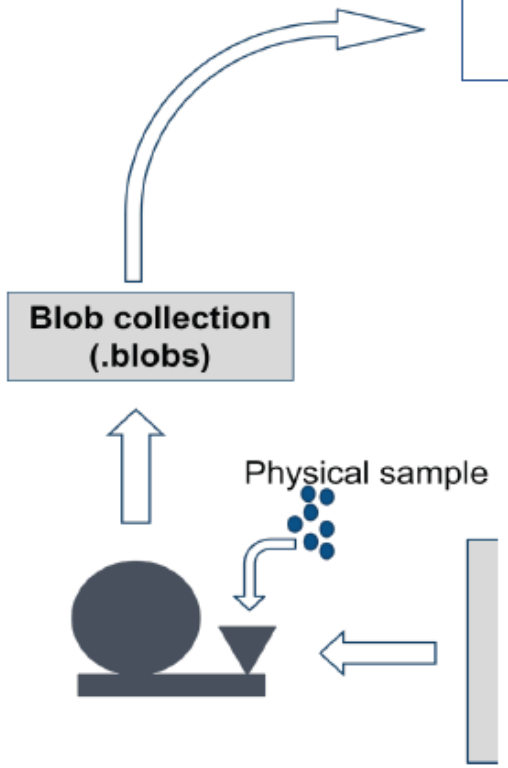
Classification of categorical descriptors – 7.5.4. Lemma color

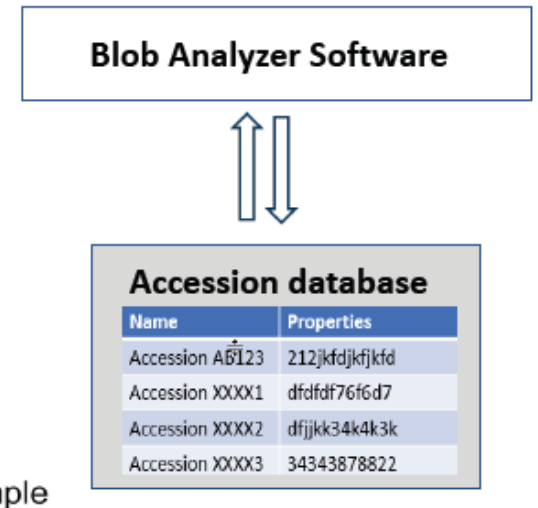


Reference \ Predicted	White	Straw	GoldAndGoldFurrows	BrownTawny	BrownSpots	BrownFurrows	Purple	ReddishLightPurple	PurpleSpots	PurpleFurrows	Black	Referenced	Misclassified
White	100.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	6.2	0.0
Straw	0.0	97.7	0.0	0.0	2.3	0.0	0.0	0.0	0.0	0.0	0.0	11.2	2.3
GoldAndGoldFurrows	0.0	0.0	89.1	2.2	0.0	8.7	0.0	0.0	0.0	0.0	0.0	5.8	10.9
BrownTawny	0.0	2.2	8.7	89.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	5.8	10.9
BrownSpots	0.0	2.6	0.6	1.3	82.5	9.7	0.0	0.0	0.0	0.0	3.2	19.6	17.5
BrownFurrows	0.0	1.8	0.0	2.7	3.6	89.2	0.0	0.0	0.0	2.7	0.0	14.1	10.8
Purple	0.0	0.0	0.0	0.0	0.0	0.0	100.0	0.0	0.0	0.0	0.0	2.7	0.0
ReddishLightPurple	0.0	0.0	0.0	0.0	0.0	0.0	8.0	88.0	0.0	4.0	0.0	3.2	12.0
PurpleSpots	0.9	0.9	0.0	0.0	3.7	0.0	0.0	0.0	89.9	4.6	0.0	13.9	10.1
PurpleFurrows	0.0	0.0	0.0	0.0	6.3	8.8	2.5	0.0	31.3	51.3	0.0	10.2	48.8
Black	0.0	0.0	0.0	0.0	1.7	0.0	0.0	0.0	0.0	0.0	98.3	7.4	1.7
Predicted	6.4	11.9	5.8	6.0	18.2	15.9	3.2	2.8	15.6	6.4	7.9	787	
Misclassified	2.0	8.5	10.9	12.8	11.2	20.8	16.0	0.0	20.3	18.0	8.1		13.3

Future: Comparison of seed accessions

Scan unknown seed sample and compare with accession database





Accession list with similarity score

Accession AB165	0.81
Accession BD765	1.27
Accession GR123	1.53
Accession GR123	1.72
Accession GR123	2.28

Thanks for your attention!

Contact: Karsten Hartelius
Videometer A/S
kah@videometer.com