

Liberté Égalité Fraternité

> Métaprogramme DIGIT-BIO Axe 2 : Phenotypes prediction

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PHEN

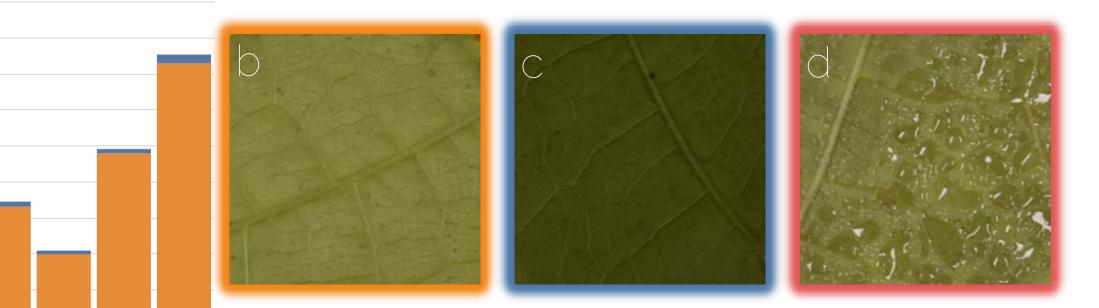
 Introduction/ Context - Downy mildew is a plant disease that affects all cultivated European grapevine varieties. The current strategy to control this threat relies on repeated applications of fungicides. The most eco-friendly and sustainable alternative solution would be to use bred-resistant varieties. Some wild *Vitis* species have been used as resistance sources to introduce resistance *loci* in *Vitis vinifera* varieties. The development of a high-throughput machine learning phenotyping method is now essential for identifying new resistance *loci*.

## Methods OIV 452-1, a Standard Scale





INRAZ lipme

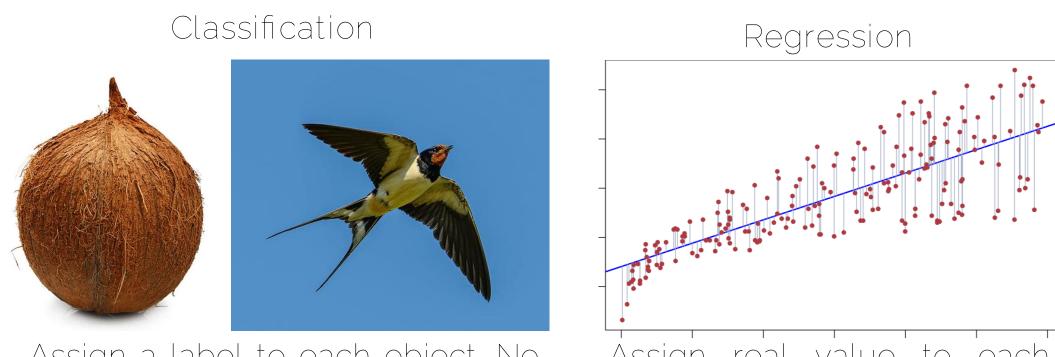


The dataset contains 3449 images distributed along the 5 values of the OIV 452-1 scale (a). The images are square patches extracted from the center of the leaf discs (b,c,d). The dataset contains well exposed images (b), under exposed images (c) and, images containing water droplets produced by condensation (d). These 3 types of images correspond to the ones more commonly generated during the experiments.

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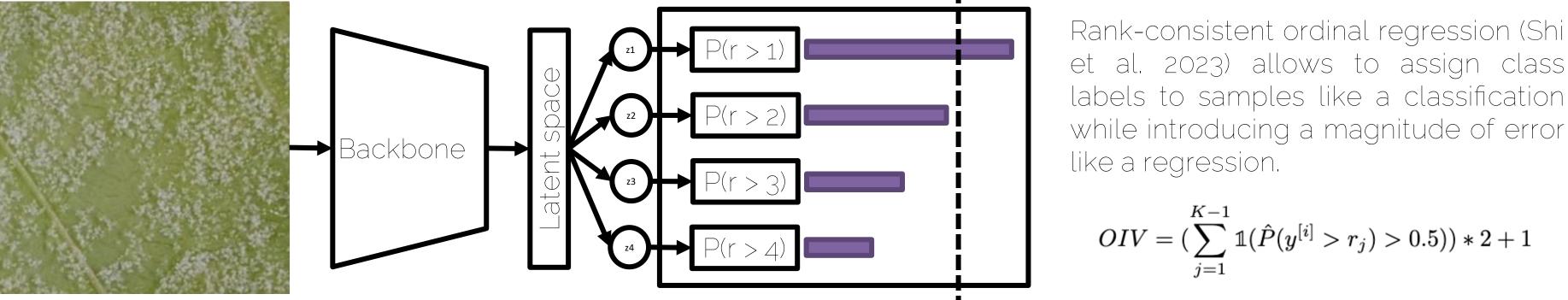
#### Neither Classification Nor Regression

plant's necrosis, also known as hypersensitve response.

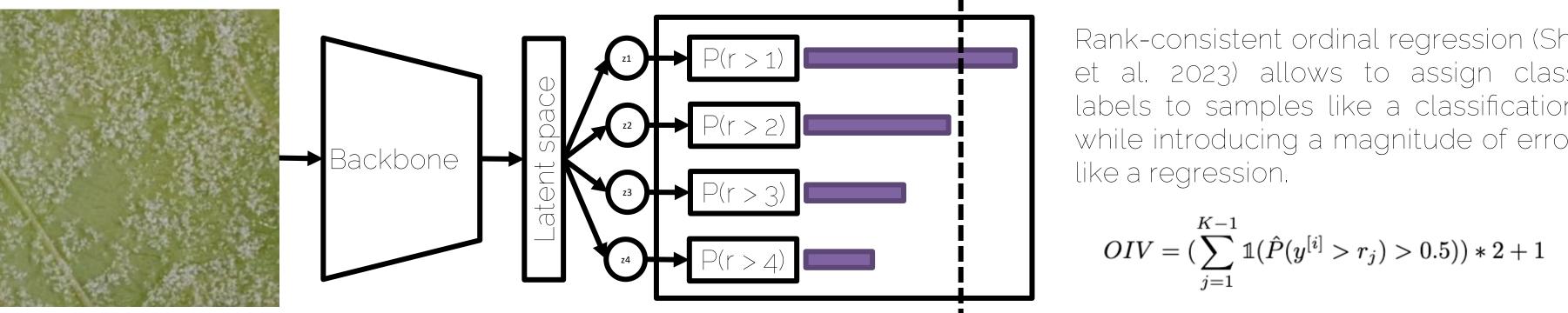


## Something completely different

Rank-Consistent Ordinal Regression (CORN)



1 3 5 7 9



Rank-consistent ordinal regression (Shi et al. 2023) allows to assign class labels to samples like a classification

Assign a label to each object. No ordinal relationship between classess. All errors are equal

Assign real value to each object. Ordinal relationship between objects.

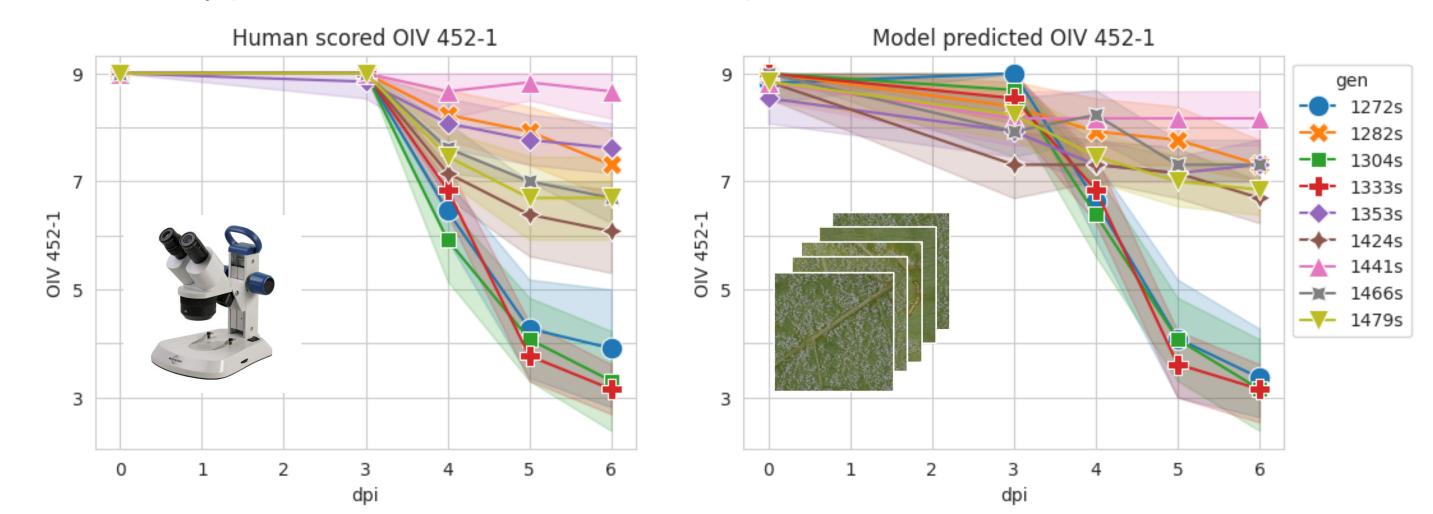
# Results

Metrics

							F1-score		
	1	109	4	$\bigcirc$	$\bigcirc$	$\bigcirc$	0,9277		
дþ	3	13	68	12	$\bigcirc$	$\bigcirc$	0,7556		
ctual labe	5	$\bigcirc$	15	63	5	$\bigcirc$	0.7545		
	7	$\bigcirc$	$\bigcirc$	9	76	19	0,78136		
$ \forall ($	9	$\bigcirc$	$\bigcirc$	$\bigcirc$	28	96	0.8033		
		1	3	5	7	9			
Predicted label									

The model obtained an MSE of 0.203 on the test dataset. Thanks to the ordinal regression there are no errors over 1 class value.

#### Genotype differentiation experiment



We performed an experiment with new material to assess the model's performance when differentiating 9 genotypes resistance level to the pathogen. We compared human observations on a stereo-microscope to the model's predictions on low resolution images.

en 1	gen 2	meandiff_pred	p-adj_pred	lower_pred	upper_pred	reject_pred	meandiff_obs	p-adj_obs	lower_obs	upper_obs	reject_obs
	12825	3.9441	0.000000	2.6017	5.2864	True	3.3986	0.000000	1.6792	5.118	True
	13046	-0.2098	0.999900	-1.5522	1.1326	False	-0.6014	0.971844	-2.3208	1.118	False
	13336	-0.2098	0.999900	-1.5522	1.1326	False	-0.7552	0.898723	-2.4746	0.9641	False
	1353s	3.9441	0.000000	2.6017	5.2864	True	3.7063	0.000000	1.9869	5.4257	
	14 <u>2</u> 4s	3.3287	0.000000	1.9863	4.671	True	2.1678	0.003724	0.4484	3.8872	
	14415	4.803	0.000000	3.4353	6.1708	True	4.7576	0.000000	3.0057	6.5095	
	14.66s	3.9441	0.000000	2.6017	5.2864	True	2.7832	0.000046	1.0638	4.5026	
	1479s	3.4825	0.000000	2.1401	4.8249	True	2.7832	0.000046	1.0638	4.5026	
	1304s	-4.1538	0.000000	-5.4391	-2.8686	True	-4.0	0.000000	-5.6462	-2.3538	
	1333s	-4.1538	0.000000	-5.4391	-2.8686	True	-4.1538	0.000000	-5.8	-2.5077	True
	1353a	0.0	1.000000	-1.2852	1.2852	False	0.3077	0.999616	-1.3385	1.9539	False
	1424s	-0.6154	0.845319	-1.9006	0.6698	False	-1.2308	0.312469	-2.877	0.4154	False
	1441s	0.859	0.496366	-0.4528	2.1707	False	1.359	0.215563	-0.3212	3.0391	False
	1466s	0.0	1.000000	-1.2852	1.2852	False	-0.6154	0.958195	-2.2616	1.0308	False
	1479s	-0.4615	0.967009	-1.7468	0.8237	False	-0.6154	0.958195	-2.2616	1.0308	False
	1333s	0.0	1.000000	-1.2852	1.2852	False	-0.1538	0.999998	-1.8	1.4923	False
	1353s	4.1538	0.000000	2.8686	5.4391	True	4.3077	0.000000	2.6615	5.9539	
	1424s	3.5385	0.000000	2.2532	4.8237	True	2.7692	0.000020	1.123	4.4154	
	1441s	5.0128	0.000000	3.7011	6.3246	True	5.359	0.000000	3.6788	7.0391	
	1466s	4.1538	0.000000	2.8686	5.4391	True	3.3846	0.000000	1.7384	5.0308	
	1479s	3.6923	0.000000	2.4071	4.9775	True	3.3846	0.000000	1.7384	5.0308	
	1353s	4.1538	0.000000	2.8686	5.4391	True	4.4615	0.000000	2.8154	6.1077	
	1424s	3.5385	0.000000	2.2532	4.8237	True	2.9231	0.000005	1.2769	4.5693	
	1441s	5.0128	0.000000	3.7011	6.3246	True	5.5128	0.000000	3.8327	7.193	
	1466s	4.1538	0.000000	2.8686	5.4391	True	3.5385	0.000000	1.8923	5.1846	
	1479s	3.6923	0.000000	2.4071	4.9775	True	3.5385	0.000000	1.8923	5.1846	
	1424s	-0.6154	0.845319	-1.9006	0.6698	False	-1.5385	0.086498	-3.1846	0.1077	False
	1441s	0.859	0.496366	-0.4528	2.1707	False	1.0513	0.559274	-0.6288	2.7314	False
	1466s	0.0	1.000000	-1.2852	1.2852	False	-0.9231	0.697549	-2.5693	0.7231	False
	1479s	-0.4615	0.967009	-1.7468	0.8237	False	-0.9231	0.697549	-2.5693	0.7231	False
	1441s	1.4744	0.015696	0.1626	2.7861	True	2.5897	0.000128	0.9096	4.2699	Tru
	1466s	0.6154	0.845319	-0.6698	1.9006	False	0.6154	0.958195	-1.0308	2.2616	False
	14795	0.1538	0.999987	-1.1314	1.4391	False	0.6154	0.958195	-1.0308	2.2616	False
	1466s	-0.859	0.496366	-2.1707	0.4528	False	-1.9744	0.009337	-3.6545	-0.2942	
	1479s	-1.3205	0.047151	-2.6322	-0.0088	True	-1.9744	0.009337	-3.6545	-0.2942	True
	1479s	-0.4615	0.967009	-1.7468	0.8237	False	0.0	1.000000	-1.6462	1.6462	False

When comparing model and human assessment wirth Tukey HSD tests there is a 97% accuracy.

Perspectives:

Conclusion

•Improve image quality and resolution. •Extend method to other leaf disc pathosystem with discrete scales.

•Use this method with multiple simultaneous pathogens.

### Expected impact: •Speedup leaf disc annotations by 650 times. •Replace human annotation thus removing human bias. •Facilitate transition to high throughput phenotyping.

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