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Melhoramento de Precisão: Automação no campo

**Métricas ambientípicas e suporte
na caracterização ambiental para
alocação de cultivares**

Questões a serem discutidas

“Sem por quê não tem pra quê”
– ouvi em algum lugar ou inventei

1. O que é ambiente?
2. Quais “níveis de ambiente” podemos definir?
3. Como podemos caracterizar um ambiente?
4. O que é ”interação genótipo x ambiente” (GxA)?
5. O que é norma de reação?
6. O que é plasticidade fenotípica?
7. Por quê existe GxA?
8. Qual são os desafios da GxA para o melhoramento de plantas?
9. Como o estudo do ambiente pode auxiliar o melhoramento de plantas?
10. Caracterizacao Ambiental “de alto desempenho”: o que é e pra quê serve?
11. Diferenças entre envirotyping, enviromics e caracterização ambiental?
12. O que é “tipagem de ambientes” (envirotyping) ?
13. O que são tipologias/tipos ambientais (envirotypes)?
14. Como posso criar uma estrutura de relacionamento ambiental? E pra quê fazer isso?
15. O que é preciso para criar uma plataforma de envirotyping?
16. Como conectar envirotyping com data science (ciencia de dados)?

Discorra em casa: Como o envirotyping pode auxiliar no seu campo de estudo / empresa ?

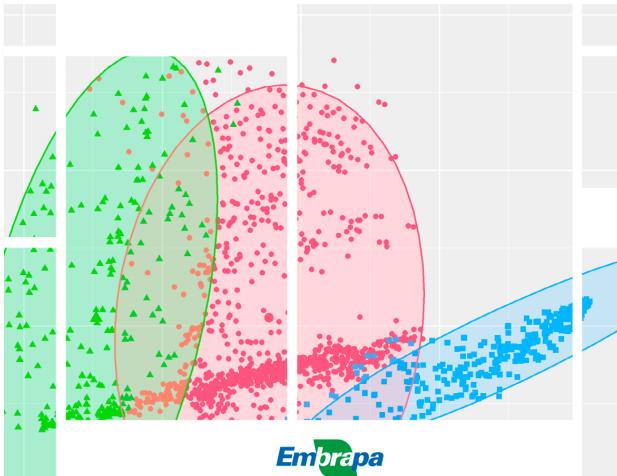
p.ex: gen.quantitativa, gen.populações, gen.molecular, biotecnologia, diversidade genética, evoluçao etc

O que eu preciso saber para trabalhar com Enviotyping?

- Programação em R/Python é útil (mas não só pra isso!)
- Noções de GIS/SIG (sistemas de informação geográfica) podem facilitar sua vida
- Agrometeorologia / ecofisiologia te ajudará a explicar o que está fazendo
- Compreender de genética quantitativa te ajudará a “encontrar os motivos” de usar enviotyping
- Estatística Experimental
- LER e PRATICAR conceitos interdisciplinares (e.g., fitopatologia, solos etc)

Uso de Informações Ambientais na Modelagem e
Interpretação da Interação Genótipo x Ambiente

Revisão Bibliográfica



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ARTICLE

Enviromics: bridging different sources of data, building one framework

Germano Costa-Neto^{1,2} and Roberto Fritsche-Neto^{2,3*}

Crop Breeding and Applied Biotechnology
21(S): e393521S12, 2021
Brazilian Society of Plant Breeding.
Printed in Brazil
<http://dx.doi.org/10.1590/1984-70332021v21Sa25>

Abstract: Enviromics is the field of applied data science that integrates databases of environmental factors into biostatistics and quantitative genet-



G3, 2021, 11(4), jkab040
DOI: [10.1093/g3journal/jkab040](https://doi.org/10.1093/g3journal/jkab040)
Advance Access Publication Date: 6 February 2021
Software and Data Resources

EnvRtype: a software to interplay enviromics and quantitative genomics in agriculture

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OPINION article

Front. Plant Sci., 16 April 2021 | <https://doi.org/10.3389/fpls.2021.651480>

The Modern Plant Breeding Triangle: Optimizing the Use of Genomics, Phenomics, and Enviromics Data

Jose Crossa^{1,2}, Roberto Fritsche-Neto³, Osval A. Montesinos-Lopez⁴, Germano Costa-Neto³, Susanne Dreisigacker⁵, Abelardo Montesinos-Lopez⁵ and Alison R. Bentley^{*}

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⁴Facultad de Telemática, Universidad de Colima, Colima, Mexico

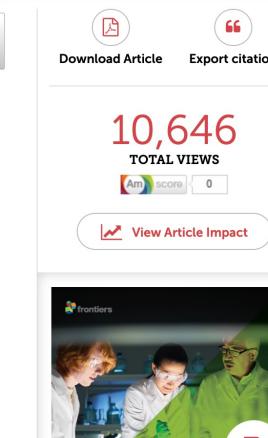
⁵Departamento de Matemáticas, Centro Universitario de Ciencias Exactas e Ingenierías (CUCEI), Universidad de Guadalajara, Guadalajara, Mexico



Xinyou Yin · Paul C. Struik *Editors*

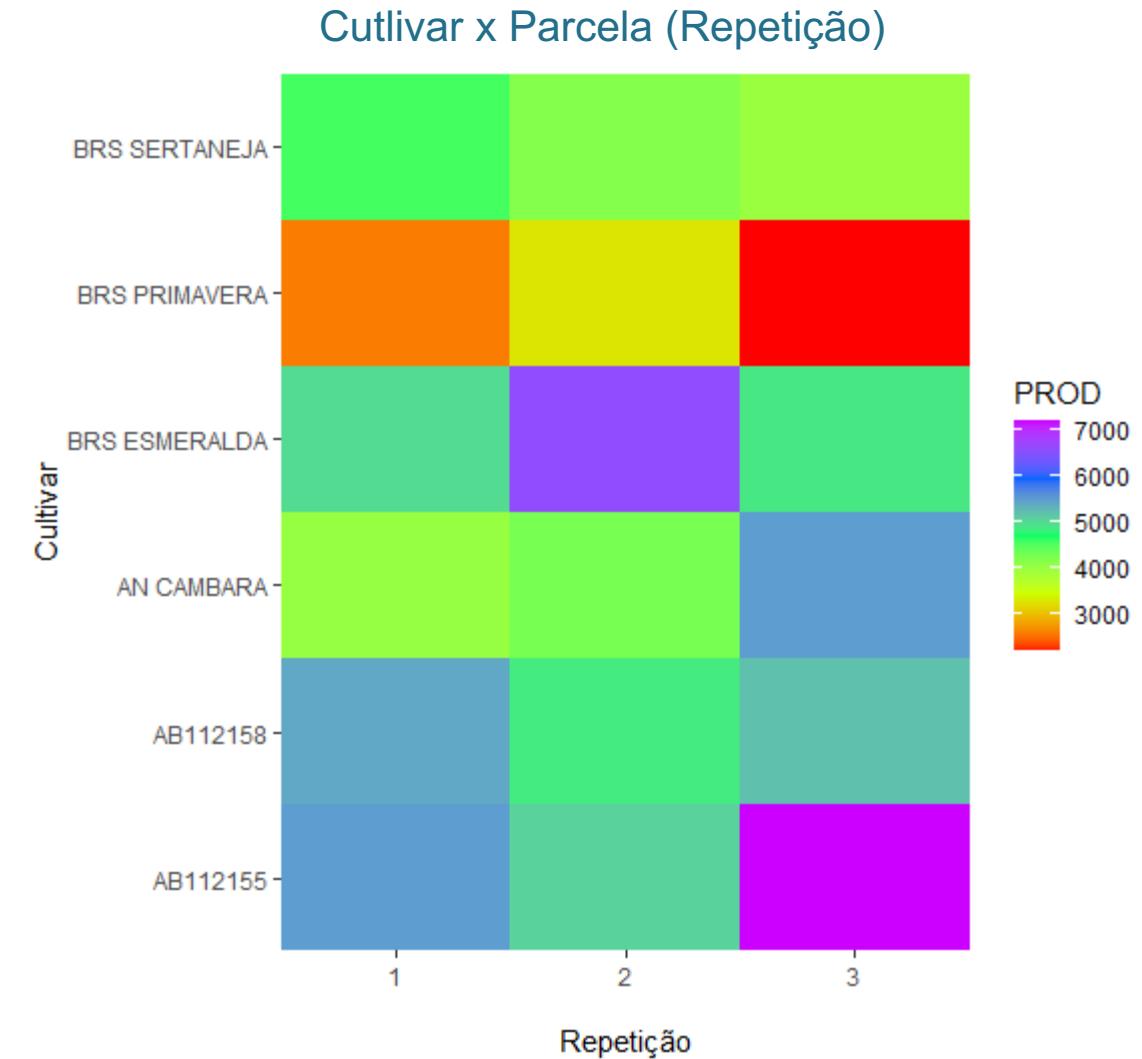
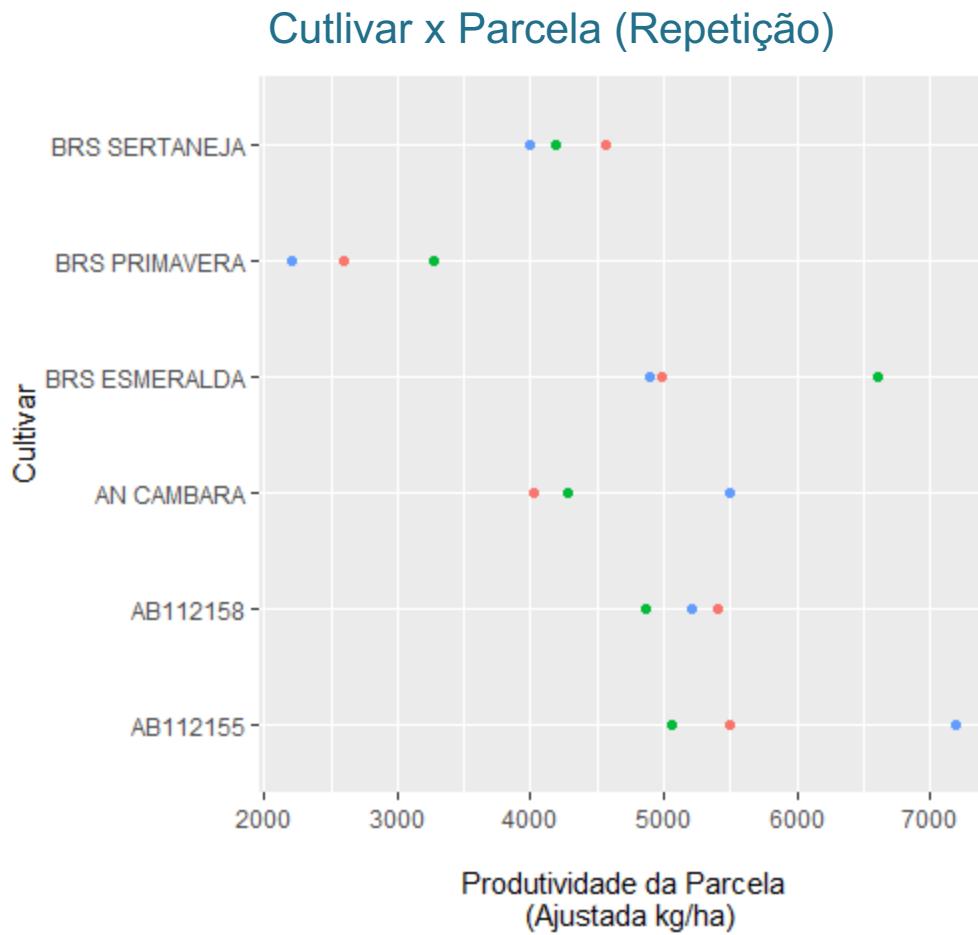
Crop Systems Biology

Narrowing the Gaps between Crop Modelling and Genetics



Decomposição da Variação Fenotípica

Dentro de um mesmo “ambiente”

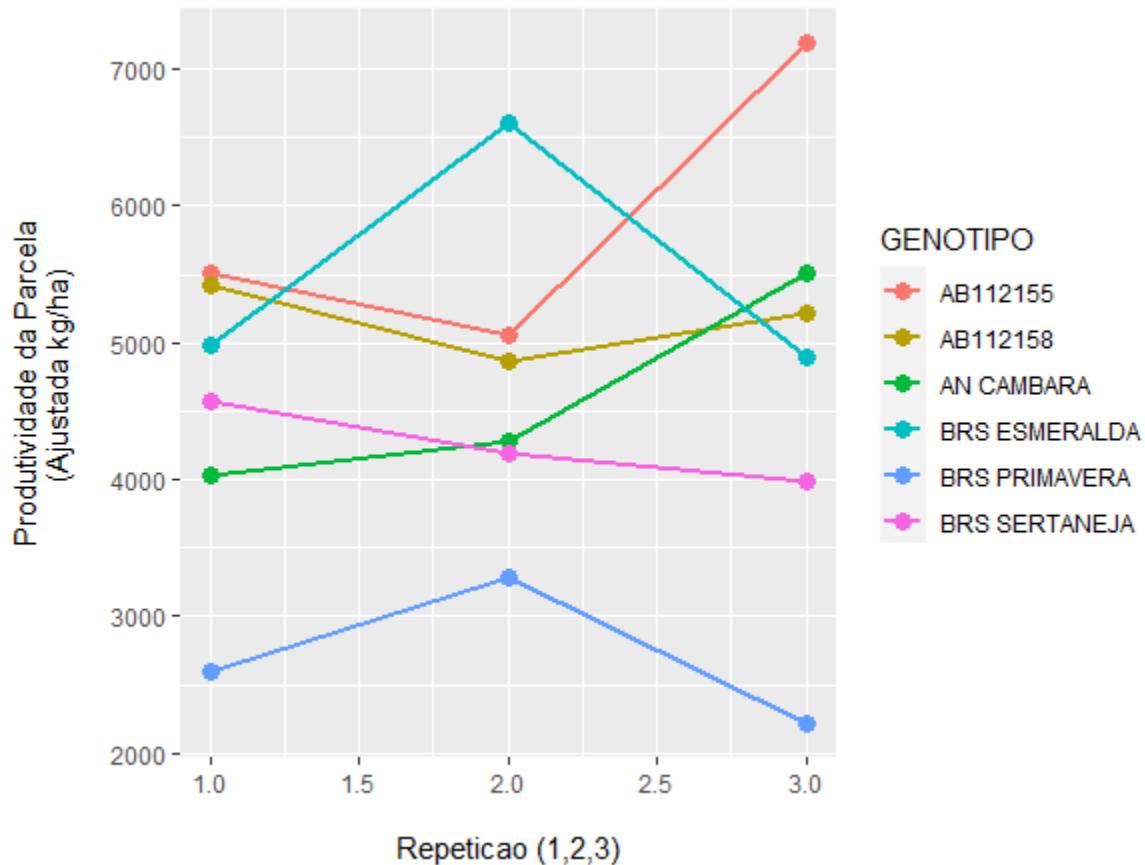


Decomposição da Variação Fenotípica

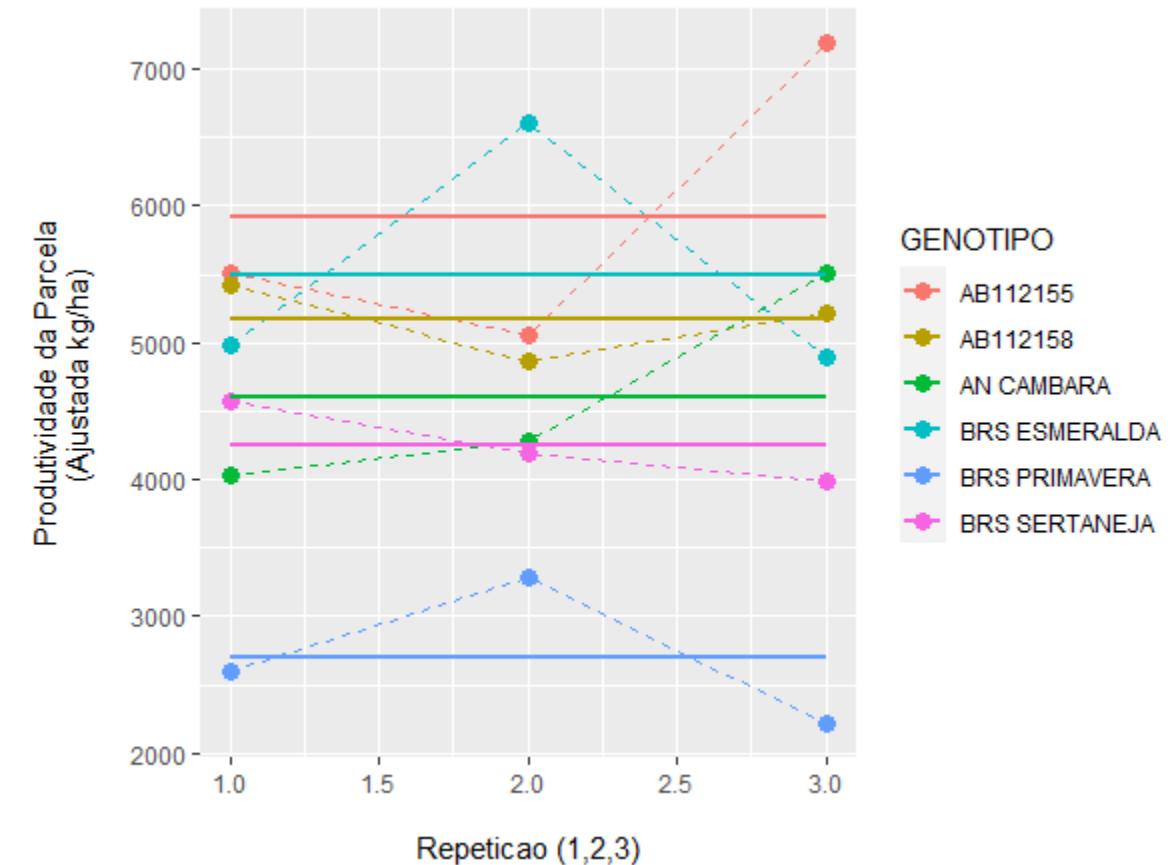
Separar “Padrão” de “Ruído”

Dentro de um mesmo “ambiente”

Dados brutos (raw data):
interação (mas há covariância?) Cutlivar x Parcela



Dados ajustados (adjusted means):
Média do Genótipo + Desvios para cada Parcela



Próximo passo?
Testar hipóteses, p.ex: (H_0 : não há diferença entre genótipos)

Decomposição da Variação Fenotípica

Ensaios individuais (único experimento de campo)

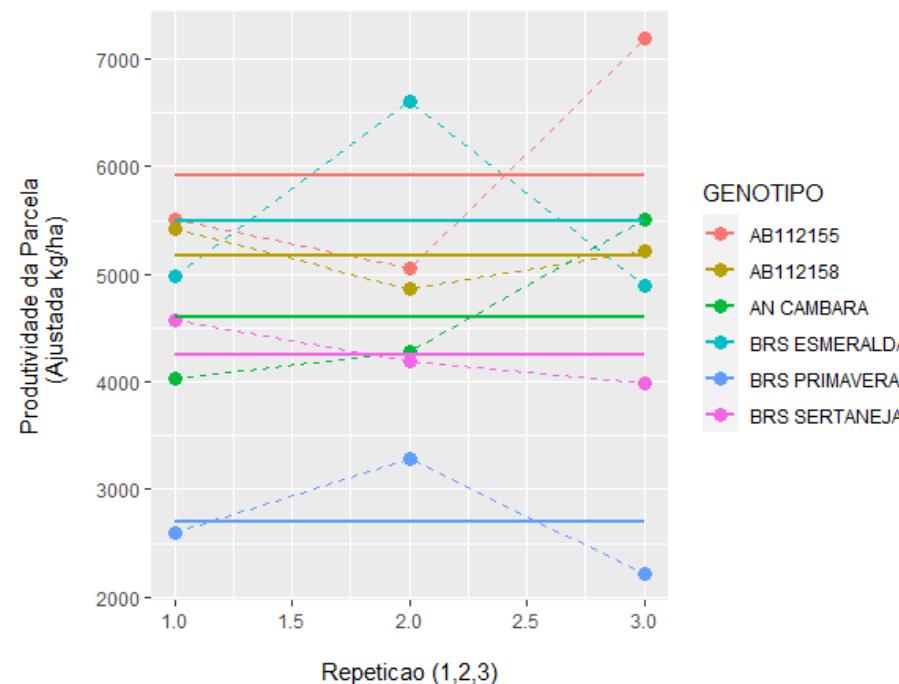
$\text{Var}(Y) = \text{Var}(G) + \text{Cov}(G,E) + \text{Var}(R)$ sendo G = fatores “genéticos” e R = resíduos experimentais

Boa qualidade experimental (condução dos ensaios e ajuste do fenótipo) resulta em $\text{Cov}(G,E) = 0$ e $\text{Var}(R) \rightarrow 0$

Conclusão: $\text{Var}(Y) \approx \text{Var}(G)$, sendo $\text{Cov}(G,E) = 0$ a interação genótipo-parcela experimental

Dados ajustados (adjusted means):

Média do Genótipo + Desvios para cada Parcada



Questão: Essas médias ajustadas são as médias “reais” de cada genótipo?

São amostras aleatórias das possíveis médias que o genótipo pode atingir dada as condições ambientais ocorrentes em seu crescimento

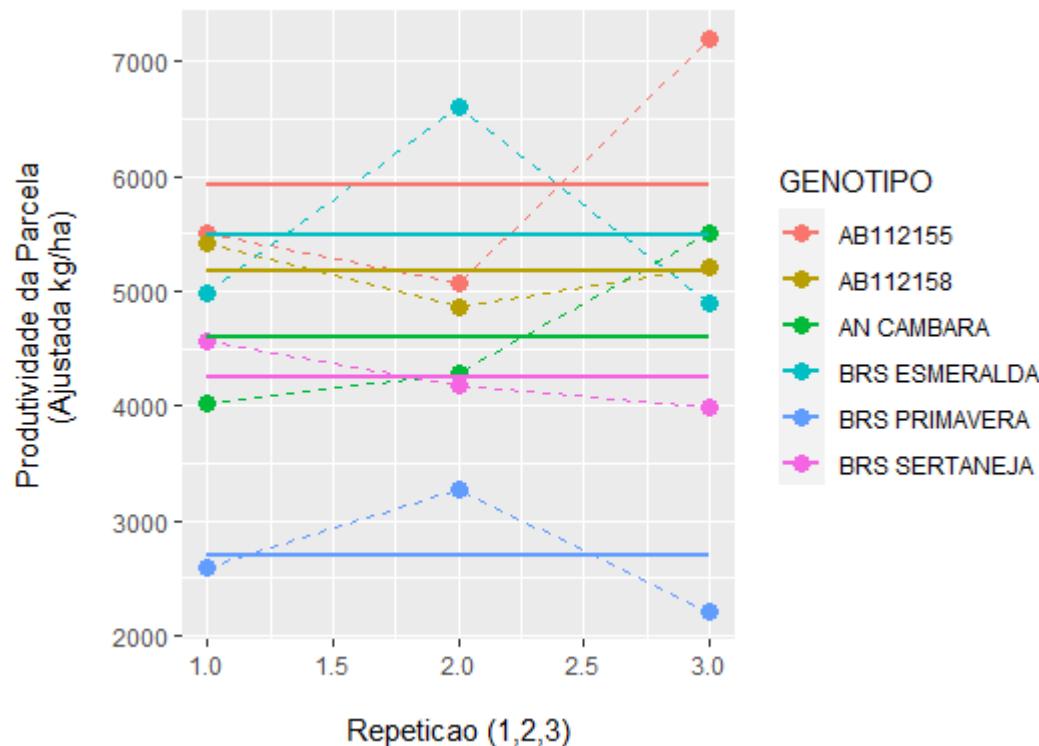
Resultado muito específico do conjunto de múltiplas interações genes x ambiente, além da estabilidade dos transcritos, proteínas e metabólitos presentes durante o ciclo de desenvolvimento da planta

Decomposição da Variação Fenotípica

- Se o genótipo é avaliado em mais de um ambiente, há variação ambiental? (**macro ambiental**)

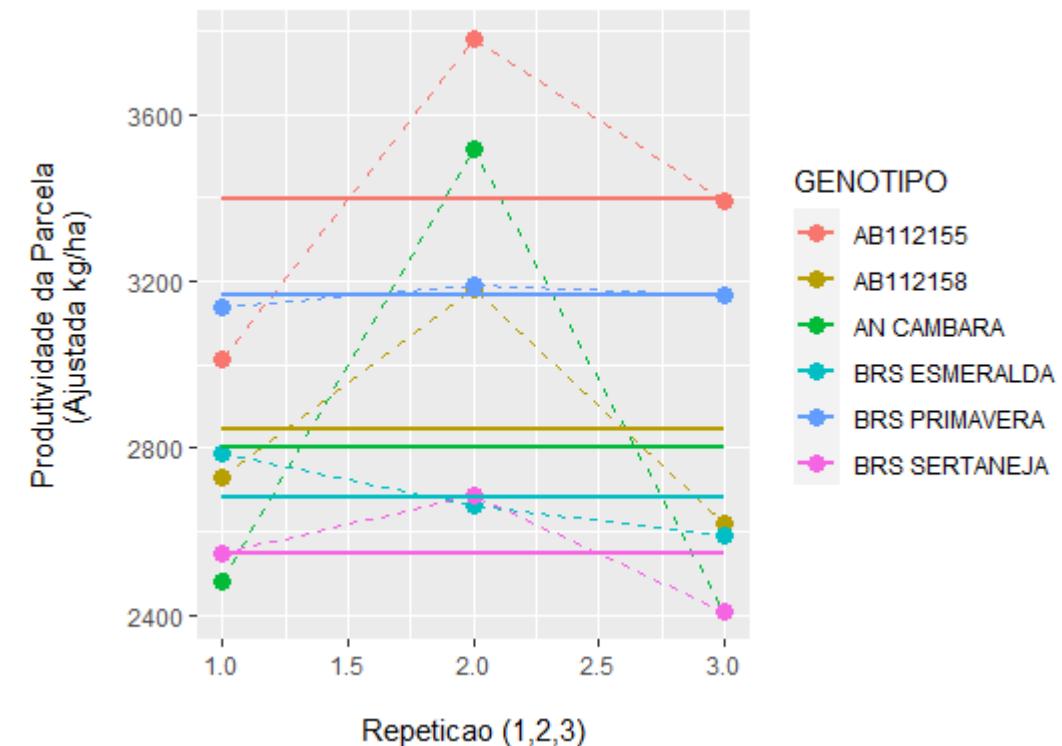
Dados ajustados (adjusted means) para **Experimento 1**

Média do Genótipo + Desvios para cada Parcela



Dados ajustados (adjusted means) para **Experimento 2**

Média do Genótipo + Desvios para cada Parcela

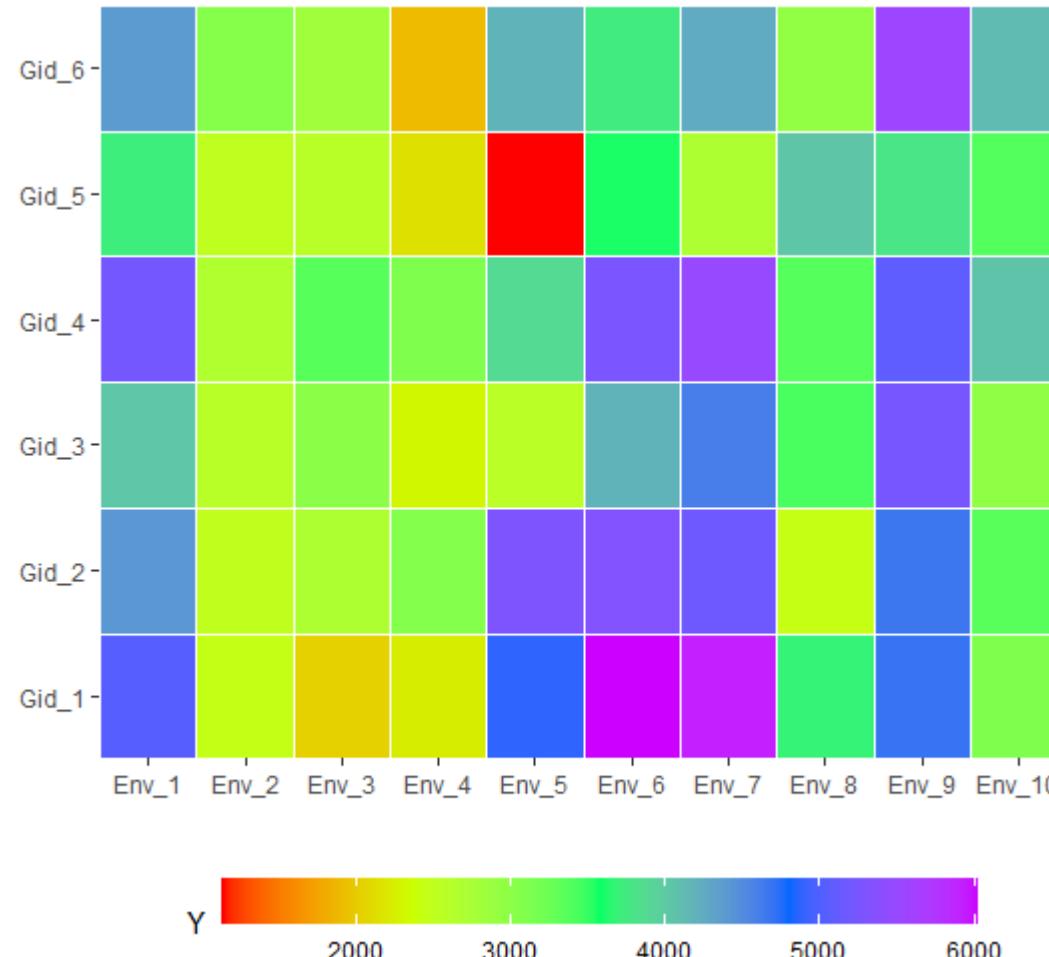


- Mudança no ranking dos genótipos (embora o melhor continua sendo o mesmo!)
- Mudança na qualidade experimental (e nível de rendimento, vide eixo y)

Questão: Dá para confiar na repetição 2?
Sugestão: Ver [Revisões sobre análise espacial](#)

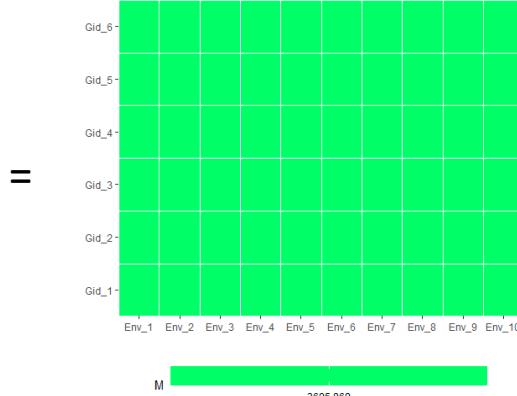
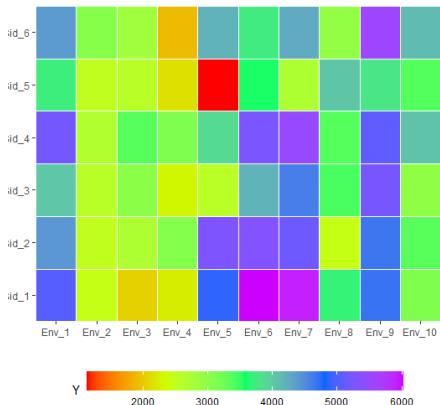
Two-way table (genótipos por ambientes)

$$\mathbf{Y}_{pq} = \begin{bmatrix} \hat{Y}_{11} & \cdots & \hat{Y}_{1q} \\ \vdots & \ddots & \vdots \\ \hat{Y}_{p1} & \cdots & \hat{Y}_{pq} \end{bmatrix} = (\mathbf{1}_{pq} \otimes \boldsymbol{\mu}) + (\mathbf{1}_p \otimes \mathbf{E}'_q) + (\mathbf{1}'_q \otimes \mathbf{G}_p) + \mathbf{G}\mathbf{E}_{pq}$$

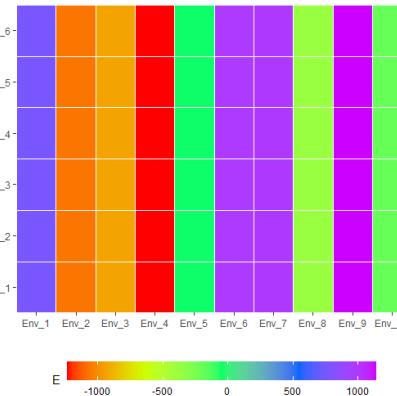


Two-way table (genótipos por ambientes)

$$Y_{pq} = \begin{bmatrix} \hat{Y}_{11} & \dots & \hat{Y}_{1q} \\ \vdots & \ddots & \vdots \\ \hat{Y}_{p1} & \dots & \hat{Y}_{pq} \end{bmatrix} = (\mathbf{1}_{pq} \otimes \boldsymbol{\mu}) + (\mathbf{1}_p \otimes E'_q) + (\mathbf{1}'_q \otimes G_p) + GE_{pq}$$

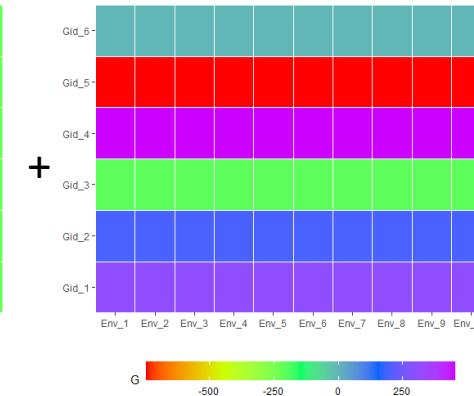


+



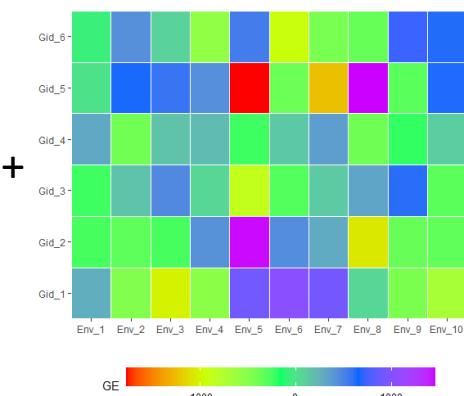
E

Efeito “ambiental”
(macro-Ambiental)



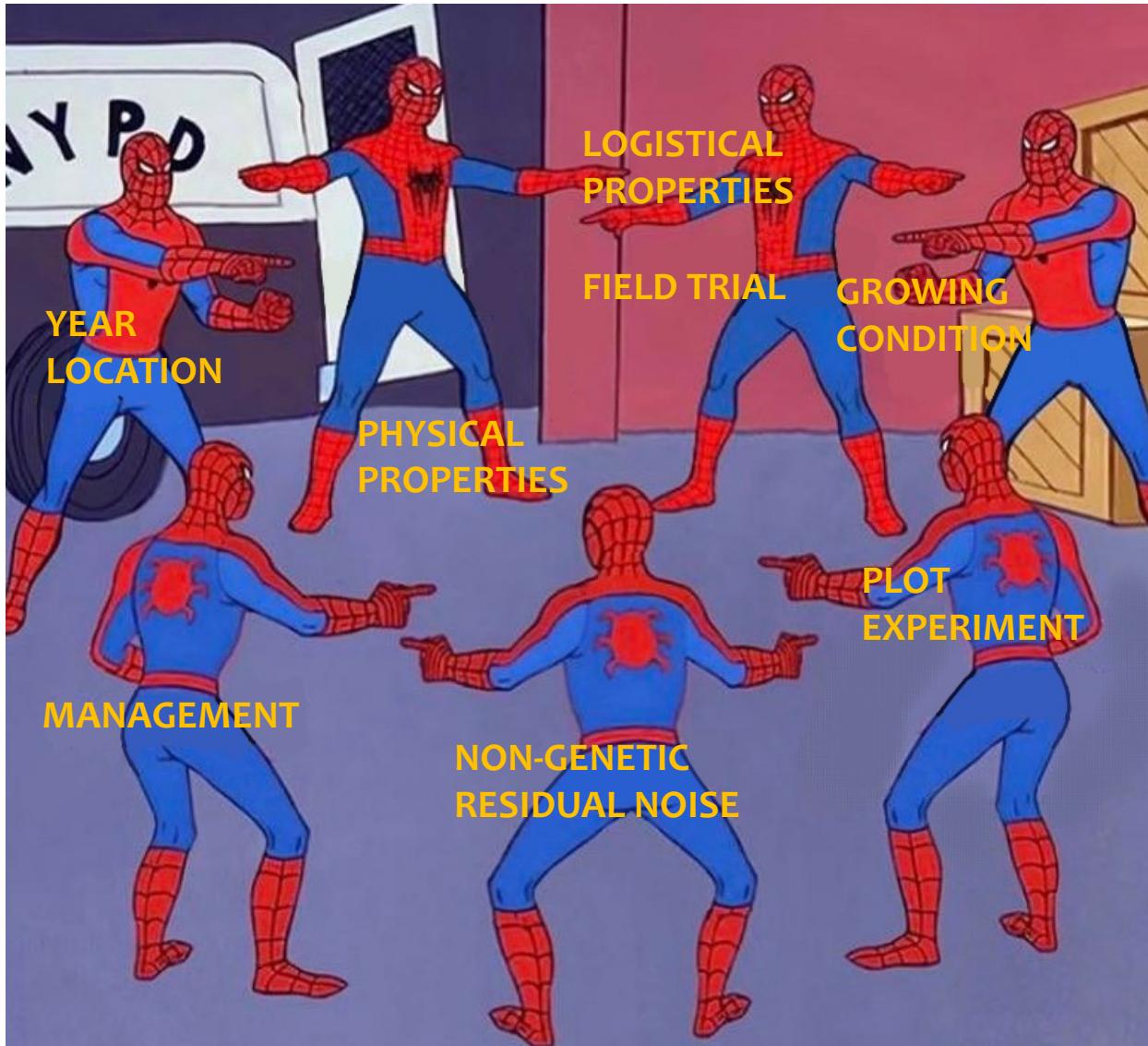
G

Efeito “Ambiental”

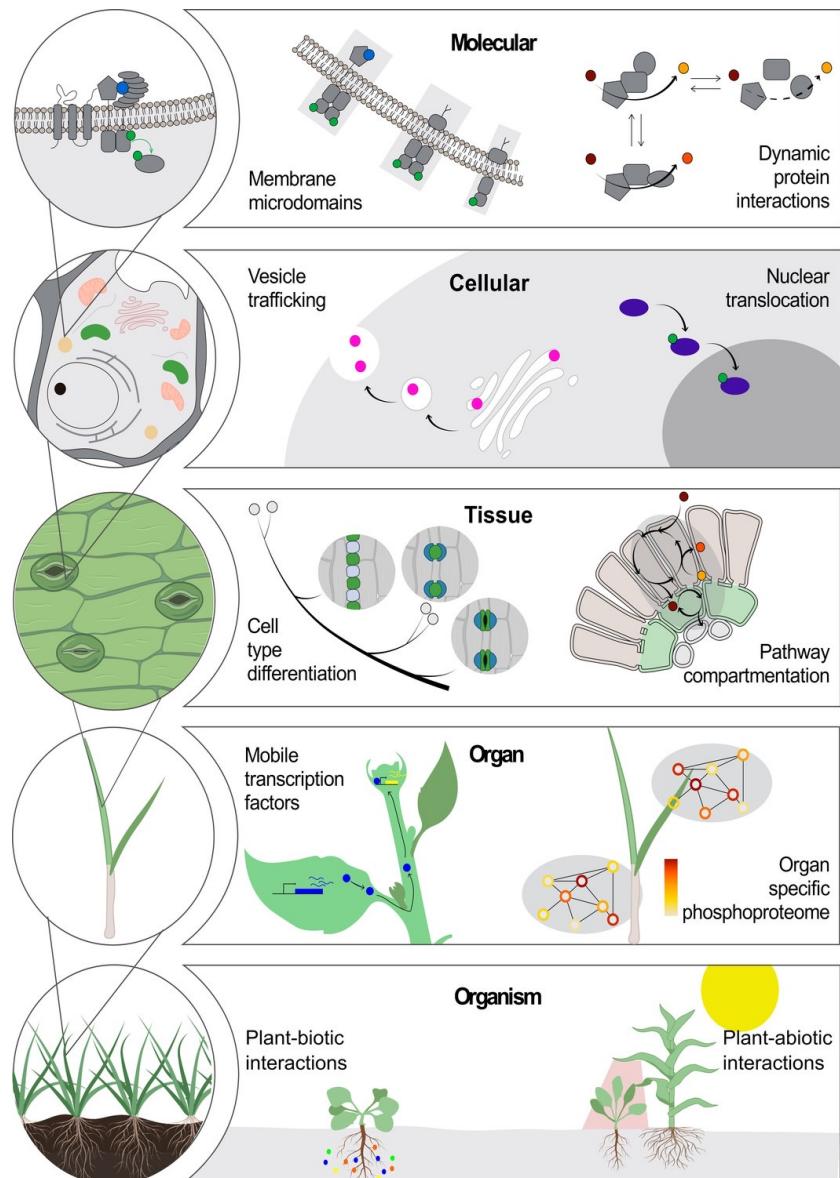


GE

What is “Environment”?



What is “Environment”?



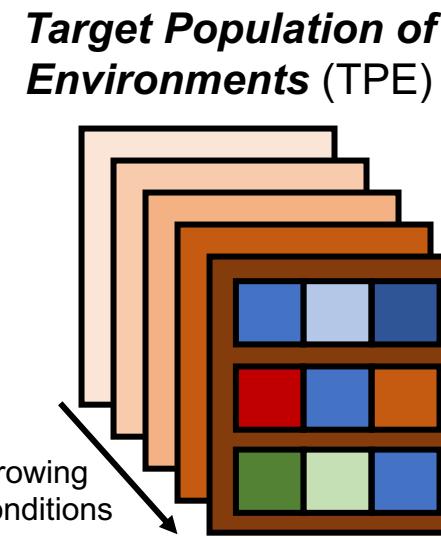
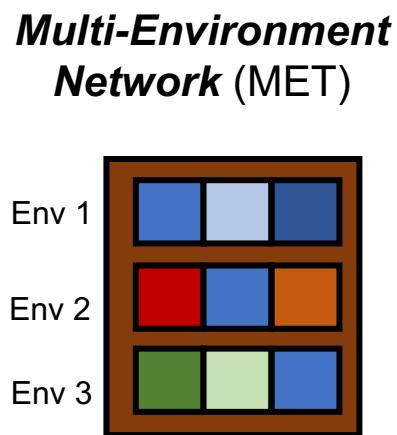
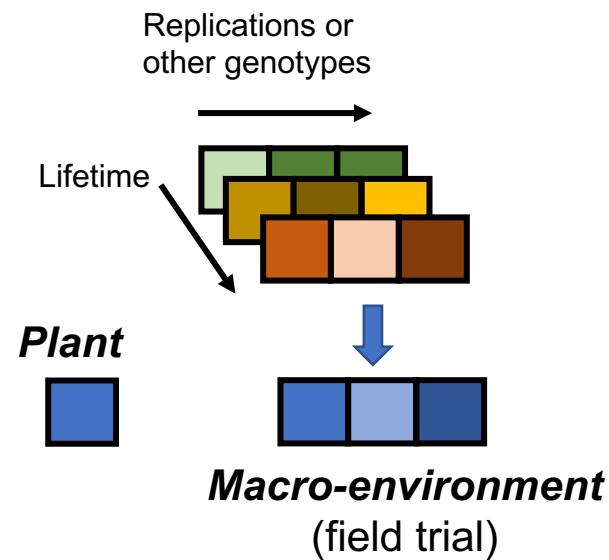
(Surrounded Plant's Growing) Environment

- **Pool of (a)biotic events** driving physical and biological process and its plant-pathogen / soil-plant-atmosphere dynamics
- Balance of **input availability (amount and frequency)** and their resource absorption/allocation demanded by plants
- **Ecophysiology moment** (time window of the crop lifetime)
- **Time-scale** (daily, phenology, planting-date)
- **Physical-scale** (see figure and next slide)

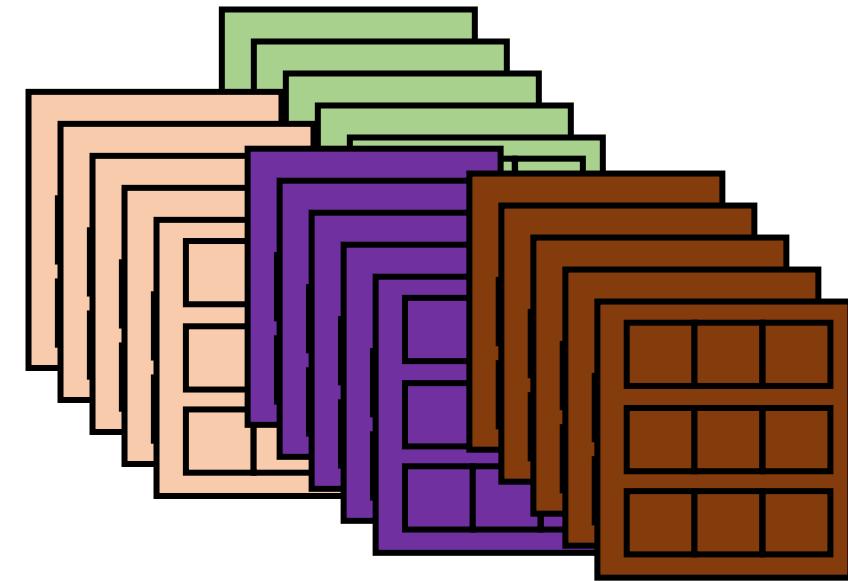
Dimensions: From Environment to Envirome in Plants

Teixeira et al., 2011; Cooper et al., 2014; Xu, 2016; Resende et al. 2021; Costa-Neto et al. 2017;2020,2021,2022

Experimental Statistical Analysis Standpoint (breeding)

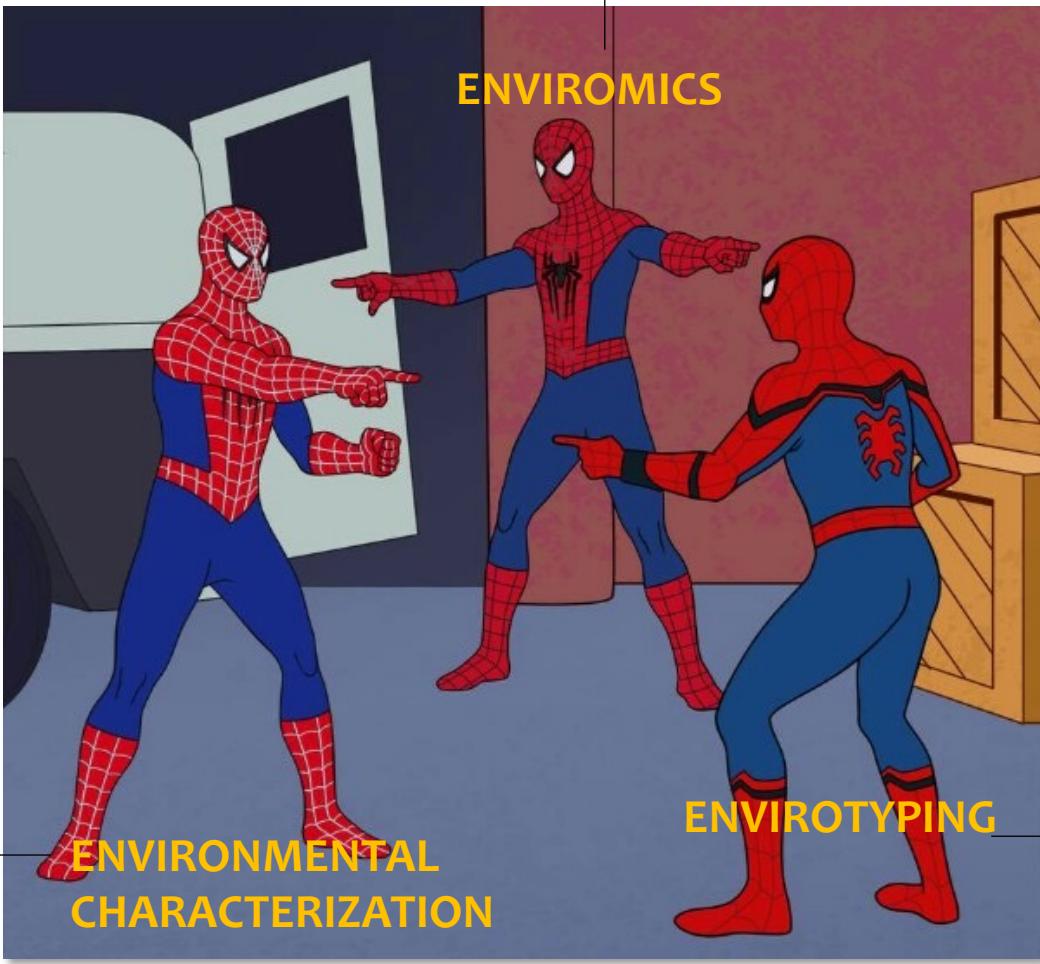


Envirome
(pool of TPEs and natural environments)



Environmental Diversity

Conceptual Multiverse



Ambiente como
tratamento ou
caracterizado por
meio do fenótipo-alvo

Back in the 60s

Within trials: back in early 20th century
Prior characterization: Backs to Sir. Ronald Fisher!
Post characterization: using end-trait or additional information (1960-90s)

Recent years

Humans (psychiatry, 1995)

Cell Enviromics

Teixeira et al (2011)

Plants

Terminology adapted by Resende et al (2020)

Discussed by

Crossa et al (2021), Costa-Neto (2021a,b)

Cooper & Messina (2021)

Costa-Neto & Fritsche-Neto (2021)

Back in the 90s-2000s

Terminology by Cooper et al 2014; Xu, 2016

tipagem de ambientes por meio
da coleta e processamento e
dados ambientais

O Quadro completo
em diferentes níveis
espaciais, temporais
e biológicos

Then, what is envirotyping? enviromics? envirome?

- **Envirotyping** (environmental + typing) gathers the steps of collecting, processing and analyzing environmental data, which can involve the association with phenotypic data, in order to understand the typology of environments for some experimental network, set of growing conditions or target population of environments (TPE) of some breeding program.
- **Enviromics** is the “high throughput” envirotyping, based on the large-scale collections of environmental data across time and space, in order to establish a global association between a certain *envirome* (the core of TPEs for a certain genotype or specie) and the possible phenotypic, genomic or other “omic” variation driving GxE.

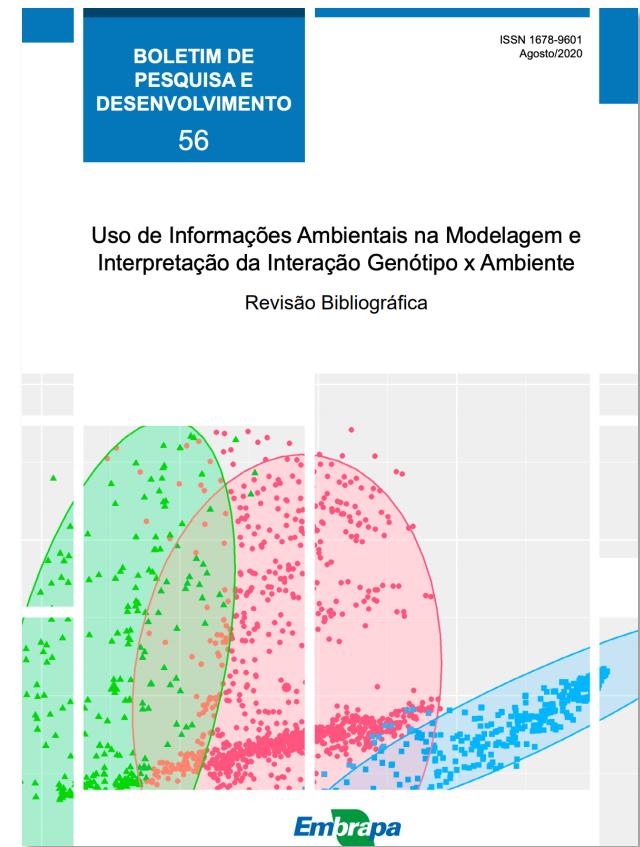
Why is envirOMICS? adapted from Teixeira et al. (2011) for “cell enviromics”; Resende et al 2021

- **Because it can bridge different omics!**

A história esquecida (ou ignorada)

“...an index independent of the experimental varieties and obtained from environmental factors would be desirable. Unfortunately, our present knowledge of the relationship between these factors and yield does not permit the computation of such an index. Until we can measure such factors to formulate a mathematical relation with yield, the average yield of the varieties in a particular environment must suffice” (Eberhart and Russell, 1966, p.37). (7,689 cite)

Fisher em 1923: sugere modelar as relações entre chuva e a variação do rendimento de trigo



Costa-Neto (2017);
Costa-Neto et al. 2020

Interpretação “Biológica” (GE ou G+GE)

Algoritmo

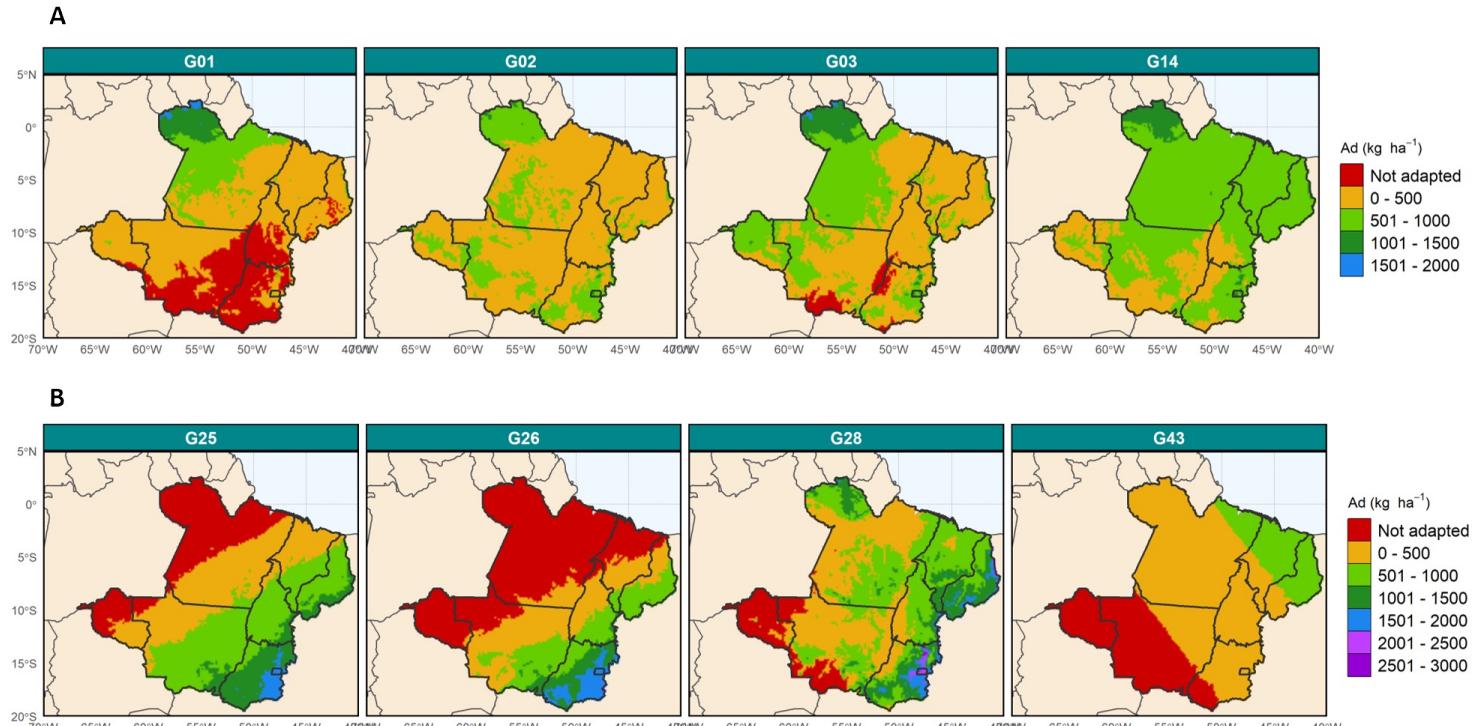
1. Ajustamos as médias de cada genótipo em cada ambiente (análise conjunta)
2. Para cada genótipo, ajustamos suas médias ao longo dos ambientes usando o modelo FR e dados ambientais
3. Temos a soma de quadrados original (sem decomposição). Comparamos com a capturada pelo modelo.
4. Para cada genótipo teremos um coeficiente de responsividade a cada fator ambiental. E o quanto que este fator explicou para o dado genótipo.
5. A soma das variancias para cada genótipo resulta na soma total explicada pelo modelo
6. Opcional: bootstrap/leave-one-out

OBS: (1) é feito com **Adij**, lembrando que este depende do seu germoplasma e da sua rede experimental

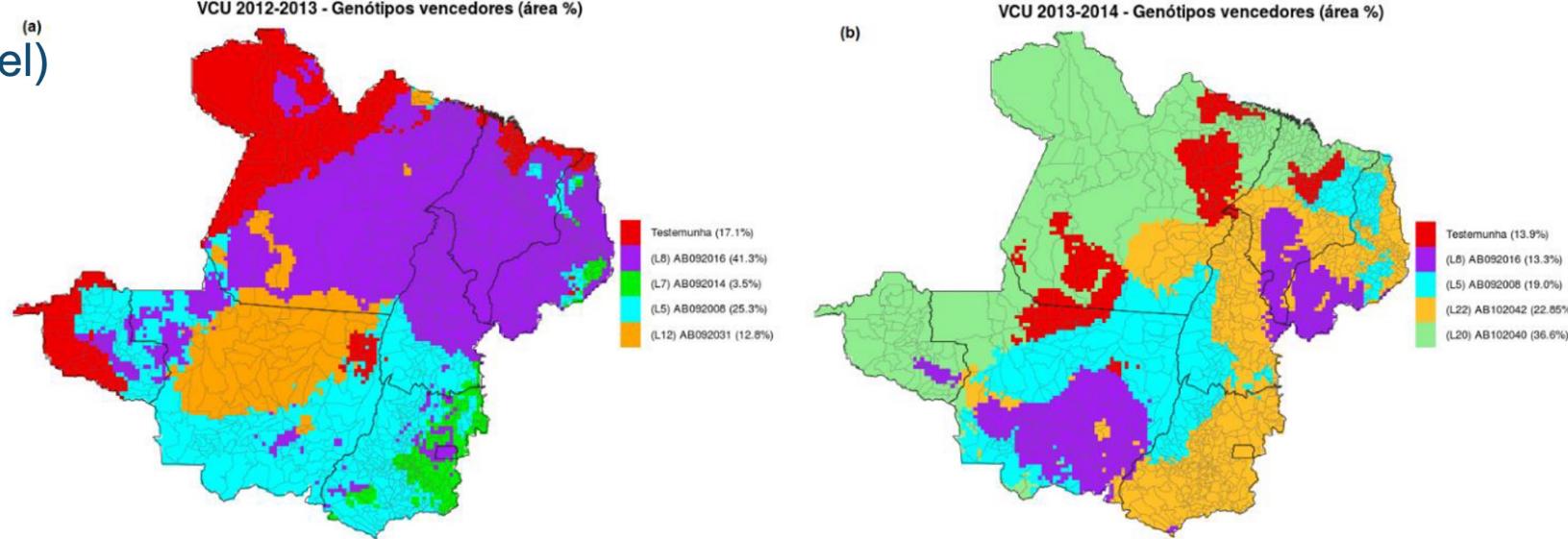
Specie	Region	Author	Env. Information	%SS
Potato	Germany	Baril et al. (1995)	DFLo, Tmax, Tmed	44,40
Ryegrass	France	Balfourier et al. (1997)	Tmin	72,80
Maize	USA	Magari et al. (1997)	GDv, GDf, Pracm	45,80
Maize	France	Epinat Le Signor et al (2001)	Tmax, Tavg, GDv, GDf	60,00
Winter Wheat	Spain	Voltas et al. (2005)	EHv, GDv, Tmaxf	71,10
Winter Wheat	Spain	Voltas et al. (2005)	GDv, Tminv	58,70
Tomato	Caribbean	Ortiz et al. (2007)	Prac, DFLo, Tavg, pH	91,16
Wheat	India	Joshi et al. (2010)	Urf, Tmaxv, Tminv, Ur, SoilChar	60,26
Wheat	Mexico	Verhulst et al. (2011)	Tminf, Racf	90,2
Melon	Brazil	Nunes et al. (2011)	Tmin, Tmax, Prac	79,89
Sugarcane	Brazil	Sá (2013)	Tavg, Prac	55,56
Soybean	Brazil	Cardoso Junior (2014)	Pracf, Etacm, LAT	41,00
Upland Rice	Brazil	Costa-Neto et al. (2020)	LAT, LON, ELE	53-59
Barley	Australia	Porker et al. (2020)	Tavg, Photoperiod	69,00

Regional adaptation (GIS-based maps)

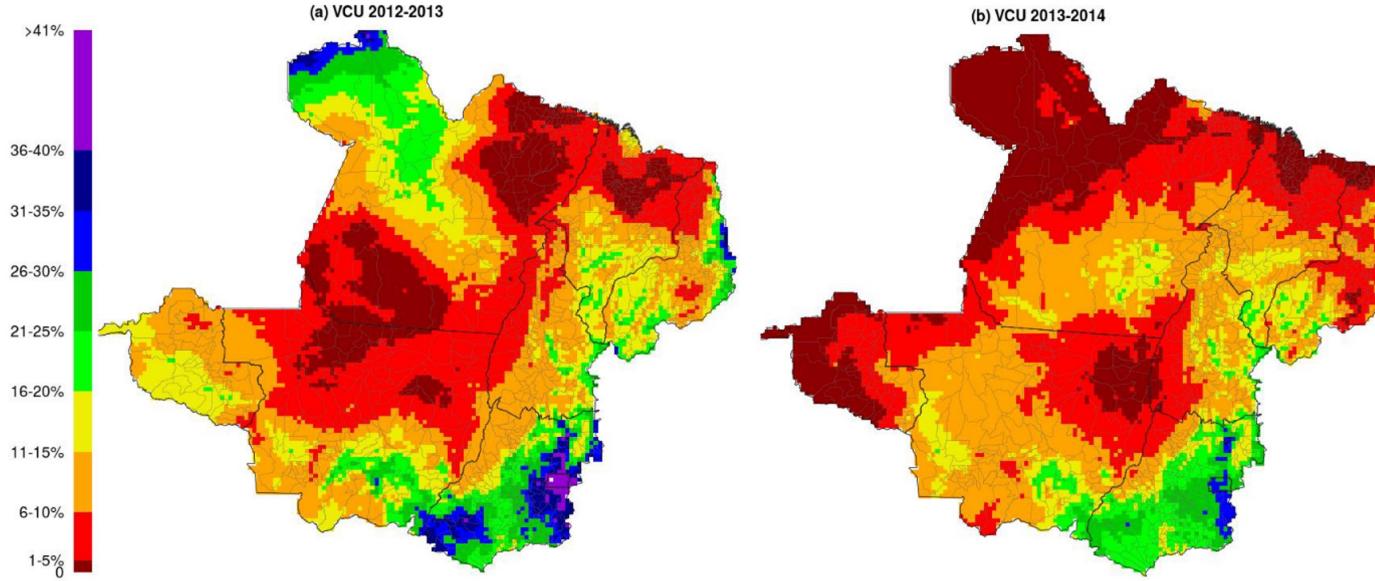
- Factorial Regression (Denis, 1980, Eeuwijk 1996, Crossa 1999)
- Adilson S. Martins (2004 , now KWS Tropical maize Breeding lead)
- Joao Batista Duarte & Several students from 2004-2019 (Luiz Antonio, Renata Sá, Odilon, Rafael)
- GGE-GIS (Costa-Neto et al., 2016, conference – EMBRAPA CERNAGEN)
- frGIS (Costa-Neto et al., 2020)



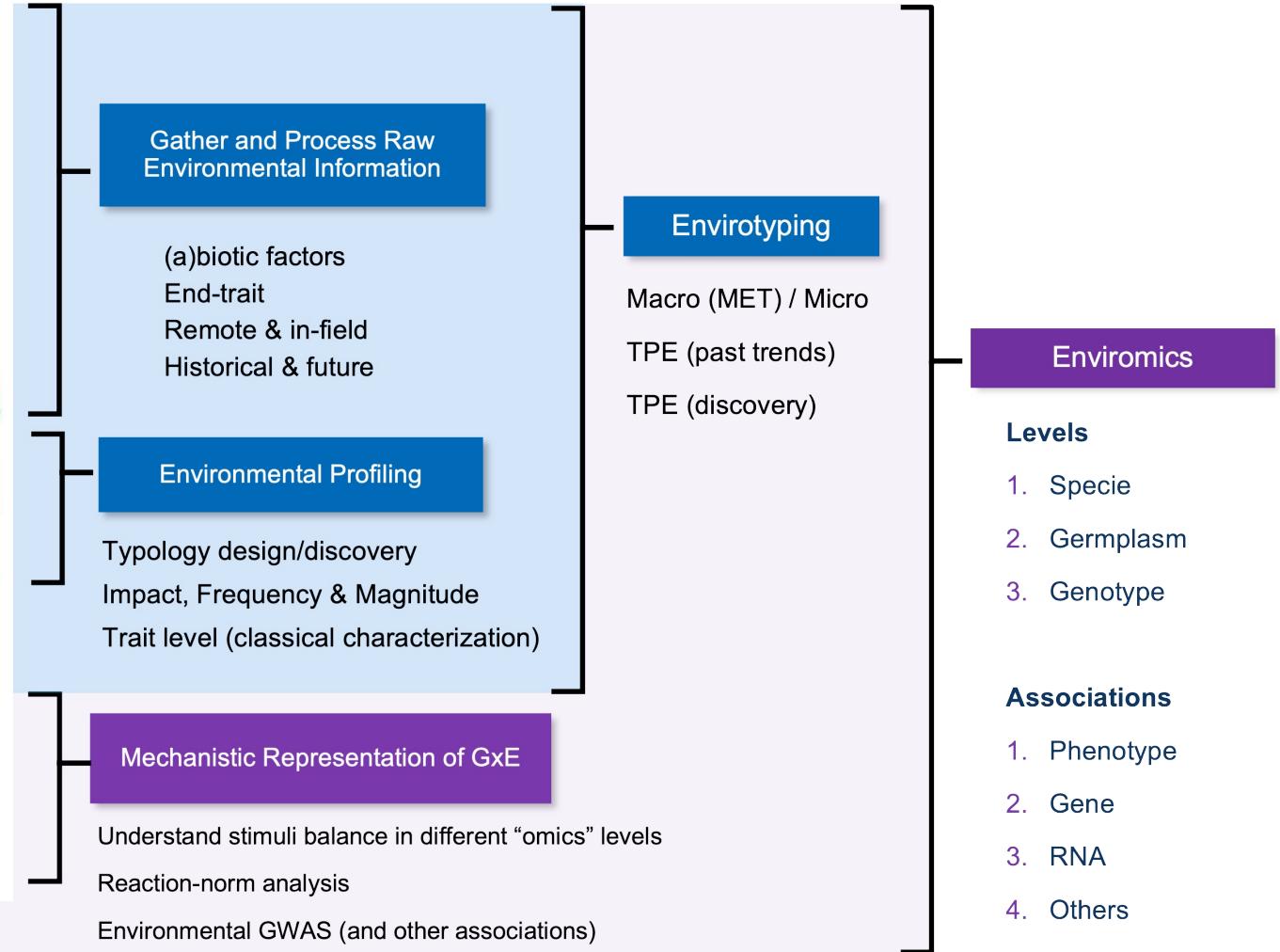
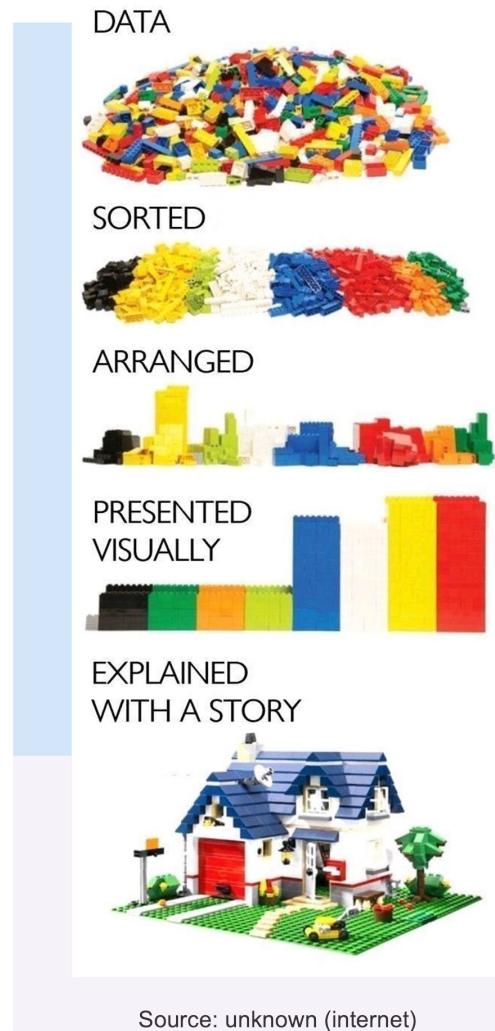
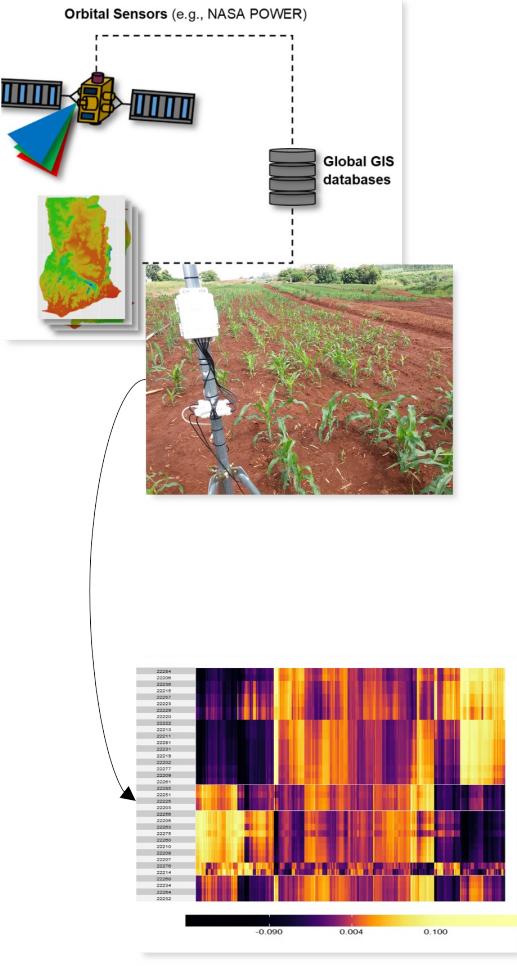
Winners (by pixel)



Best candidates vs Best checks



Diferença entre dado, informação e história



Assembly Enviromes and “Calling envirotype markers”

ORIGINAL RESEARCH article

Front. Plant Sci., 07 October 2021 | <https://doi.org/10.3389/fpls.2021.717552>



Download Article Export citation

Enviromic Assembly Increases Accuracy and Reduces Costs of the Genomic Prediction for Yield Plasticity in Maize

Germano Costa-Neto^{1,2*}, Jose Crossa^{3,4†} and Roberto Fritsche-Neto^{1,5}

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³Biometrics and Statistics Unit, International Maize and Wheat Improvement Center (CIMMYT), Mexico City, Mexico

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Quantitative genetics states that phenotypic variation is a consequence of the interaction between genetic and environmental factors. Predictive breeding is based on this statement, and because of this, ways of modeling genetic effects are still evolving. At the same time, the same refinement must be used for processing environmental information. Here, we present an “enviromic assembly approach,” which includes using ecophysiology knowledge in shaping environmental relatedness into whole genome predictions (GPs) for plant breeding (referred to as

2,366

TOTAL VIEWS

Am score 5

View Article Impact



Suggest a Research Topic >

Mensagem Chave

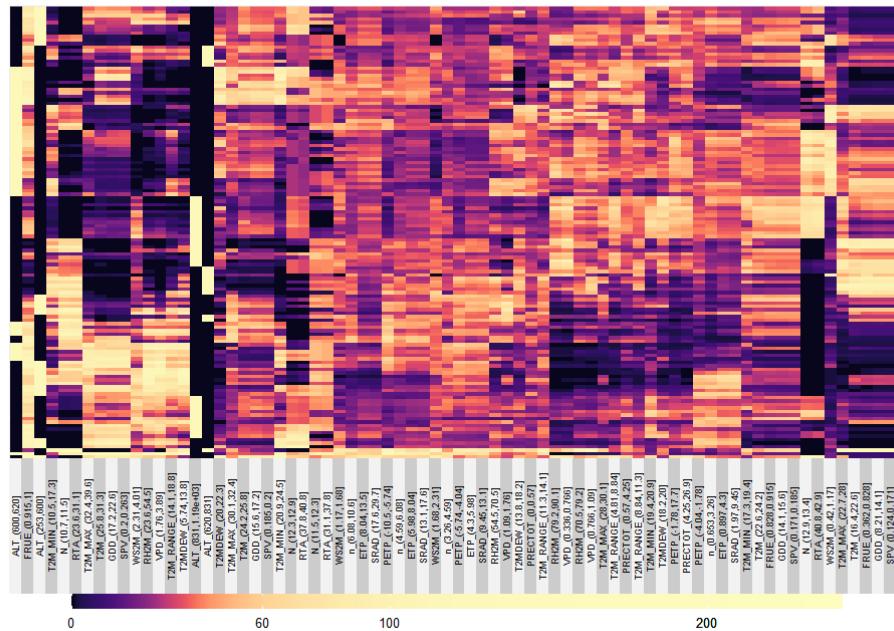
Ambiente = soma das tipologias e suas frequencias (ou seja, um mosaico de tipologias possíveis)

T-matrix = Matrix de Tipologias x Ambiente, nos quais cada “celula” é a frequencia (de 0 a 1)

Montagem de Enviromas (Envirome assembly) derivado de “Genome assembly”

Matrizes de tipologias ambientais (“marcas ambientipicas”)

Panel of Environmental Types



Used as Explicit Covariates

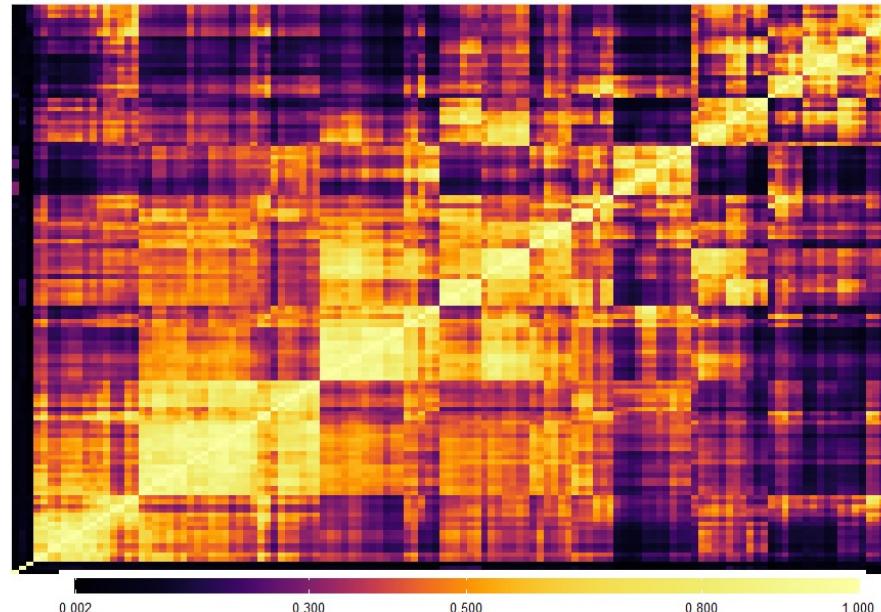
Kernelization
(env_kernel)

Environmental Relatedness

Approaching Similarity
(in silico)

Montar um kernel = Montar uma estrutura de variancia-covarancia (relacionamento)

1. Linear Kernel (same as GBLUP)
2. Nonlinear Gaussian Kernel (GK)
3. Nonlinear Deep Kernel (Arc-cosine approach)



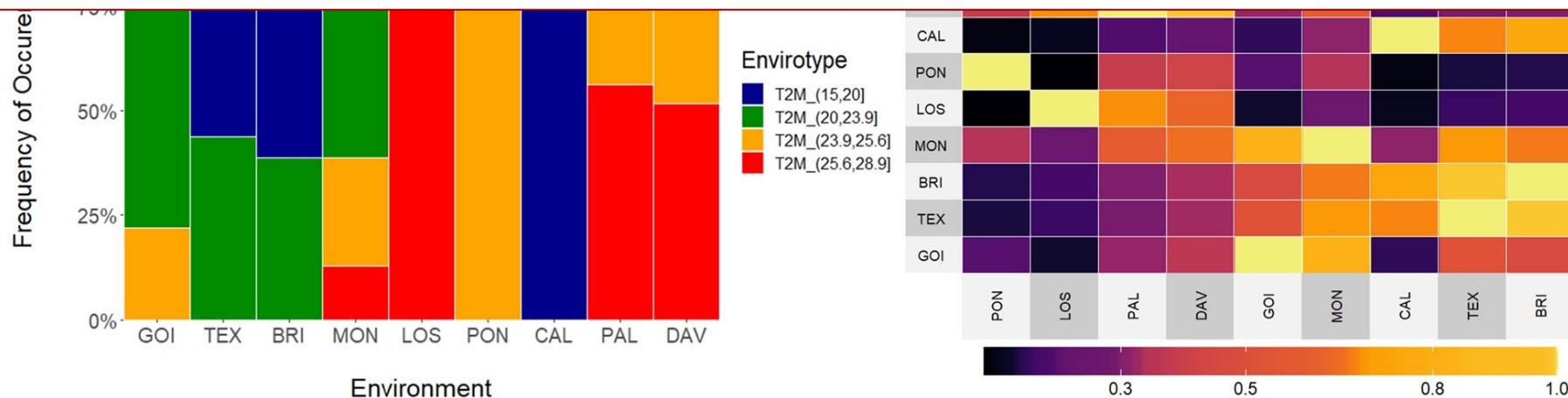
Criando “redes globais” de relacionamento

A

50°N -

Pergunta:
isso é propriedade da “localidade” ou do
cultivo/espécie nesta localidade? E se mudar a data
de plantio?

env_typing()

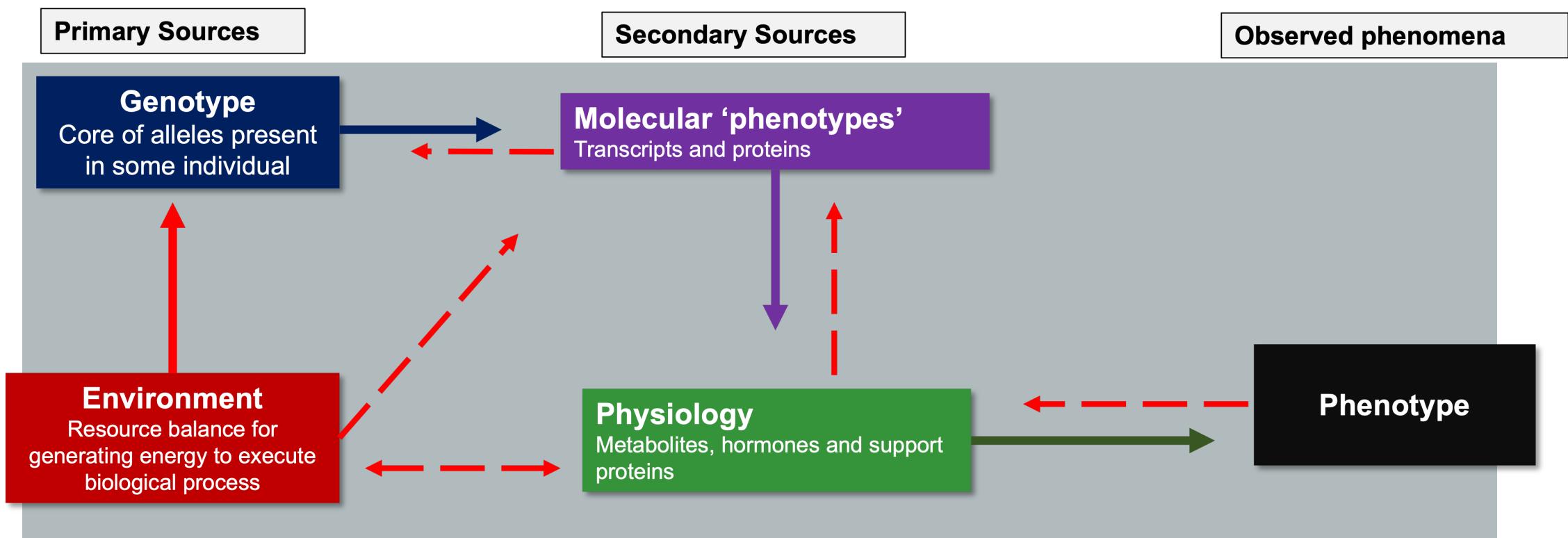


Interplay Quantitative and Molecular Genetics

- **Phenotype:** end-result of multiple interactions among expressed genes, epigenome and environmental signals
- Environmental acts at nuclear, cellular and physiological level (plant level)
- It is not a one-way road: compensatory effects, homeostasis, plasticity, pleiotropy, epigenetics...across time and space!

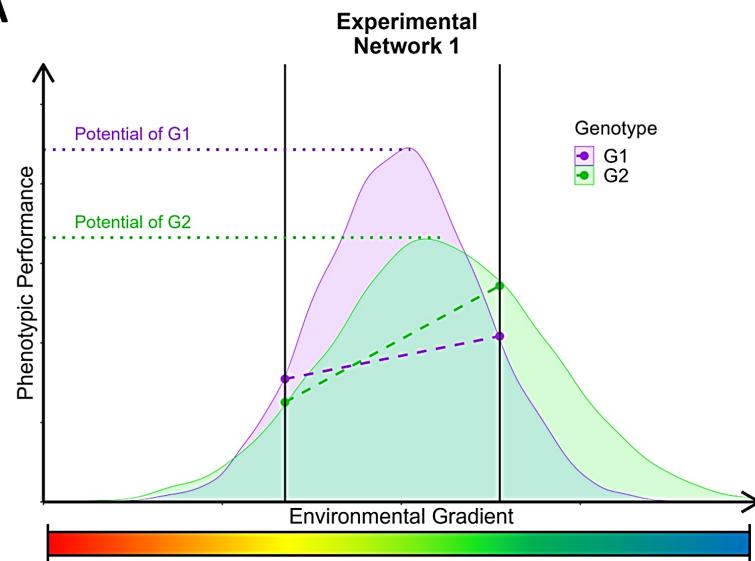
Solid lines: Central Dogma

Dashed lines: Surrounding environment outside gene level

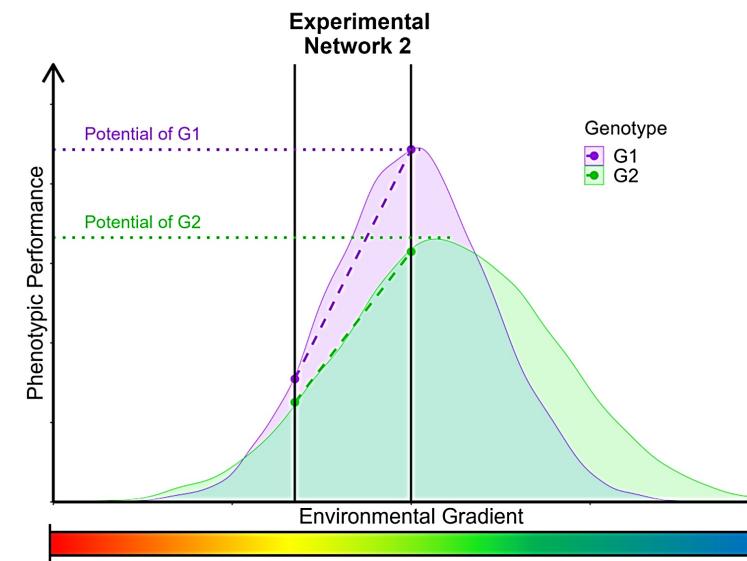


Interação Genótipo x Ambiente: uma propriedade emergente!

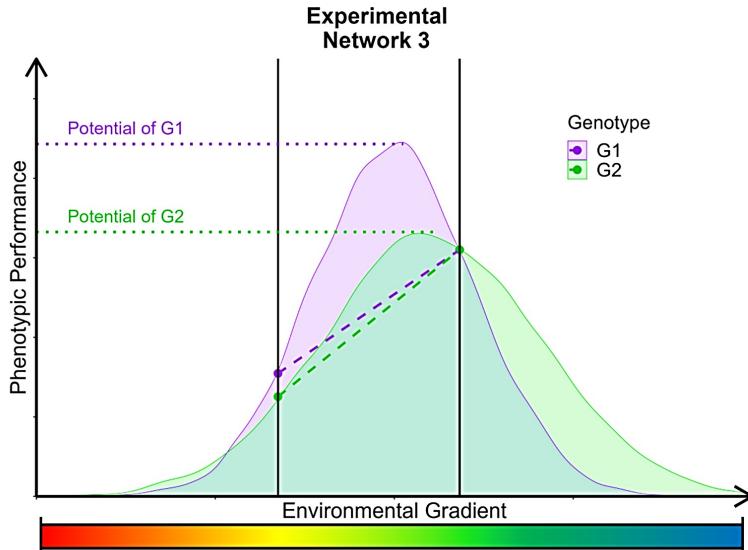
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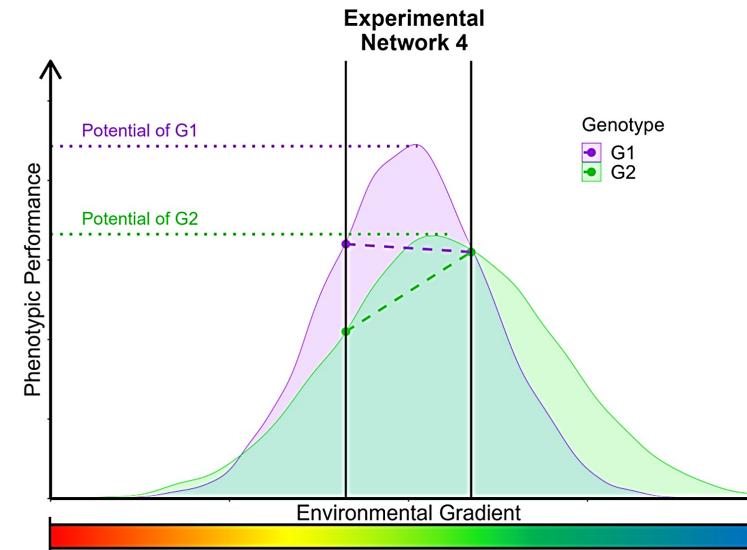
B



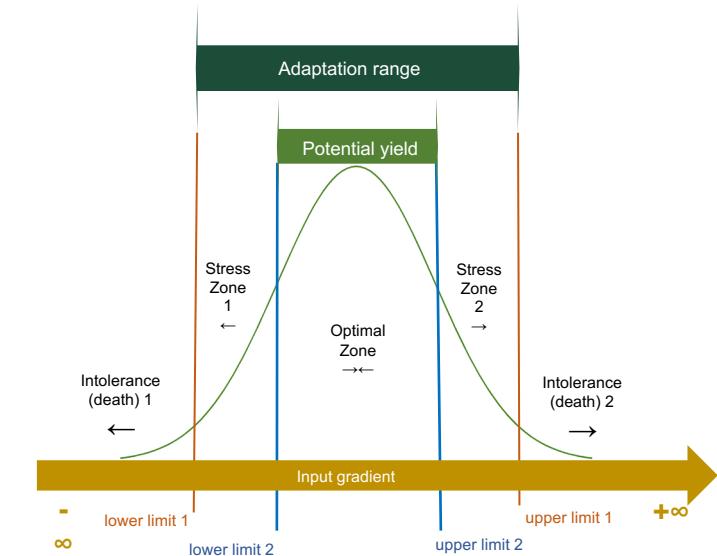
C



D

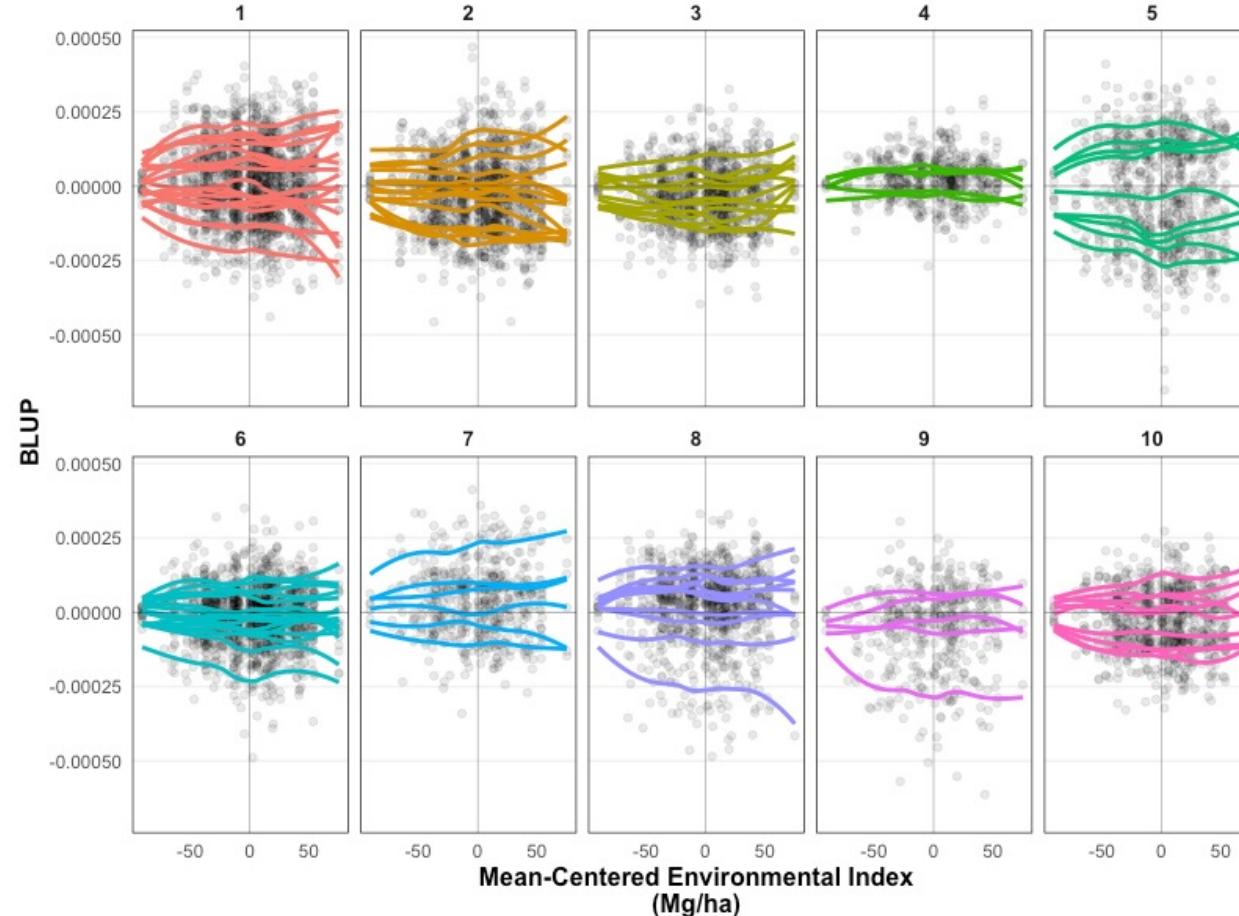


Shelford's Law

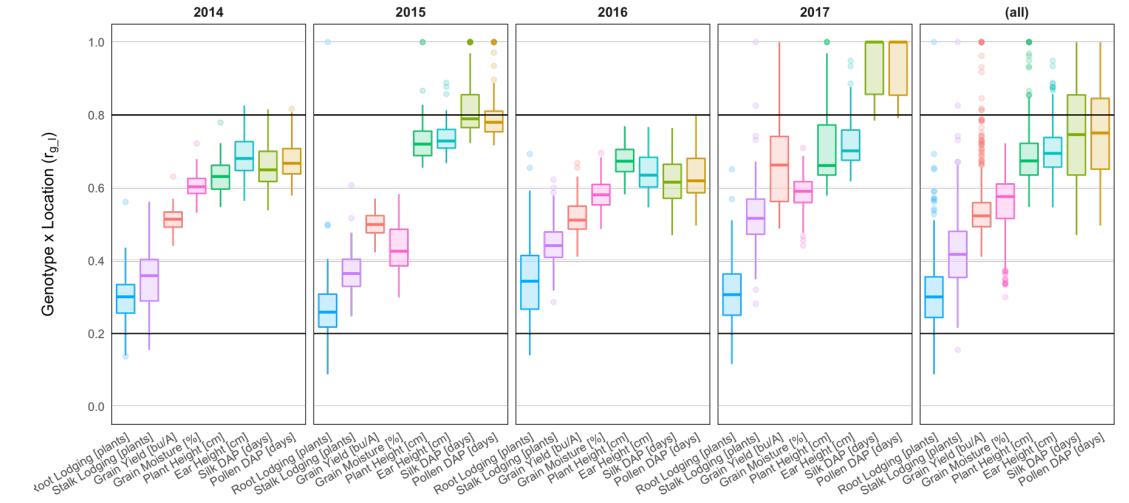


Evidencia da “efemeridade” da interacao GxA

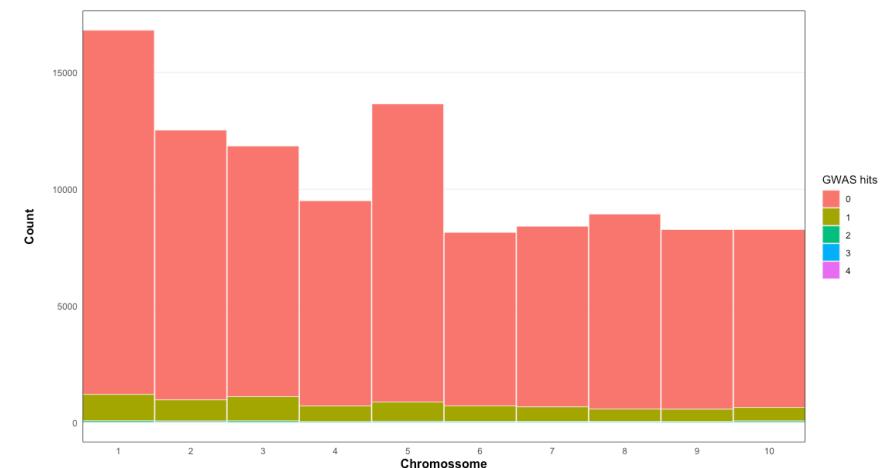
Reaction-norm of the genome regions (for each chromosome)



GxL depends on the MET sample

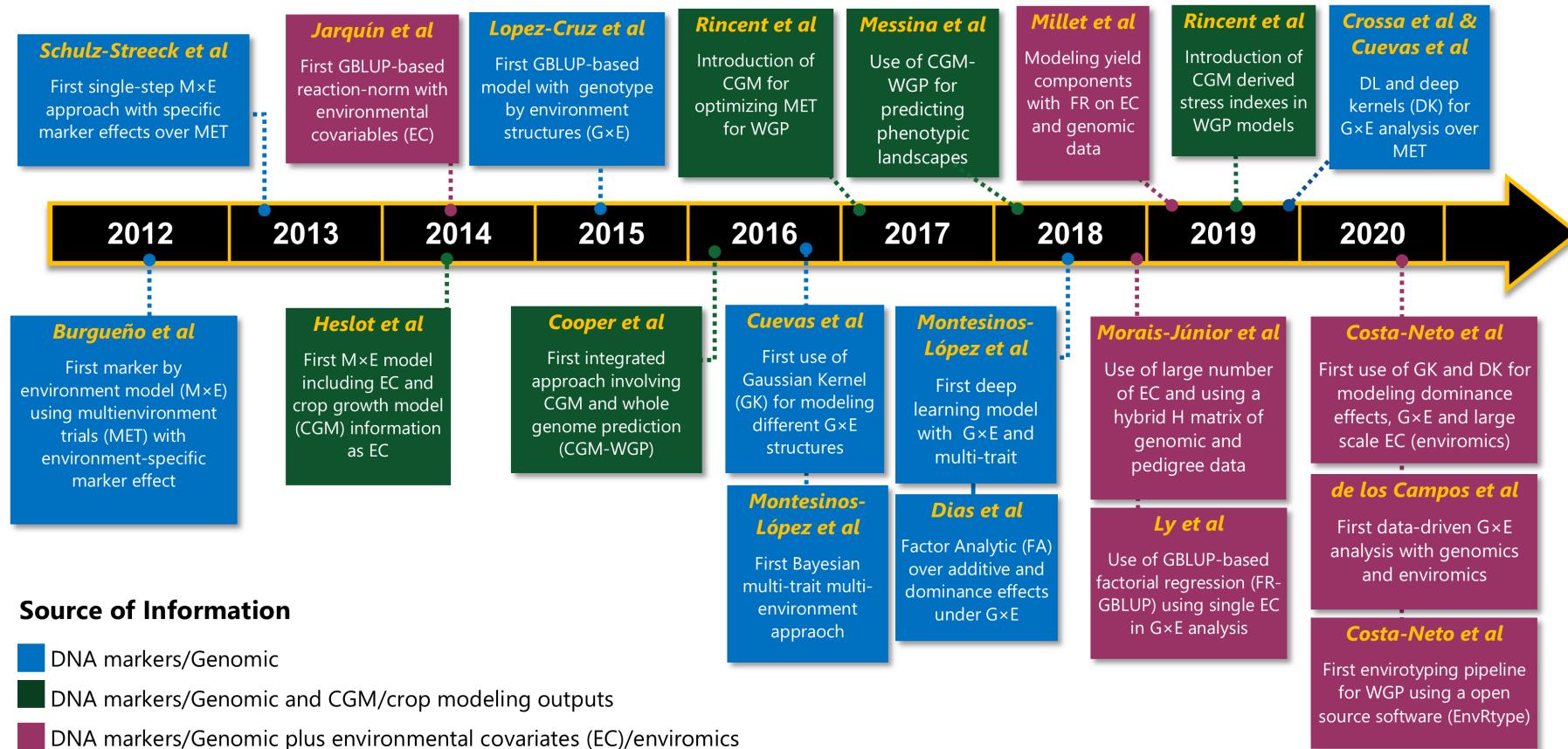


Common GWAS hits across environments

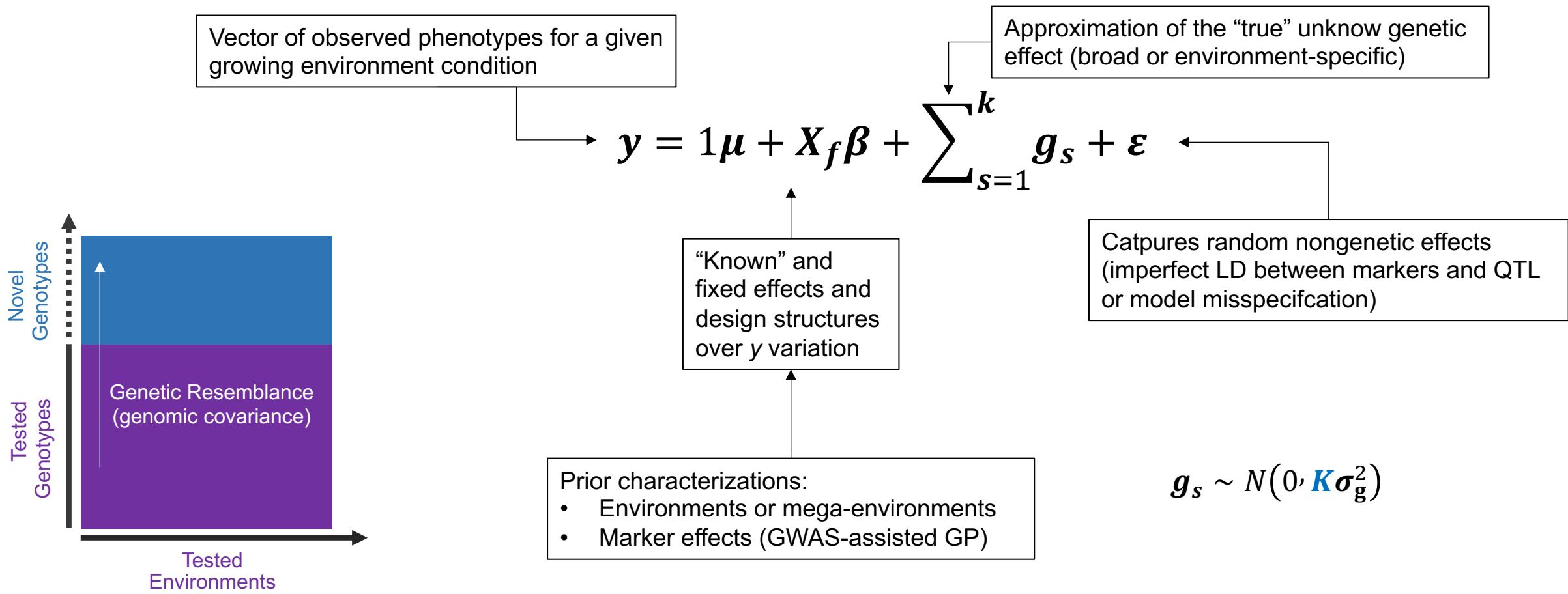


Genomic Prediction (GP, across MET)

Short history and some of the GP-MET papers (OBS: there is much more from 2012-present, definitely it must be updated)

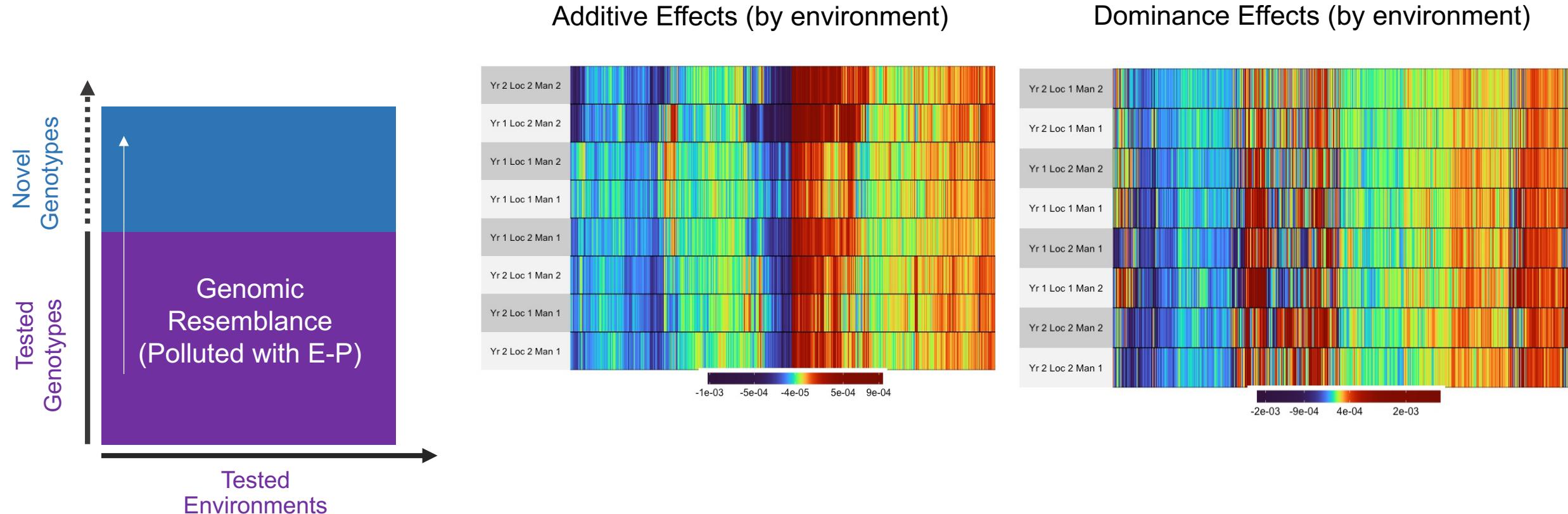


Genomic Prediction (GP, across MET)



Relações fenotipo-ambiente afetam as relações G-to-P

Ridge Regression (regressão aleatória sobre o efeito dos marcadores sobre algum fenótipo)

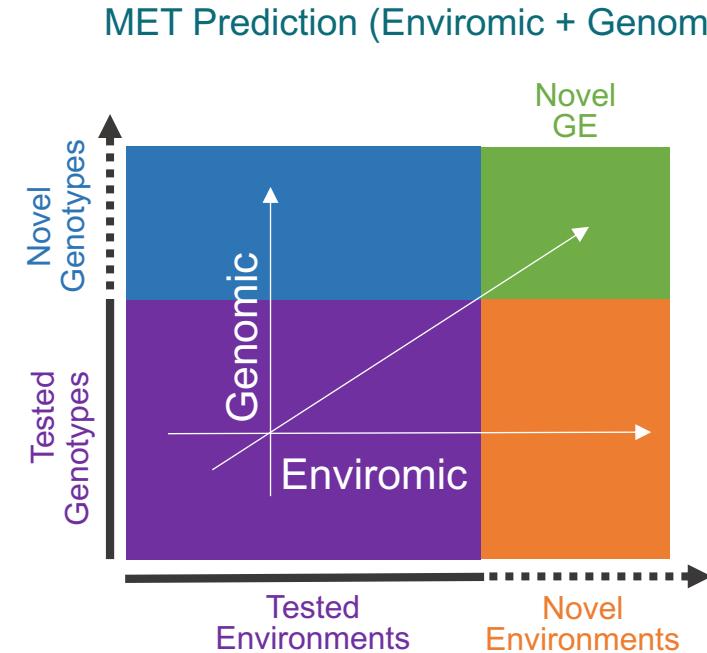
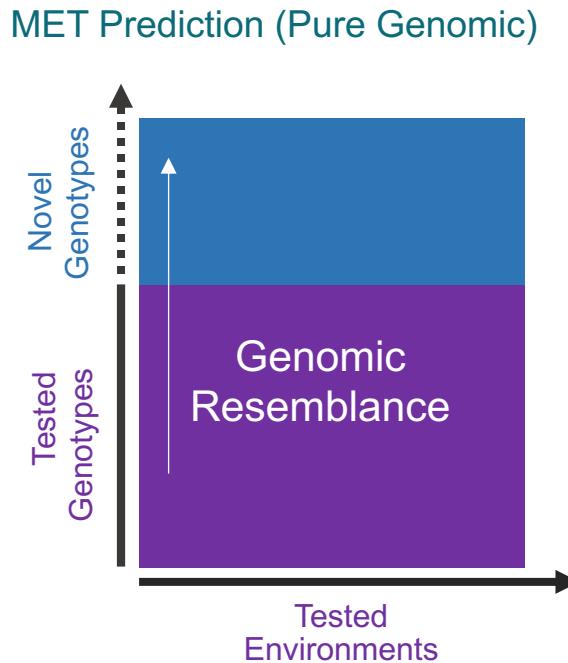


Toy Data set: 2 years, 2 locations, 2 managed nitrogen fertilizer levels. Markers were computed for each single environment (ridge regression). Grain yield

Costa-Neto et al. (in review, tropical maize)

Predição genômica “assistida” por enviromics

Linking **G** to **P** using **E** information to **mimic biological or putative** ecophysiology interactions



Adapted from Malossetti et al. (2013)

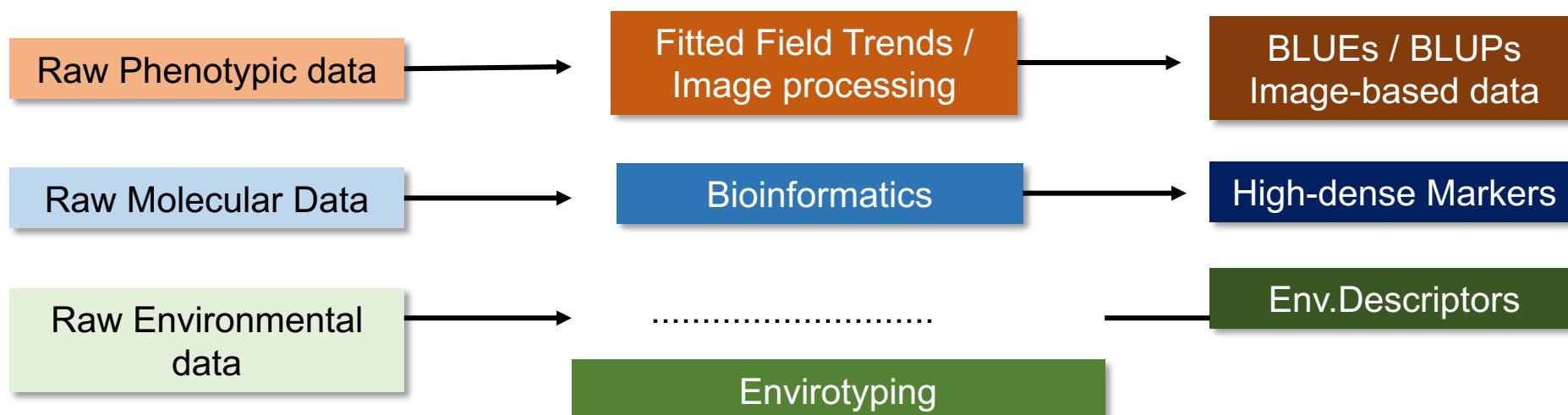
Model Generalization

- Regression models (linear/nonlinear)
- Kernel-based models
- Machine Learning
- Deep Learning

$$y = f(G, E, \dots) + \epsilon$$

Pra quê EnvRtype?

- Facilitar o estabelecimento de uma pipeline de envirotyping
- Até então não há plataformas claras: mas também não há regra “rígida”
- Primeiros passos para melhorar o PROCESSAMENTO dos dados ambientais

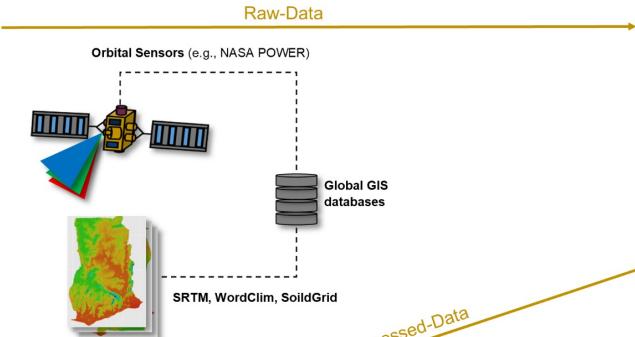


Module 1

Remote Data Collection

- `get_weather()`
- `extract_GIS()`

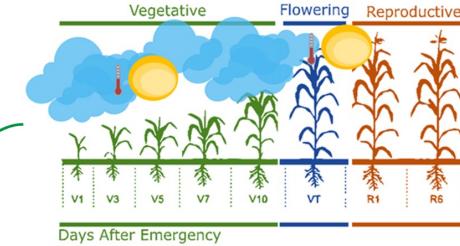
Raw-data from environmental sensors or `get_weather()` and `extract_GIS()` can be used in the further steps or processed



Raw-data Processing

- `SummaryWTH()`
- `ProcessWTH()`
- `param_temperature()`
- `param_radiation()`
- `param_atmospheric()`

Data processing involves the quality control and computation of additional variables

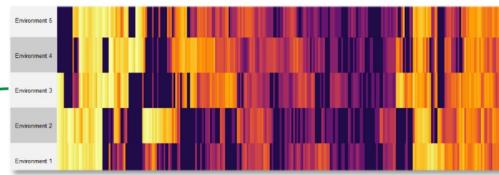


Module 2

Environmental Characterization

- `env_typering()`
- `W_matrix()`

Enviotype descriptors



Panel of enviotype descriptors or environmental covariabiles can be incorporated in predictive tools as environmental markers or to study similarity among environments

Environmental covariabiles

Module 3

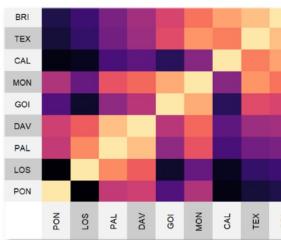
Environmental Similarity

- `env_kernel()`

Relatedness across environments derived from enviotyping data can be used to group environments with similar pattern

Enviromic Kernels

Kernel Models for phenotype prediction can be made involving genomic and enviromic-based sources derived from environmental similarity kernels



Enviromic-based Kernels Models

- `get_kernel()`
- `kernel_model()`

Models:

1. Genotypic Effects (MM and MDs)
2. Enviromic-enriched Main Effects (EMM and EMDs)
3. Enviromic-based Reaction-Norm (RNMM and RNMDs)

Genomic-based Predictions

Genomic-estimated Reaction-Norm Multi-environment Prediction

Outputs

Reaction-Norm

examples Factorial Regression GxE analysis

Environmental Grouping

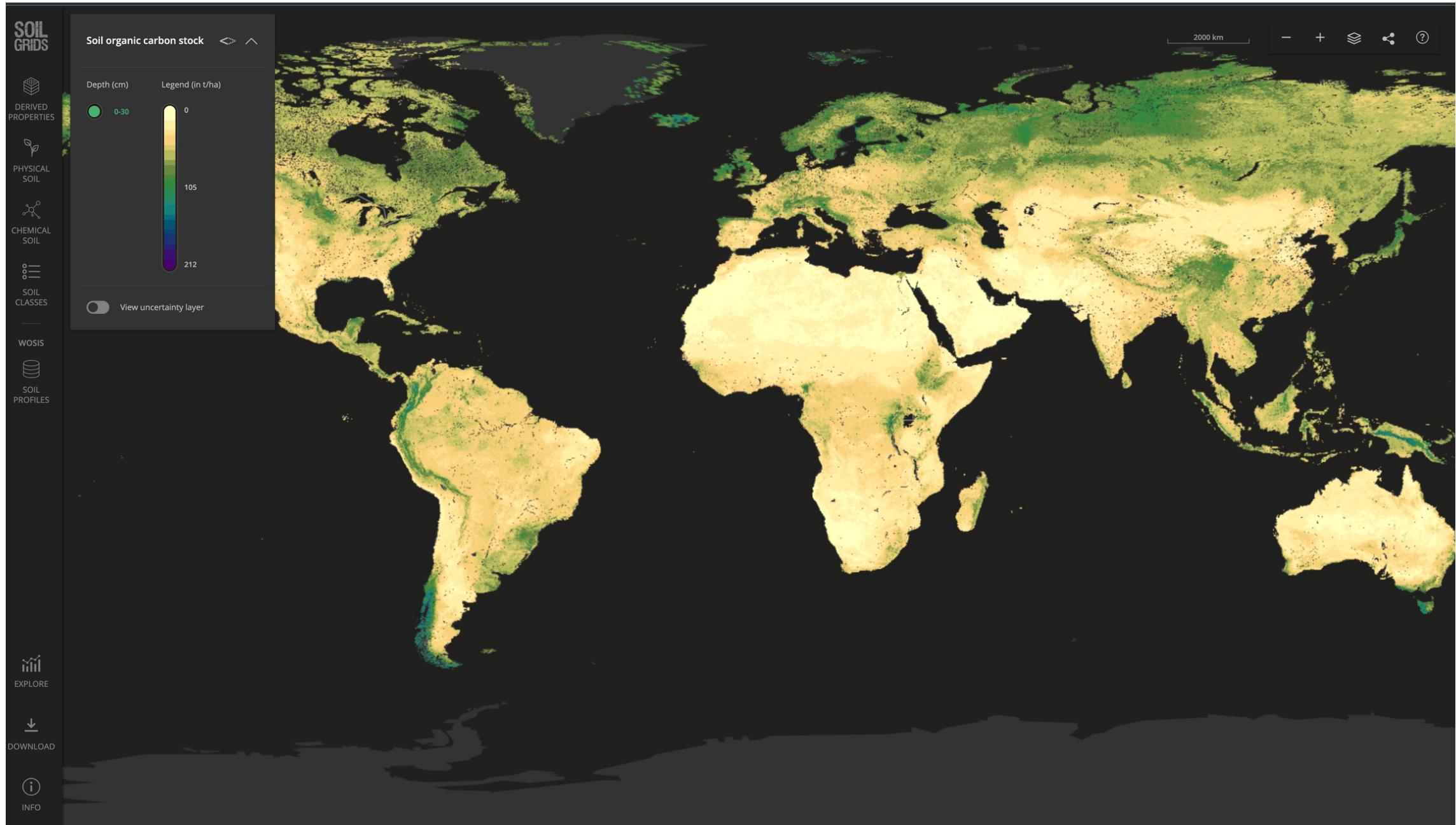
Clustering (K-mean) TPE definition

Remote Sensing (Digital Envirotyping)



Source	ID	Environmental Factor	Unit
Nasa Power ¹	ALLSKY_SFC_SW_DWN	All sky insolation incident on a horizontal surface	MJ m ⁻² d ⁻¹
	ALLSKY_SFC_LW_DWN	Thermal infrared longwave radiative flux	MJ m ⁻² d ⁻¹
	WS2M	Wind speed at 10 m above the surface of the earth	m s ⁻¹
	T2M_MIN	Minimum air temperature at 2 m above the surface of the earth	°C d ⁻¹
	T2M_MAX	Maximum air temperature at 2 m above the surface of the earth	°C d ⁻¹
	T2MDEW	Dew-point temperature at 2 m above the surface of the earth	°C d ⁻¹
	RH2M	Relative air humidity at 2 m above the surface of the earth	%
	PRECTOT	Rainfall precipitation (P)	mm d ⁻¹
SRTM ²	ALT	Elevation (above sea level)	m
Computed ³	FRUE	Effect of Temperature on Radiation use Efficiency	-
	GDD	Growing Degree-days	°C d ⁻¹
	ETP	Evapotranspiration (ETP)	mm d ⁻¹
	PETP	Atmospheric water deficit P-ETP	mm d ⁻¹
	DVP	Deficit of vapor pressure	kPa d ⁻¹
	SVP	Slope of saturation vapor pressure curve	kPa C° d ⁻¹
	T2M_RANGE	Temperature Range	°C d ⁻¹
	RTA	Global Solar Radiation based on Latitude and Julian Day	MJ m ⁻² d ⁻¹

Dados de Solo: <https://soilgrids.org/>

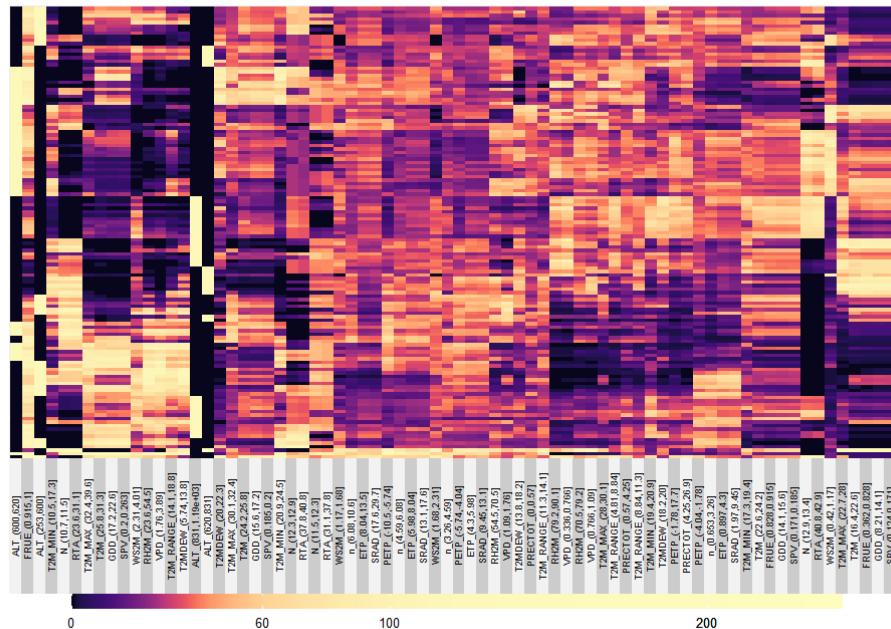


Cardinals for temperature (from literature)

Species	Suggested Cardinal Limit			
	Tbase1	Topt1	Topt2	Tbase2
Maize	8.0	30.0	37.0	45.0
Wheat	0.0	25.0	28.0	40.0
Rainfed Rice	8.0	30.0	37.0	45.0
Irrigated Rice (only vegetative stage)	8.0	28.0	40.0	45.0
Irrigated Rice (only reproductive stage)	15.0	25.0	35.0	45.0
Sorghum	8.0	30.0	37.0	45.0
Soybean	8.0	30.0	35.0	45.0
Peanut	8.0	30.0	35.0	45.0
Canola	0.0	25.0	28.0	40.0
Sunflower	8.0	30.0	34.0	45.0
Dry Bean	8.0	30.0	35.0	45.0
Chickpea	0.0	25.0	30.0	40.0
Barley	0.0	25.0	28.0	40.0
Sugarcane	5.0	22.5	35.0	40.0

Environmental Matrix (W_{matrix} or `env_typing`)

Panel of Environmental Types



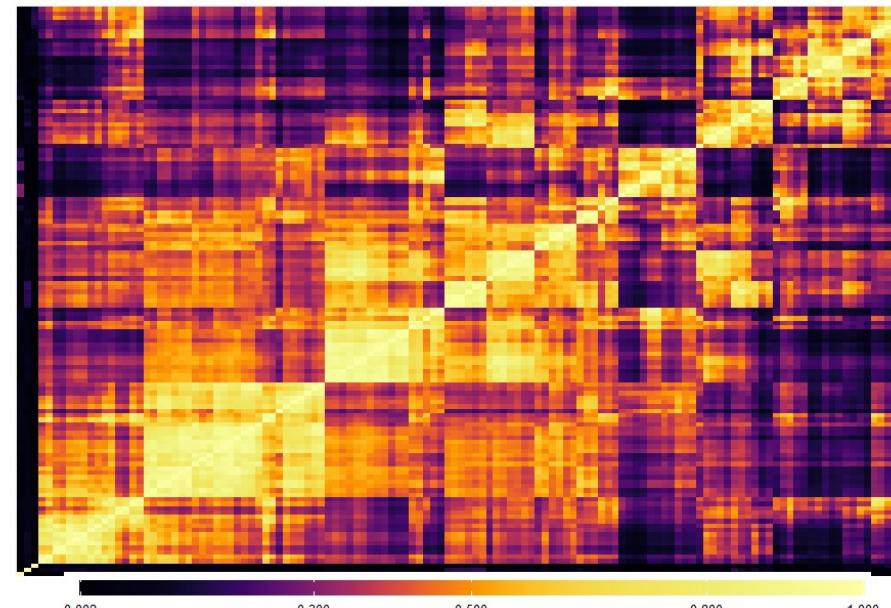
Used as Explicit Covariates

Kernelization
(`env_kernel`)

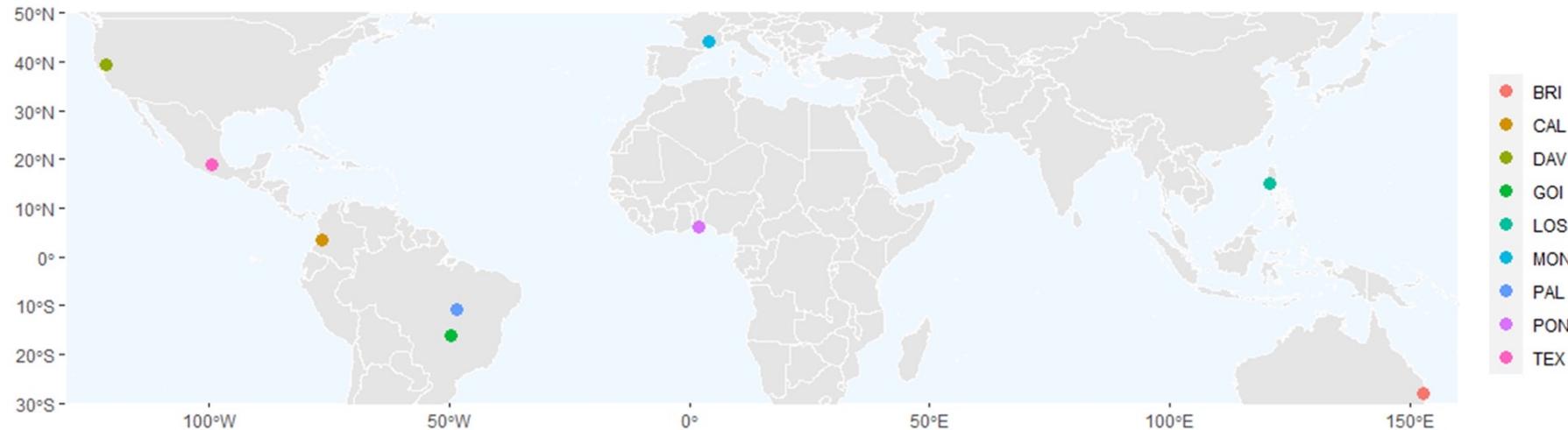
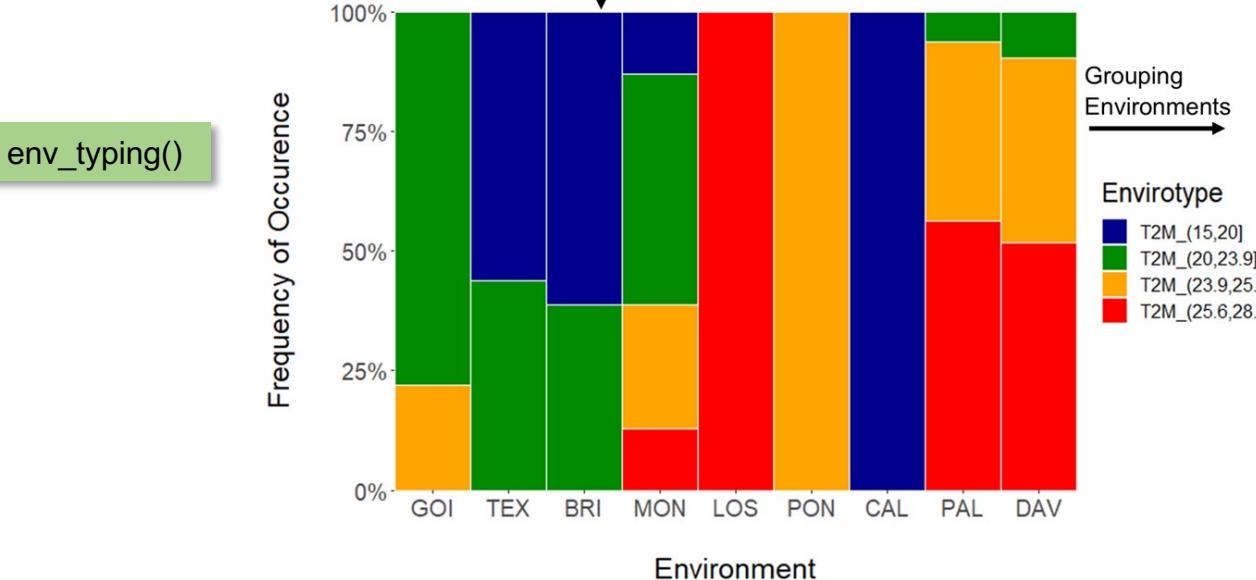
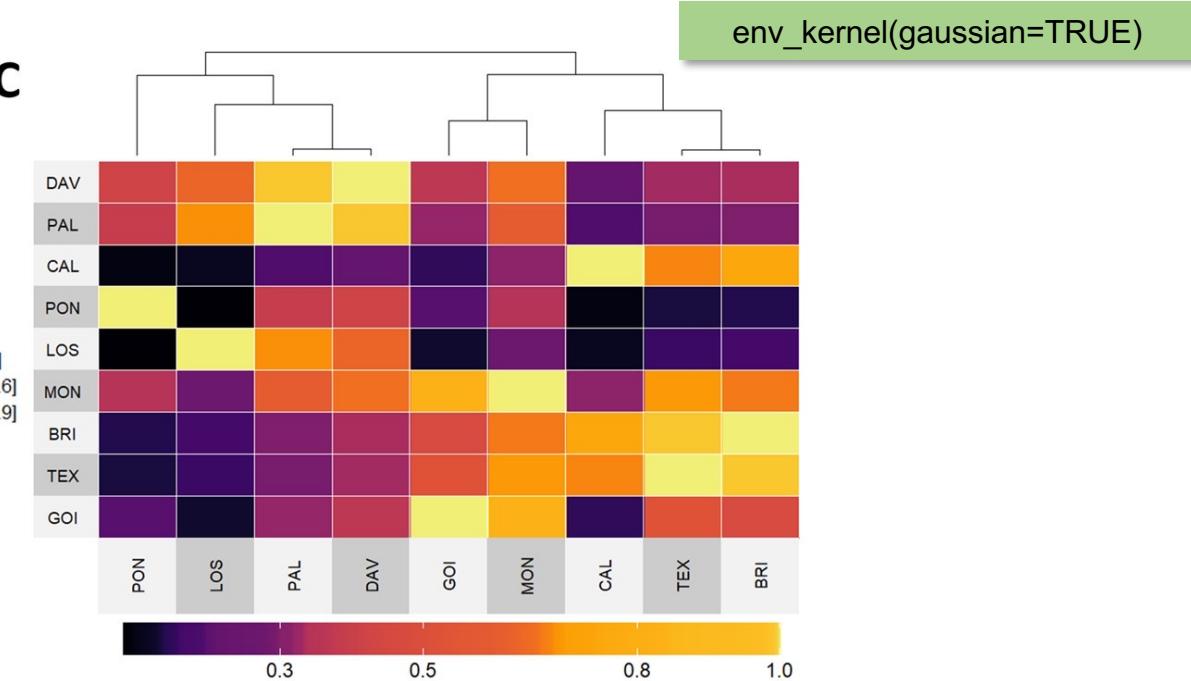
1. Linear Kernel (same as GBLUP)
2. Nonlinear Gaussian Kernel (GK)
3. Nonlinear Deep Kernel (Arc-cosine approach)

Environmental Relatedness

Approaching Similarity
(*in silico*)



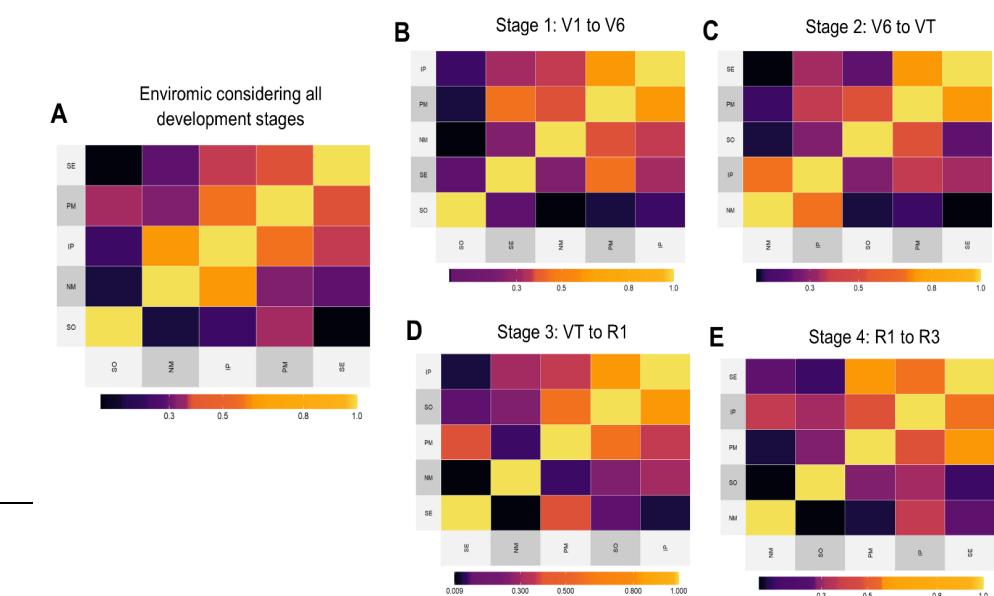
Global Envirotyping Network

A**B****C**

“New” reaction-norm approaches

GK+different model structures

Random Effect	Model		
	M1	M2	M3
Genomic (G)	0.426 [0.389;0.470]	0.509 [0.464;0.562]	0.555 [0.506;0.612]
Environment (E)	-	2.686 [2.470;2.505]	-
Stage 1 (S ₁ : V1 to V6)	-	-	3.507 [3.227;3.827]
Stage 2 (S ₂ : V6 to VT)	-	-	2.711 [2.494;2.958]
Stage 3 (S ₃ : VT to R1)	-	-	3.940 [3.626;4.300]
Stage 4 (S ₄ : R1 to R3)	-	-	4.018 [3.697;4.385]
GxE*	0.353 [0.322;0.390]	0.269 [0.246;0.297]	-
GxS ₁	-	-	0.308 [0.269;0.326]
GxS ₂	-	-	0.295 [0.278;0.337]
GxS ₃	-	-	0.306 [0.279;0.336]
GxS ₄	-	-	0.304 [0.280;0.339]
Residual	0.848 [0.773;0.936]	0.269 [0.245;0.296]	0.262 [0.238;0.289]



Model	Prediction Scenario	
	CV1	CV00
M1 (Baseline Genomic × Environment)	0.130 ± 0.047	0.102 ± 0.045
M2 (Benchmark Reaction-Norm)	0.762 ± 0.024	0.485 ± 0.211
M3 (Reaction-Norm for Each Development Stage)	0.760 ± 0.028	0.504 ± 0.194

“New” reaction-norm approaches

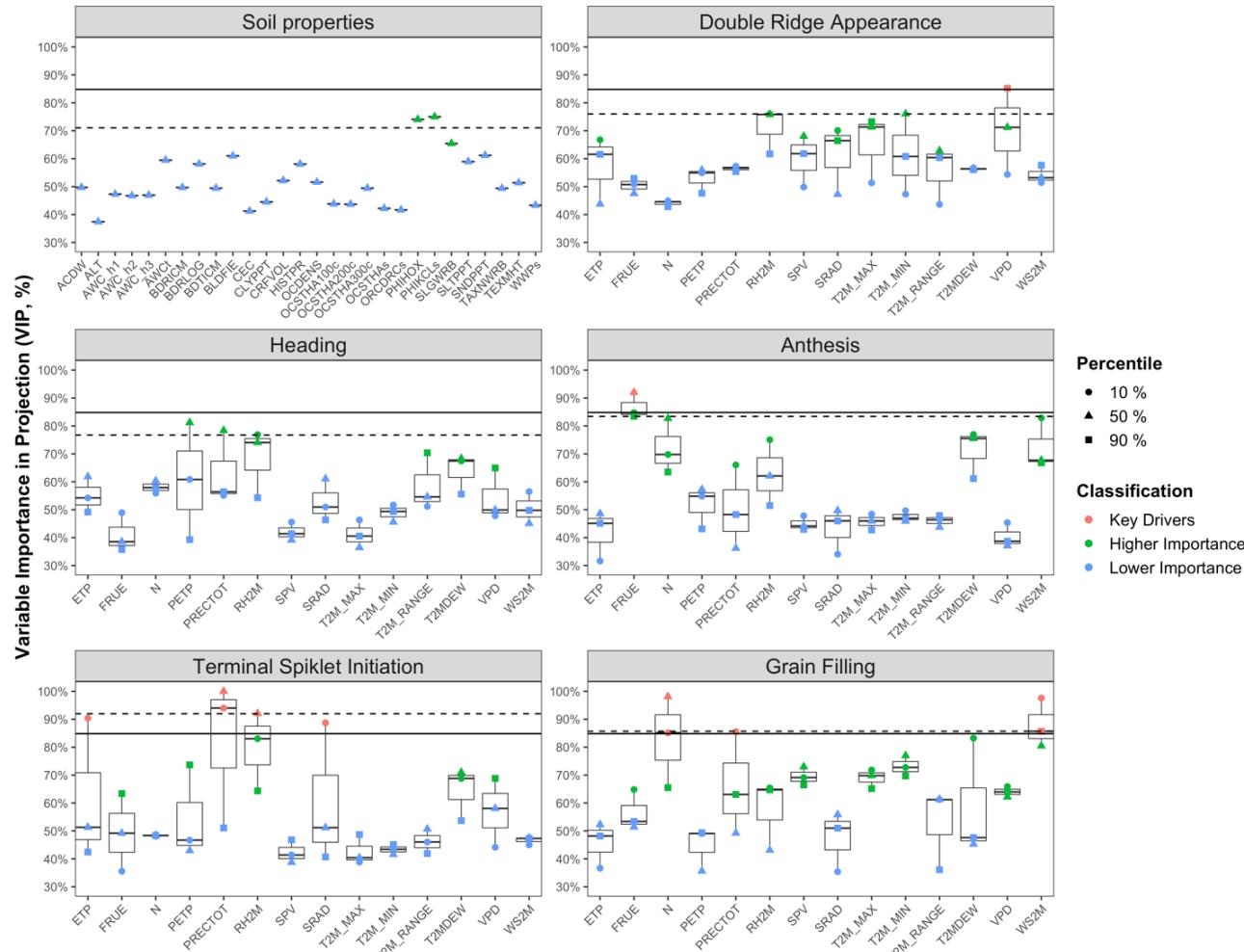
GK+specific or joint covariates effects

$$\mathbf{y} = \mathbf{1}\boldsymbol{\mu} + \mathbf{X}_f\boldsymbol{\beta} + \mathbf{g} + \mathbf{gE} + \mathbf{EC} + \mathbf{gEC} + \boldsymbol{\varepsilon}$$

Envirotyping Level	Model	Random Effect			
		Environment (E)	Genotype (G)	G×E	Residual
No Envirotyping	M0	-	0.435	0.329	0.837
Envirotyping by environment	M1	4.117	0.425	0.764	0.849
	(EC1 = FRUE)	[3.789;4.493]	[0.387;0.468]	[0.696;0.843]	[0.773;0.936]
	M2	3.440	0.384	0.786	0.726
	(EC 2 = PETP)	[3.165;3.754]	[0.350;0.423]	[0.716;0.867]	[0.662;0.801]
	M3	4.279	0.497	0.664	0.456
	(EC3=FRUE+PETP)	[3.938;4.670]	[0.453;0.548]	[0.605;0.733]	[0.416;0.503]
Envirotyping by development stage at each environment	M4	8.802	0.522	0.484	0.266
	(EC4 = FRUE)	[8.099;9.605]	[0.476;0.576]	[0.441;0.534]	[0.243;0.294]
	M5	3.514	0.548	0.425	0.267
	(EC5 = PETP)	[3.233;3.835]	[0.500;0.604]	[0.388;0.469]	[0.243;0.295]
	M6	1.595	0.514	0.464	0.262
	(EC6 = FRUE+PETP)	[1.468;1.740]	[0.468;0.566]	[0.423;0.512]	[0.238;0.289]

Compensa “selecionar covariaveis”?

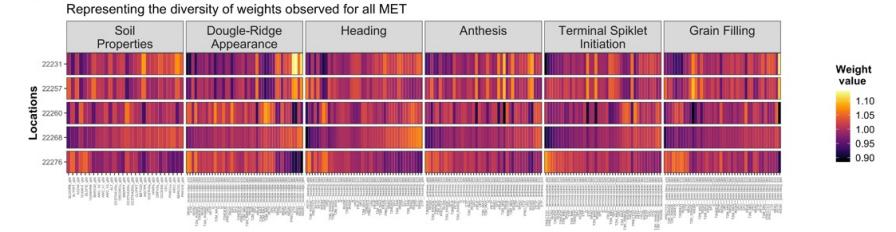
Selection of “covariabes” are a bad decision



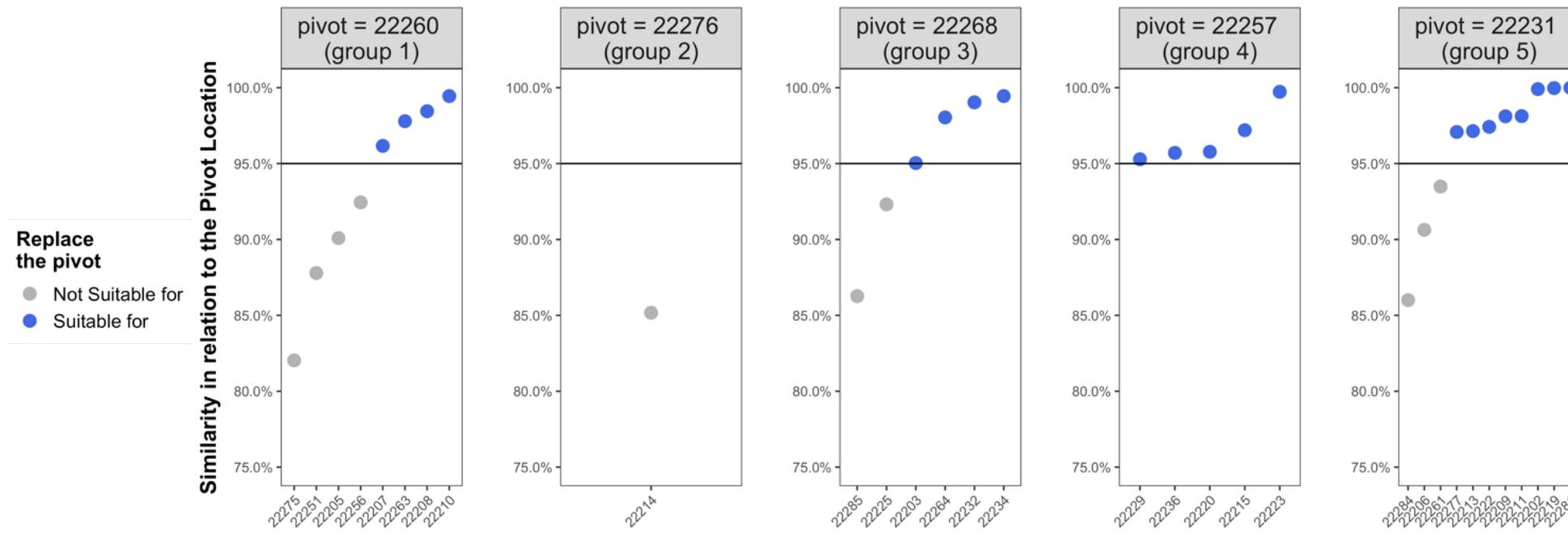
A Environmental Weights: all MET



B Environmental Weights: Pivot-Locations

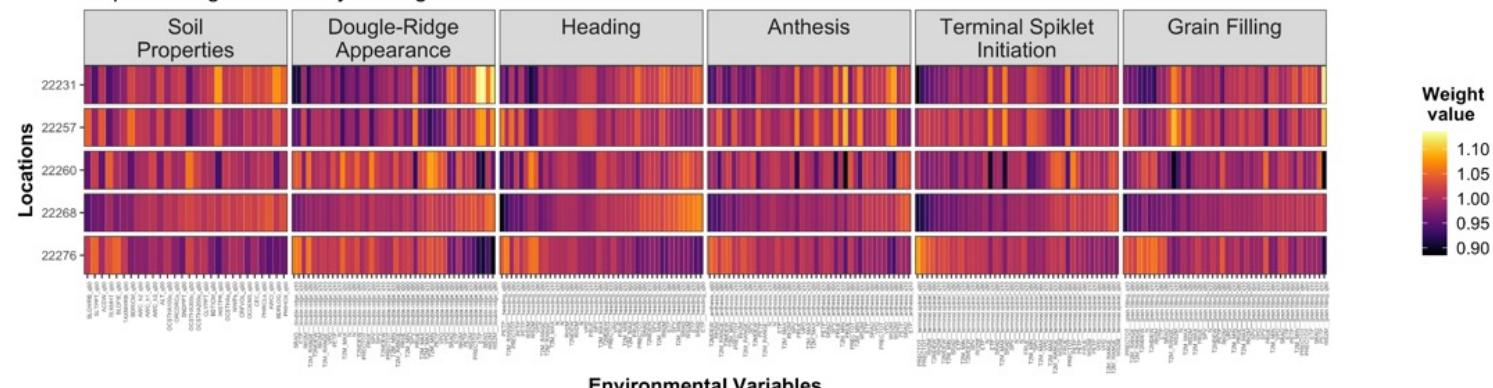


Diversidade Ambiental > Numero de ambientes



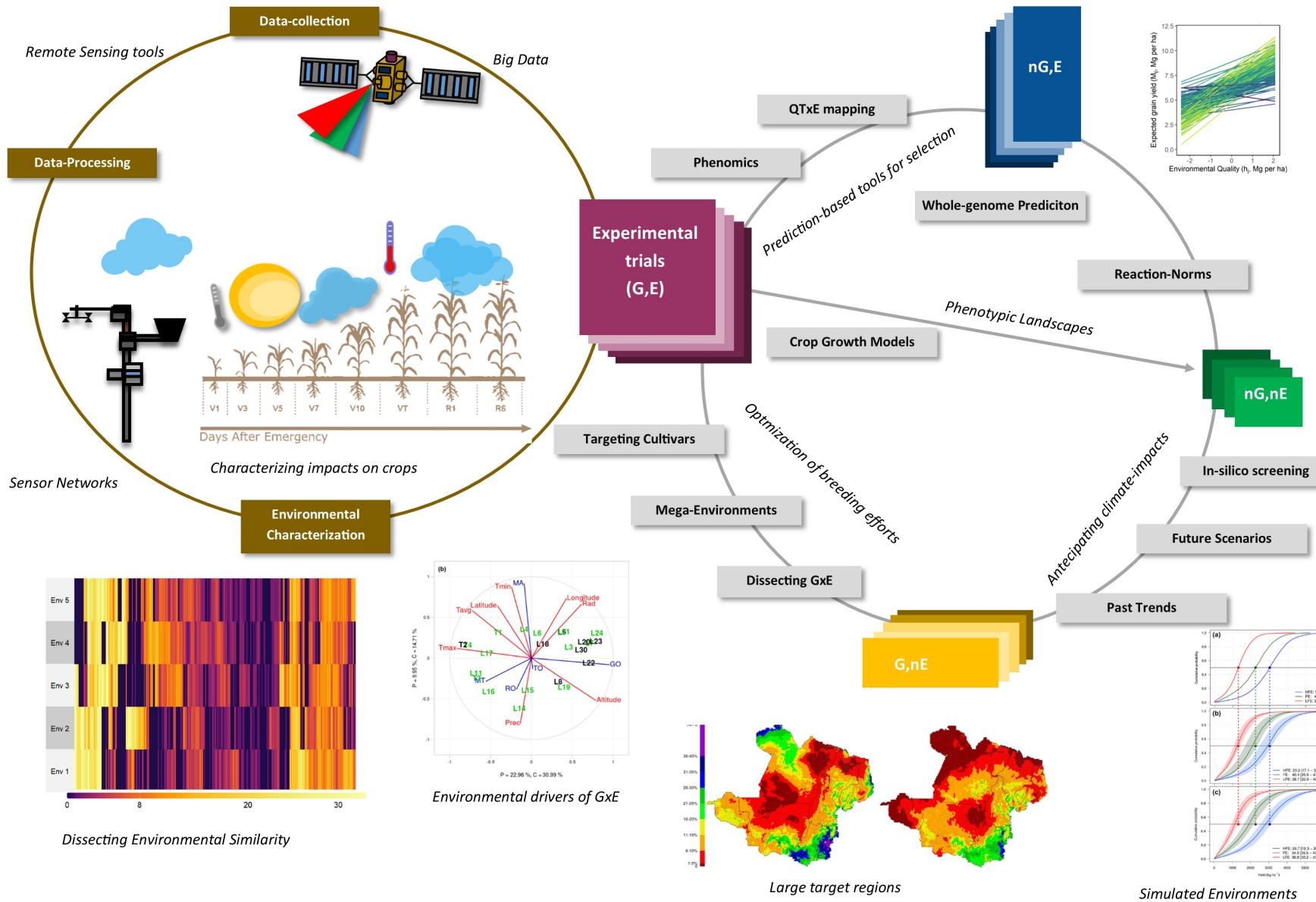
B Environmental Weights: Pivot-Locations

Representing the diversity of weights observed for all MET



Visão Geral

“[...] Enviromics é como uma caixa de chocolates: voce nunca sabe o que vai encontrar dentro”



Futuro: parte integral do “data science” e “research analytics”

Reinventando o desenho experimental

- Combinada com a Fenômica (fenotipagem de alto rendimento / baseada em imagens) como reflexo dos micro-ambientes a nível de parcela ou planta;
- Integração de técnicas de agricultura de precisão para melhor controle local (blocagem);
- Conexão entre diferentes experimentos – diferentes estágios de breeding/postbreeding
- Compreender ganhos genéticos para adaptação

Auxilio no estudo da diversidade genética e populacional

- Mineração de alelos de adaptação em populações naturais

Modelagem sob diferentes níveis da “biologia de sistemas” visando melhor entender a expressão genica

- Associação com proteômica e transcriptômica como formas de “melhor entender a norma de reação”
- Modelos de aprendizado de maquina (e.g., CNN) acoplando “layers ambientais” (e.g., Washburn et al., 2021)