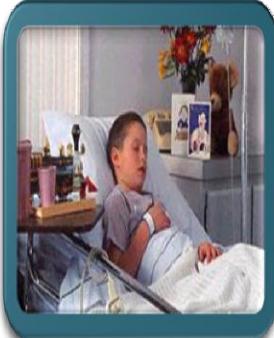


Clinical Dietitian Routine

Case study



PSA, male, 7 years old

- Fever, abdominal cramps, steatorrhea, flatus, bloody stools, diarrhea, vomiting, lactose intolerance, abdominal cramps**



Early exposition to cow milk (2 months of age); weight loss (8% in 2 weeks; anorexia)

- 21kg (p 50 = 23kg); 121 cm (p 50); Body mass index = 14.4kg/m² (p15 - p50)**

Clinical Dietitian Routine

Case study



Leucocytes = 18000 cells/ 10^9 ; C-reactive protein = 33mg/dl; albumin = 2.7g/dl

- Acute Phase response
- Nutritional diagnosis: acute protein malnutrition



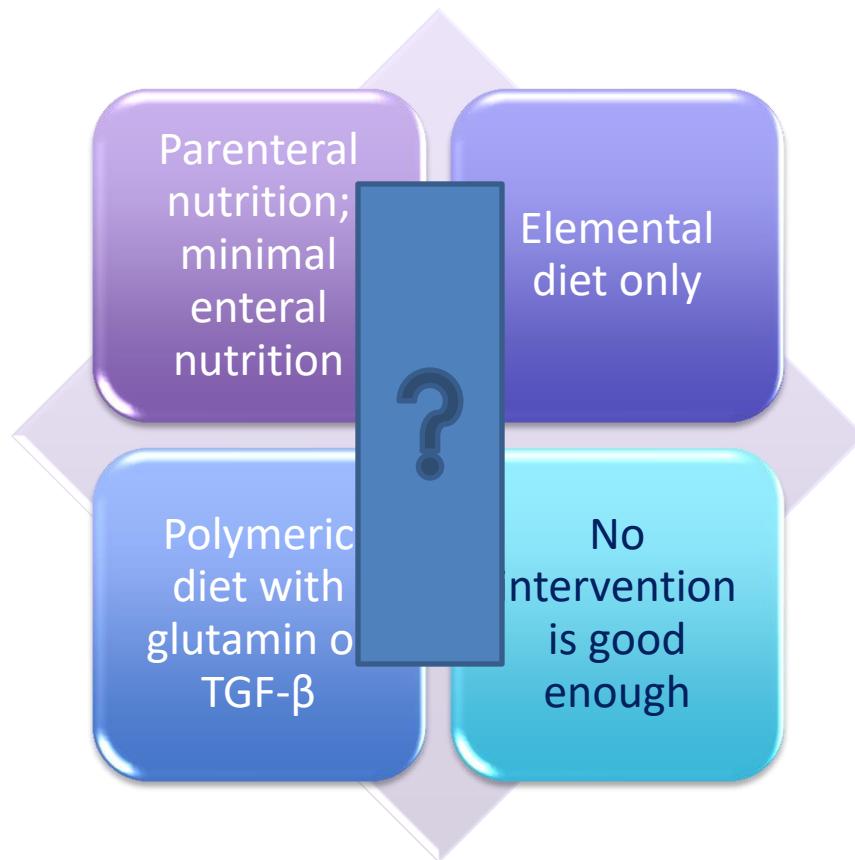
Malabsorption

- Lipid, electrolytes
- Medical Diagnosis: Crohn's disease (disease activity index > 20)

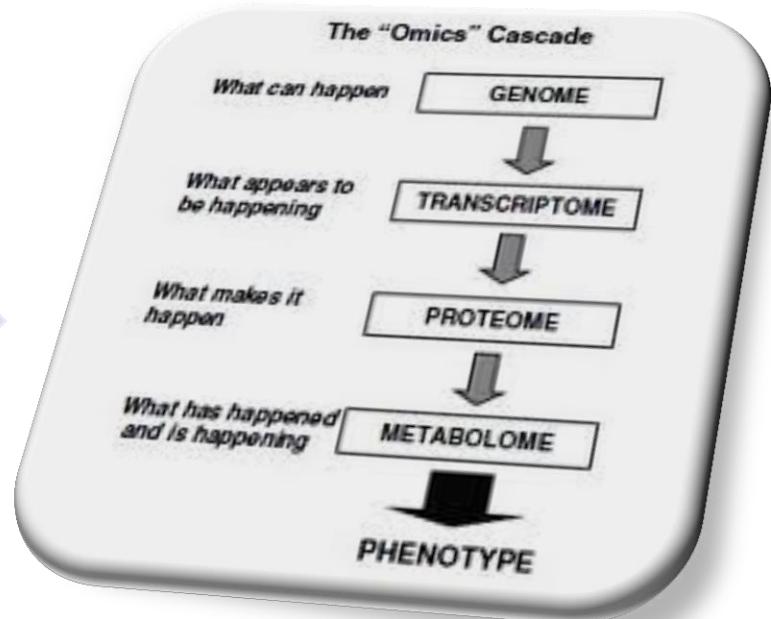


Clinical Dietitian Routine

Clinical significance of intervention?



Systems Biology





Variações das respostas às doenças

TIPO DE RESPOSTA METABÓLICA À INTERVENÇÃO NUTRICIONAL



Alguns respondem positivamente.



Alguns não respondem.



Alguns respondem negativamente.

Respondem devido às diferenças genéticas interagindo com o meio ambiente

Obesidade como exemplo...

Uma dieta rica em lipídios não define que o indivíduo será obeso!...

Alguns estudos indicam que o consumo médio de alimentos está ↓ mas a obesidade está ↑...

Será que a obesidade não está necessariamente associada a alta ingestão alimentar? (Blundell JE & Cooling J, 1999)

A escolha por alimentos ricos em gordura é um fenômeno biológico ou do meio ambiente? E como as variações genéticas interferem neste processo?



Tabela 9 - Análise descritiva da ingestão energética e porcentagem de macronutrientes da dieta de adolescentes atendidos no CMSCVL e divididos por grupo, de acordo com o estado nutricional

Variáveis*	Grupo 1	Grupo 2	Grupo 3
Energia (Kcal)	2226 (1083-5092)	2199 (1294-3747)	2179 (1174-5489)
Proteínas(% VE)**	17,2 (10,7-24,1)	17,5 (13,3-30,9)	18 (11,1-26,6)
Carboidratos (% VE)	45,4 (25,5-59,9)	43,6 (27,6-52,2)	43,6 (34-51,7)
Lipídios (% VE)	36,6 (20,1-53)	38,3 (31-48,3)	38,2 (26,7-47,8)

* p > 0,05; **VE = Valor Energético



Respostas variadas ao tratamento

Alguns estudos não encontram associação entre ingestão alimentar e obesidade

Alguns perdem peso!

Alguns não perdem peso!



Diferentes necessidades nutricionais?

Qual a contribuição das variações genéticas?

Interação gene-nutriente?

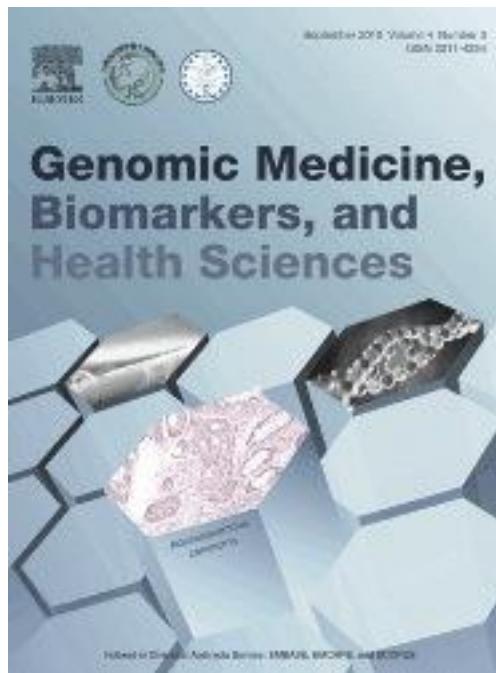


Bezerra IN & Sichieri
R. 2011
Int J Behavioral Nut
and Physical Activity

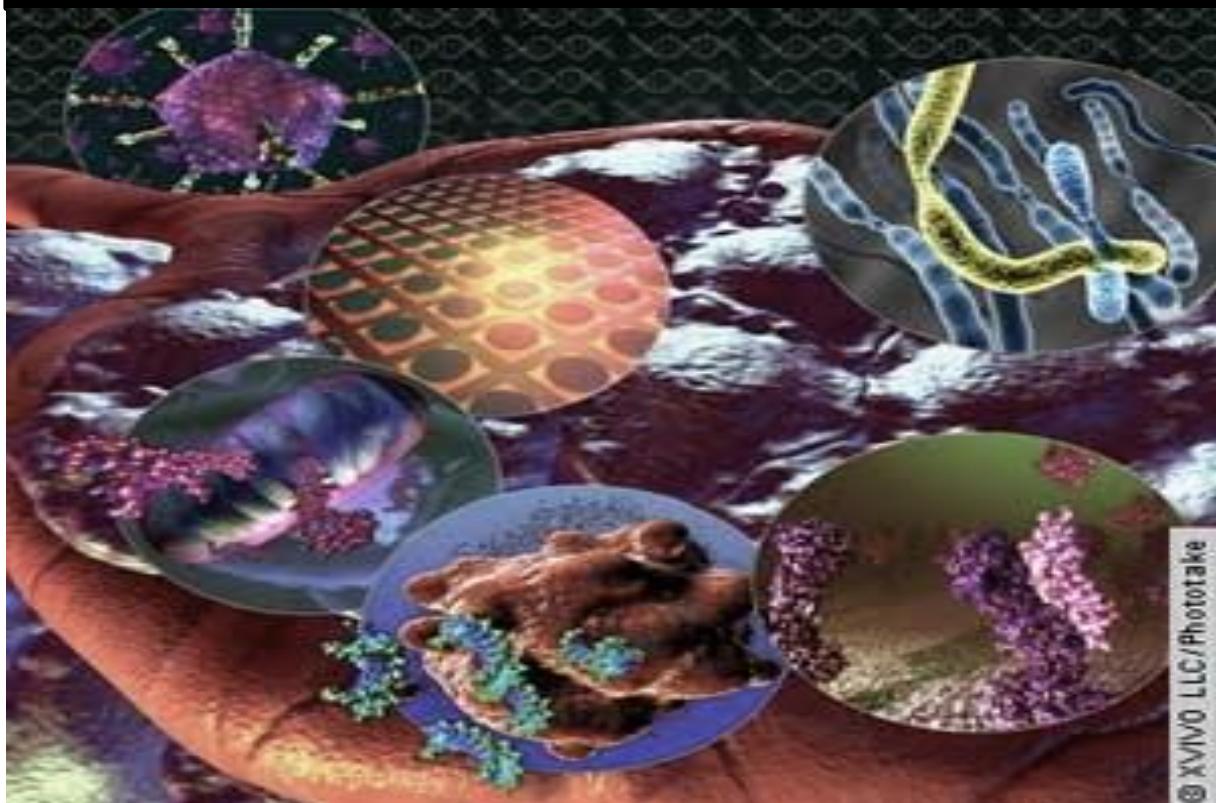




WIKIPEDIA
The Free Encyclopedia

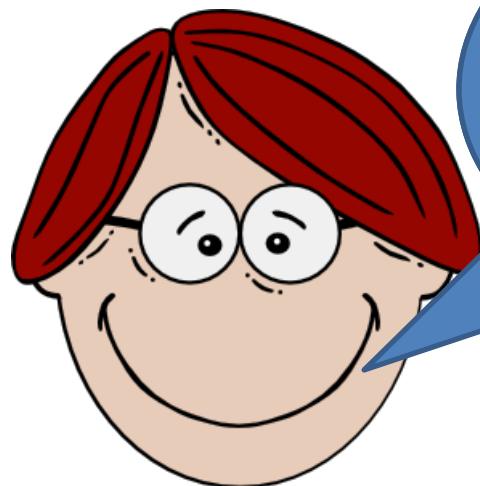


A **biomarker**, or **biological marker**, generally refers to a measured characteristic which may be used as an indicator of some biological state or condition.

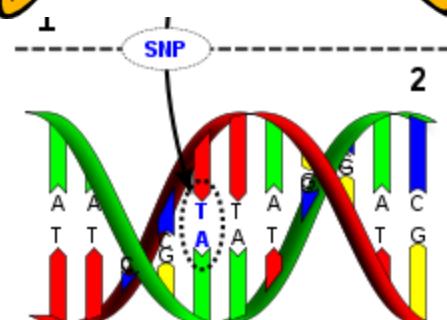
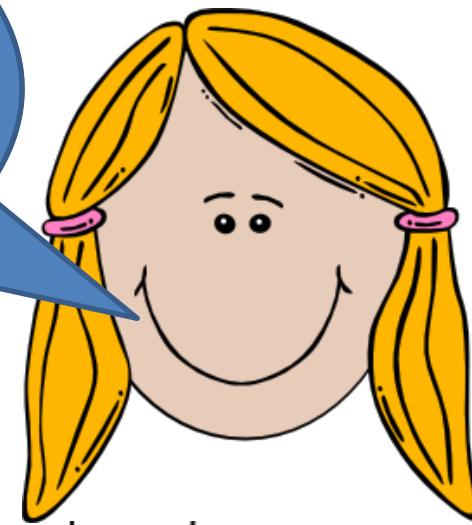
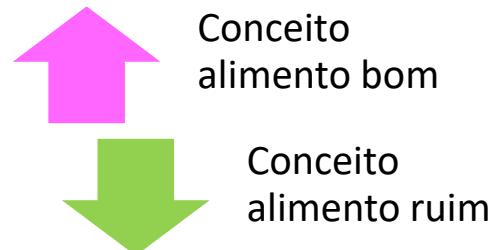
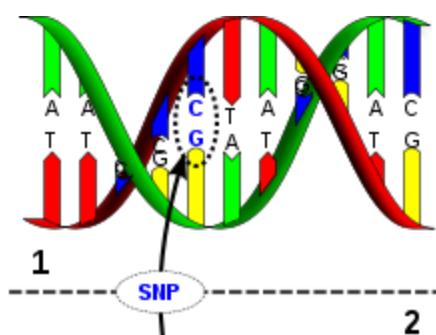


A **biomarker** can detect early stage of the development of a disease or indicate risk of a future disease.

Tendências da pesquisa sobre nutrição personalizada



Se o nosso genoma é o mesmo porquê os cientistas estão dizendo que temos diferenças genéticas? Se isso é verdade então podemos ter diferentes necessidades nutricionais!!!!



Rideout TC. 2011;
Lovegrove JA &
Gitau R. 2008



GENÔMICA DA NUTRIÇÃO NÃO É SIMPLES E ESTAMOS APENAS ENGATINHANDO...



Doutora, porquêigo tudo direitinho e meu LDL continua alto e
meu HDL continua baixo?

Se você tem um polimorfismo na APOA1 do tipo GG você só
terá ↑ HDL se PUFA < 4% VCT; agora se você tem
polimorfismo do tipo GA, seu HDL vai ↑ quando PUFA > 8%

Talvez não seja
tão simples
assim...

ESTUDAR UMA VARIAÇÃO GENÉTICA AJUDA?



Dieta pobre em
lipídios e colesterol é
boa para todos?

- Depende do polimorfismo da APOE

AJUDA MAS
NÃO É
SUFICIENTE
PARA TRADUZIR
A ADEQUADA
INFORMAÇÃO
PARA O
PACIENTE...

APOE3/E3

APOE4/E4

APOE4/E3



Uusitupa MIJ
et al.1992



Common genetic determinants of vitamin D insufficiency: a genome-wide association study

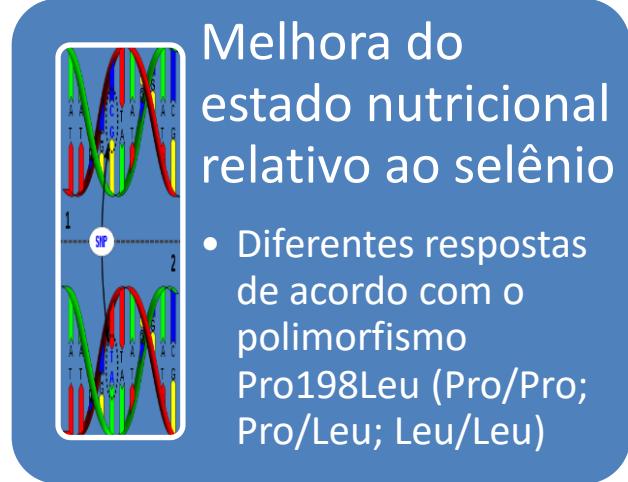
Thomas J. Wang e colaboradores
Lancet. 2010 July 17

Table 3

Genetic variants and risk of vitamin D insufficiency

	< 75 nmol/L		< 50 nmol/L	
	Odds ratio*	P-value	Odds ratio*	P-value
<u>Individual variants</u>				
GC (rs2282679)	1.63 (1.53-1.73)	3.5×10^{-50}	1.49 (1.40-1.59)	7.5×10^{-33}
DHCR7 (rs7944926)	1.21 (1.14-1.29)	4.1×10^{-10}	1.21 (1.14-1.29)	4.7×10^{-9}
CYP2R1 (rs10741657)	1.21 (1.45-1.29)	9.4×10^{-11}	1.06 (1.00-1.13)	0.06
<u>Genotype score</u>				
Quartile 1	1.0 (Referent)		1.0 (Referent)	AJUDA MAS
Quartile 2	1.29 (1.15-1.46)		1.10 (0.97-1.25)	NÃO É
Quartile 3	1.56 (1.39-1.75)		1.38 (1.22-1.57)	SUFICIENTE
Quartile 4	2.47 (2.20-2.78)		1.92 (1.70-2.16)	PARA TRADUZIR
P-for-trend	2.3×10^{-48}		1.0×10^{-26}	A ADEQUADA INFORMAÇÃO PARA O PACIENTE...

Gene da Glutationa Peroxidase-1 (GPx1)



Melhora do estado nutricional relativo ao selênio

- Diferentes respostas de acordo com o polimorfismo Pro198Leu (Pro/Pro; Pro/Leu; Leu/Leu)

37 obesas mórbidas

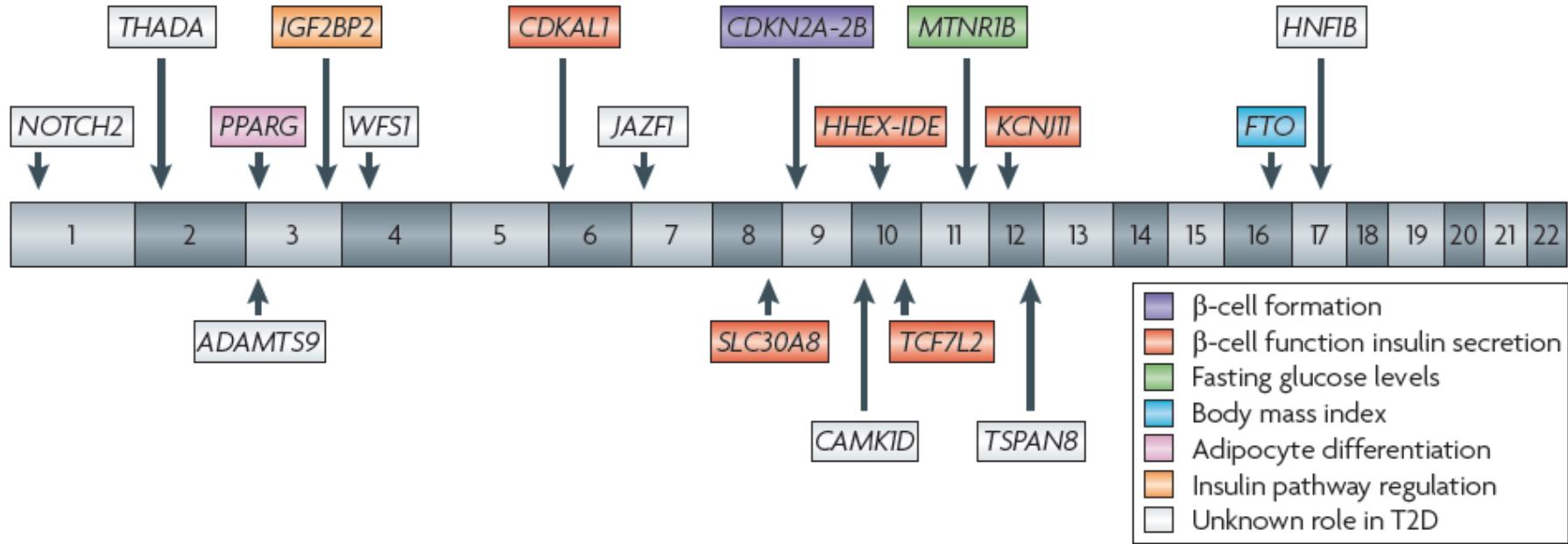
1 castanha durante 8 semanas (290 μ g de selênio por dia)

AJUDA MAS
NÃO É
SUFICIENTE
PARA TRADUZIR
A ADEQUADA
INFORMAÇÃO
PARA O
PACIENTE...



Cominetti C
et al. 2011
Nutrition

T2DM Genes (GWAS)



Tag SNP for a LD bin *statistically associated* with trait

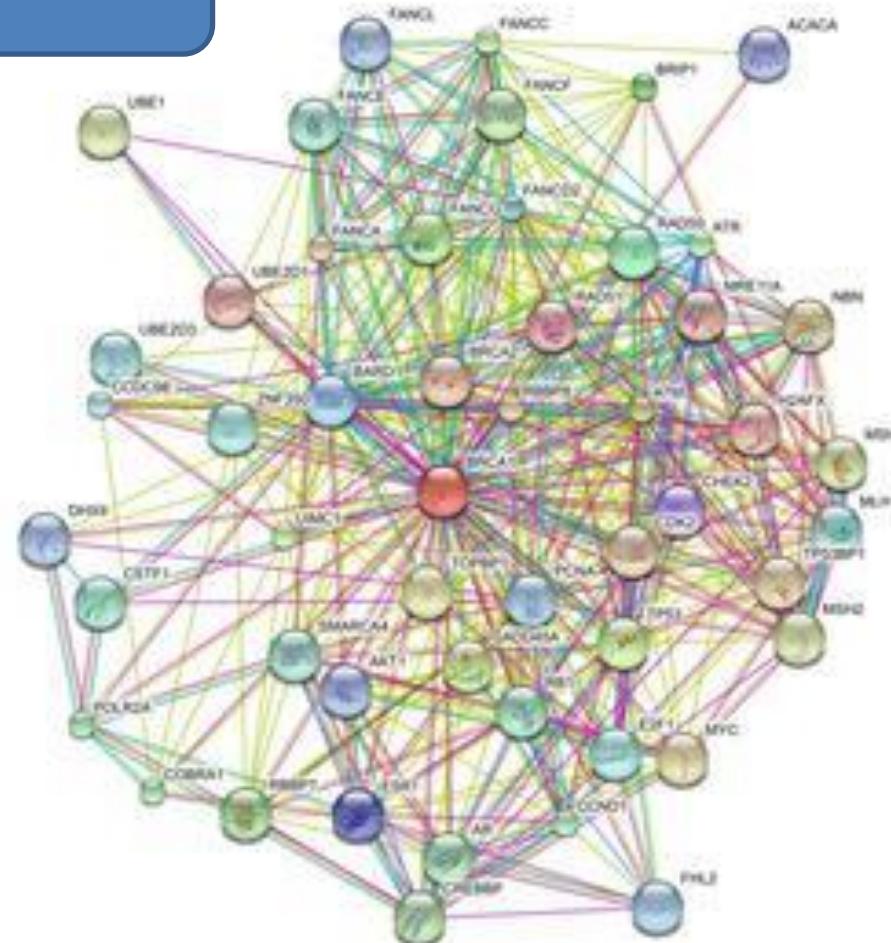
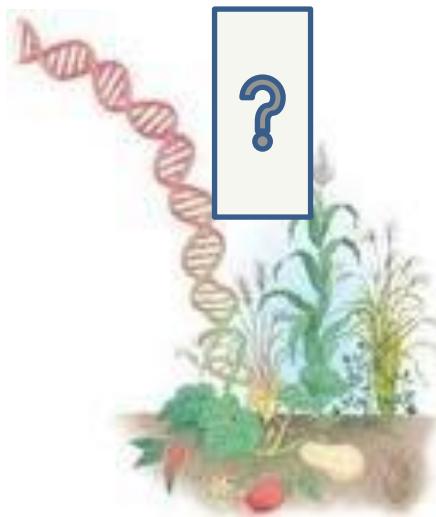
Collectively “explains” ~0.5% - 2.4% of individual’s risk

~96% of participants were Europeans

1 interação gene-nutriente no contexto de Sistemas Biológicos?



Complexa e delicada rede de interações que desafia a simplicidade e torna a orientação nutricional um desafio

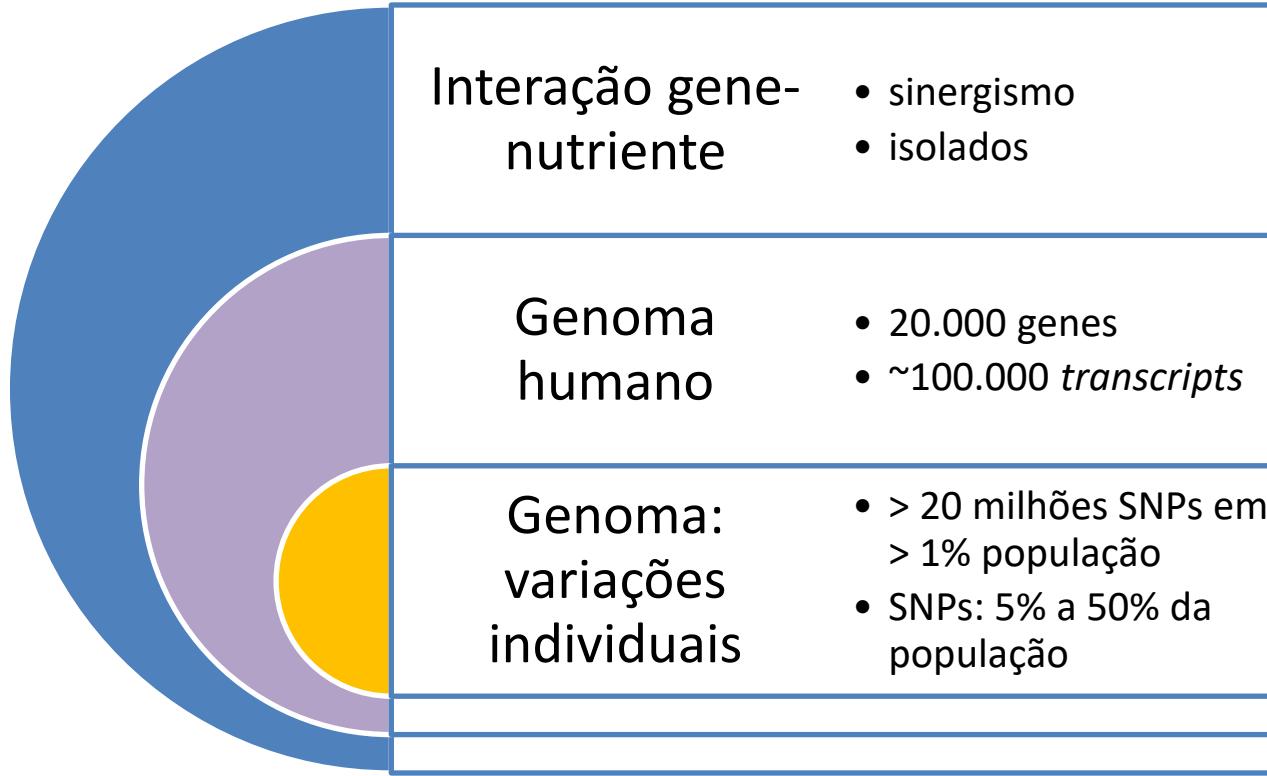


Many nutrient-nutrient interactions exist and are fundamental part of the growth and development process

Nutritional Systems

Focusing on a single nutritional cause obscured the broader nutritional phenotype that exists in a person

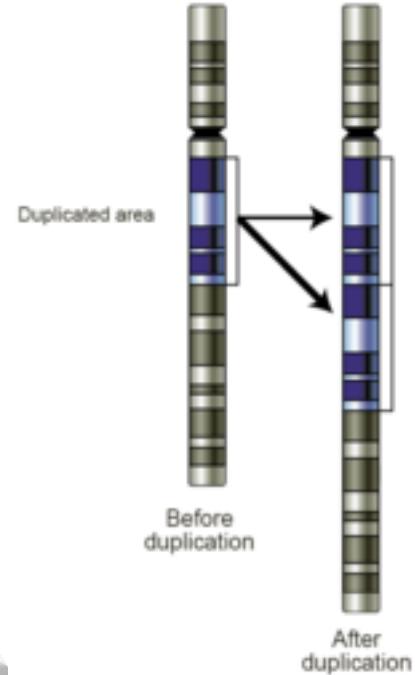
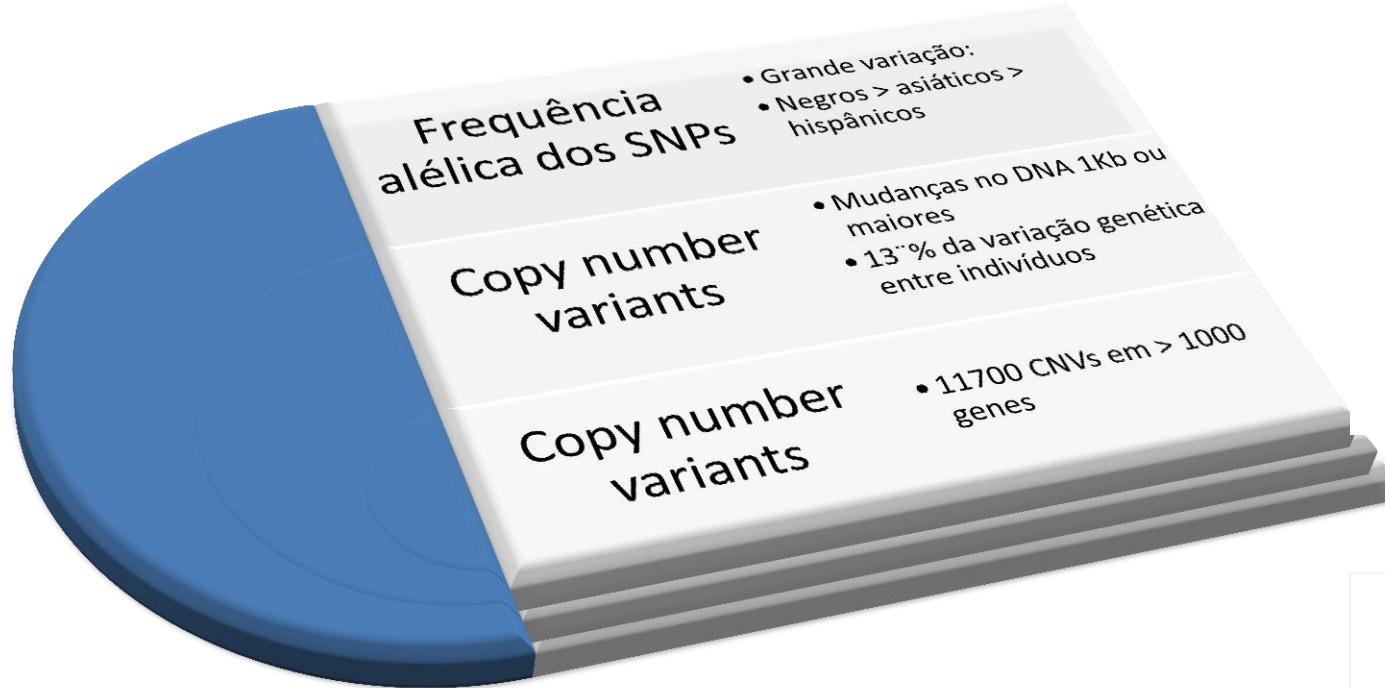




McVean G
et al. 2005

Personalized Nutrition Research in the Era of Nutrigenomic



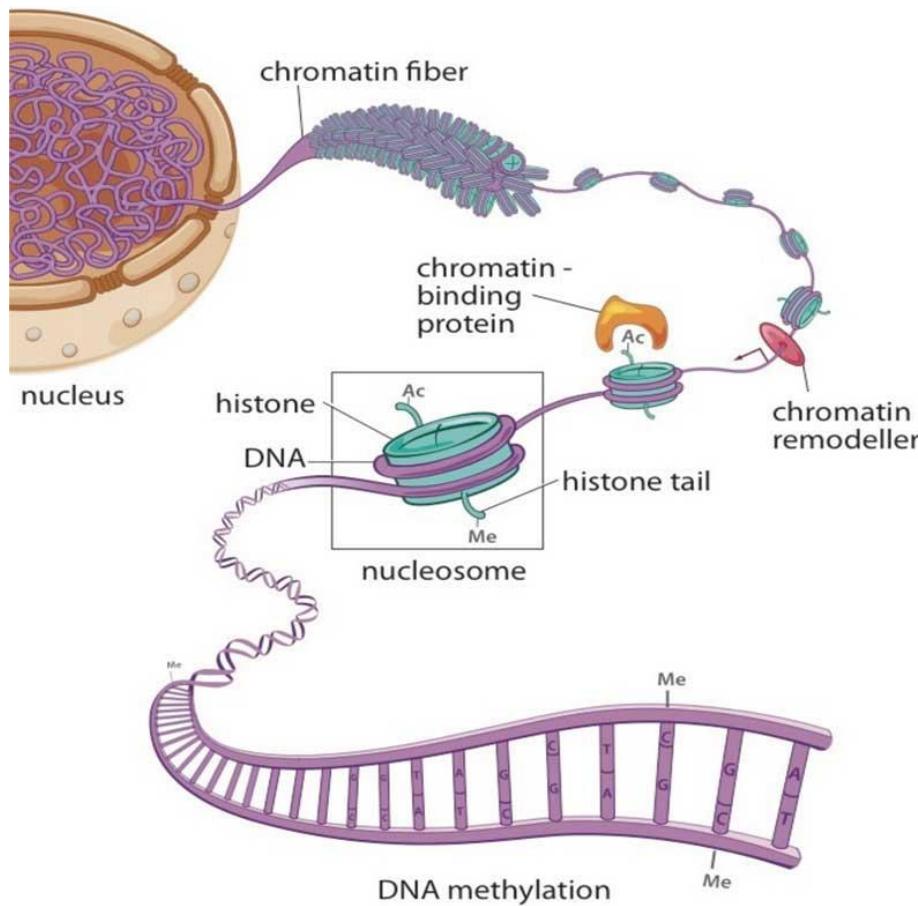


This gene duplication has created a copy-number variation. The chromosome now has two copies of this section of DNA, rather than one.



Varma V et al.
2010; Myles S et
al. 2008
Simopoulos AP. 2010

Metilação de DNA

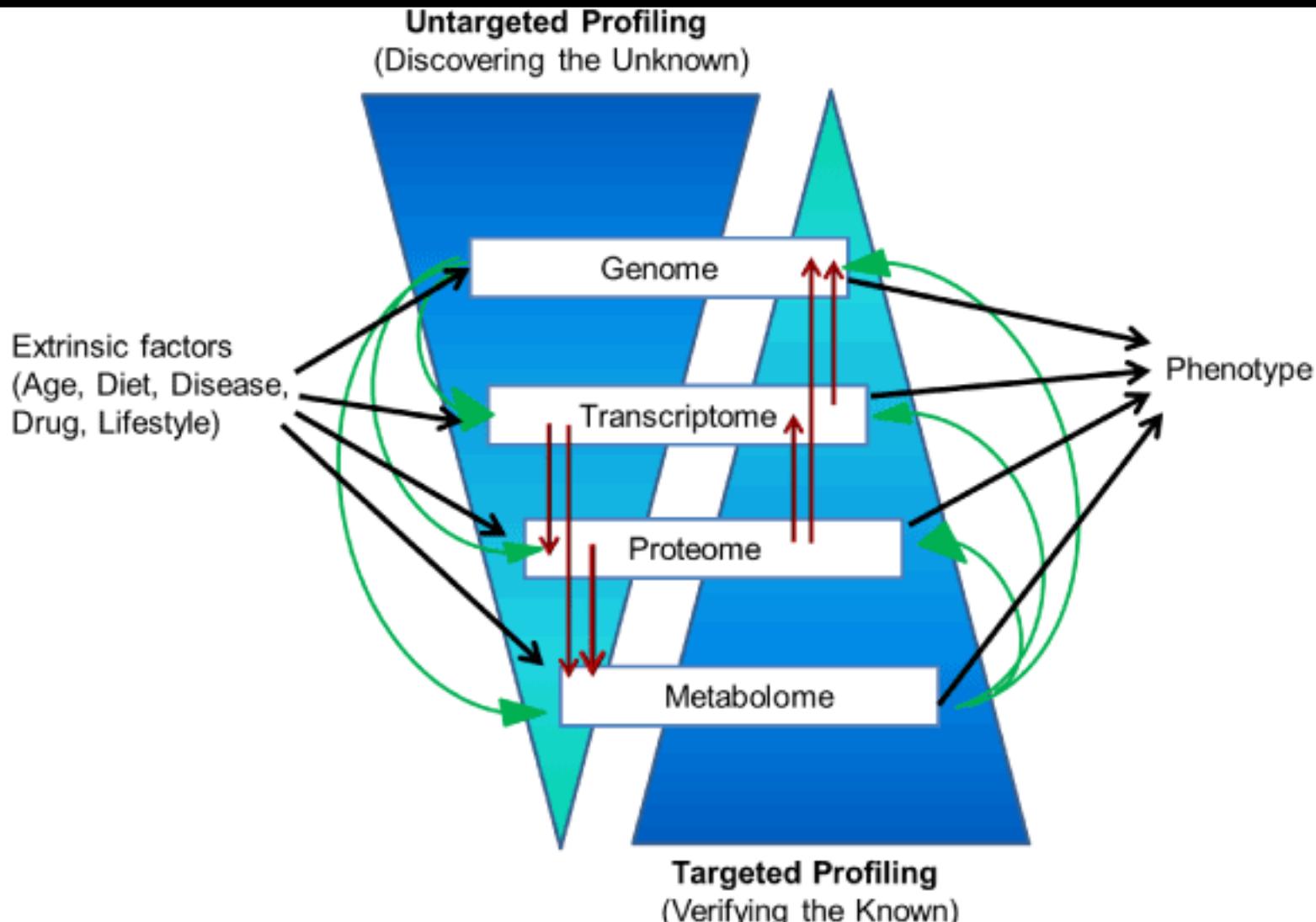


Nutriente altera a estrutura do DNA mas não a sequencia de nucleotídeos



Zeisel SH. 2007

Ciências ômicas se referem a categorias de biomarcadores moleculares sendo estudados, mensurados ou descritos.



Fenótipo metabólico é o termo para um conjunto de metabólitos cuja abundância em fluidos biológicos reflete o estado de saúde/doença de um indivíduo. É preciso construir e validar ferramentas que forneçam mais informações sobre os processos que integram

Compostos bioativos são constituintes “extra-nutricionais” que ocorrem em pequenas quantidades nos alimentos.

É preciso entender a complexidade das interações entre os componentes da dieta e o genoma, a proteômica e a metabolômica para que possamos entender as diferentes respostas à mesma intervenção

Technologies All models – SYSTEMS BIOLOGY

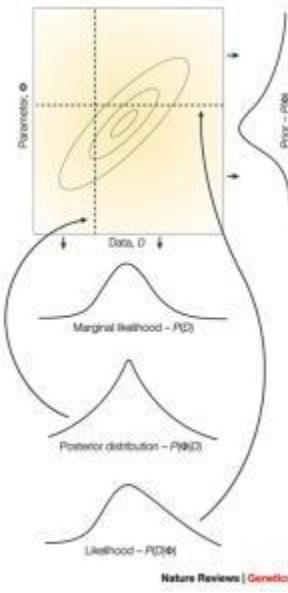
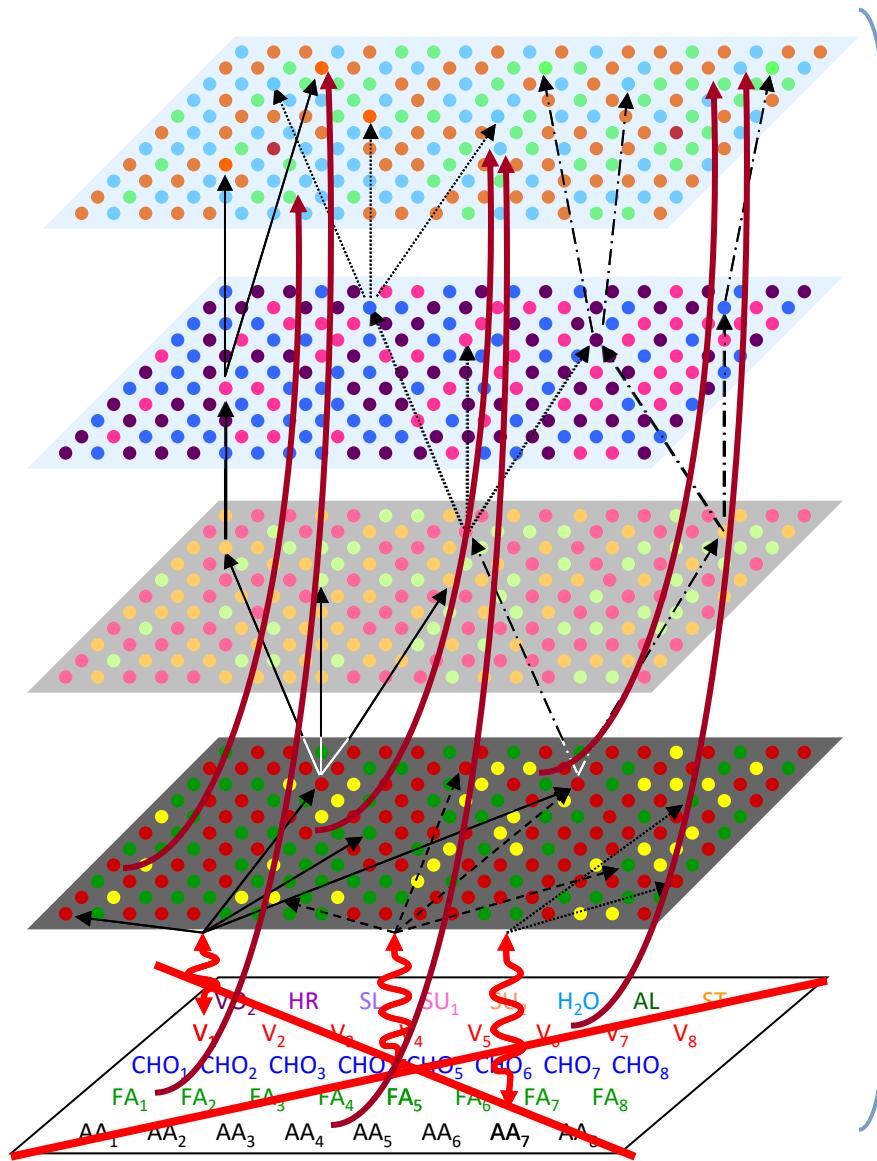
Clinical
& Metabolomics

Proteomics

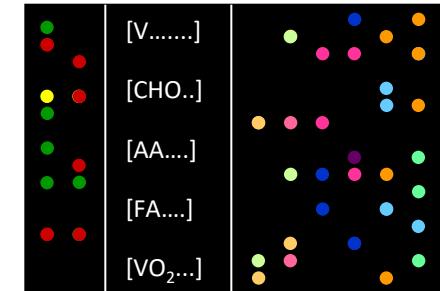
Transcriptomics

Genomics
& Epigenomics

Diet & Lifestyle



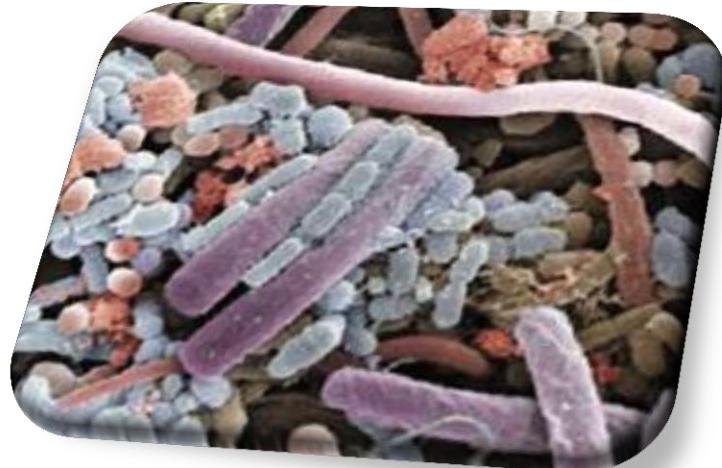
$$\int \sum (G \times E) \quad | \quad \text{Group}$$



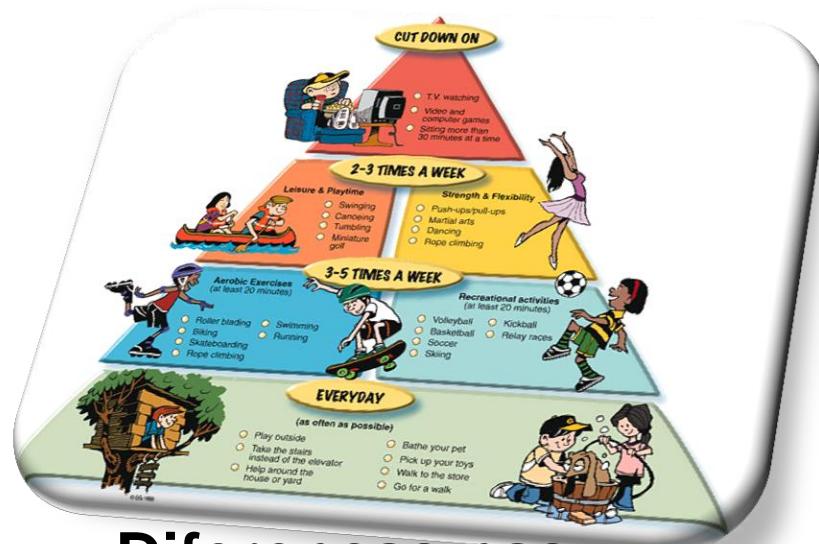
DESAFIOS AO ANALISAR AS INTERAÇÕES GENE-NUTRIENTE



Heterogeneidade genética
e as interações gene-gene



Microbiota

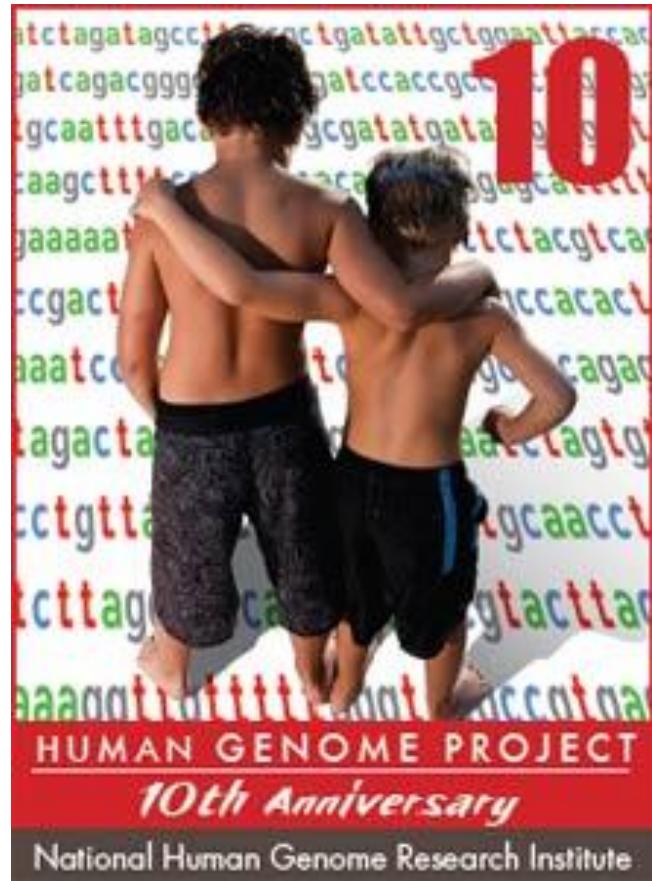


Diferenças nas



Meio ambiente: Diferenças nos
Padrões Dietéticos e Interação

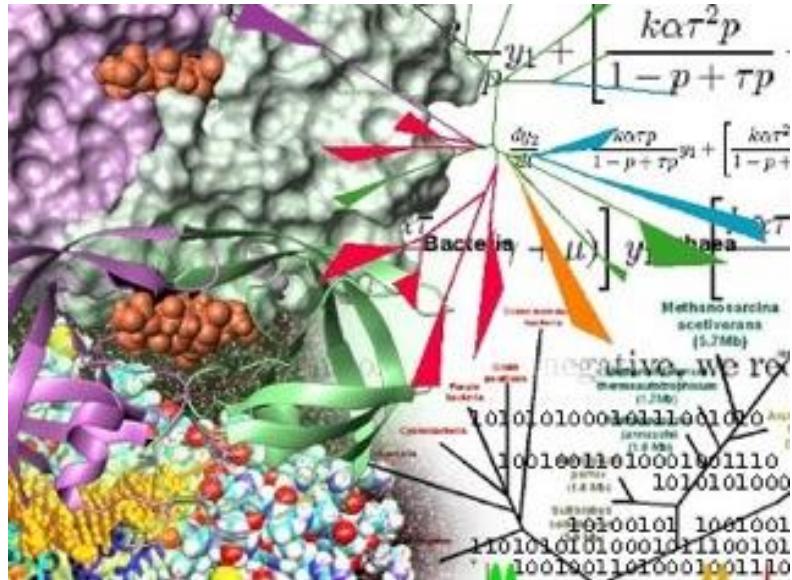
Approximately 228,000 human genomes have been sequenced by the start of 2015 and estimates are that 1.6 million genomes were sequenced in 2017



Each new genome sequence confirms that individuals are genetically unique and hence will have unique responses to environmental factors including diet, lifestyle, and medicines

Algorítmo e Sistemas Biológicos

Permite identificar padrões, agrupar genes relacionados que regulam as vias metabólicas e agrupar vias metabólicas relacionadas

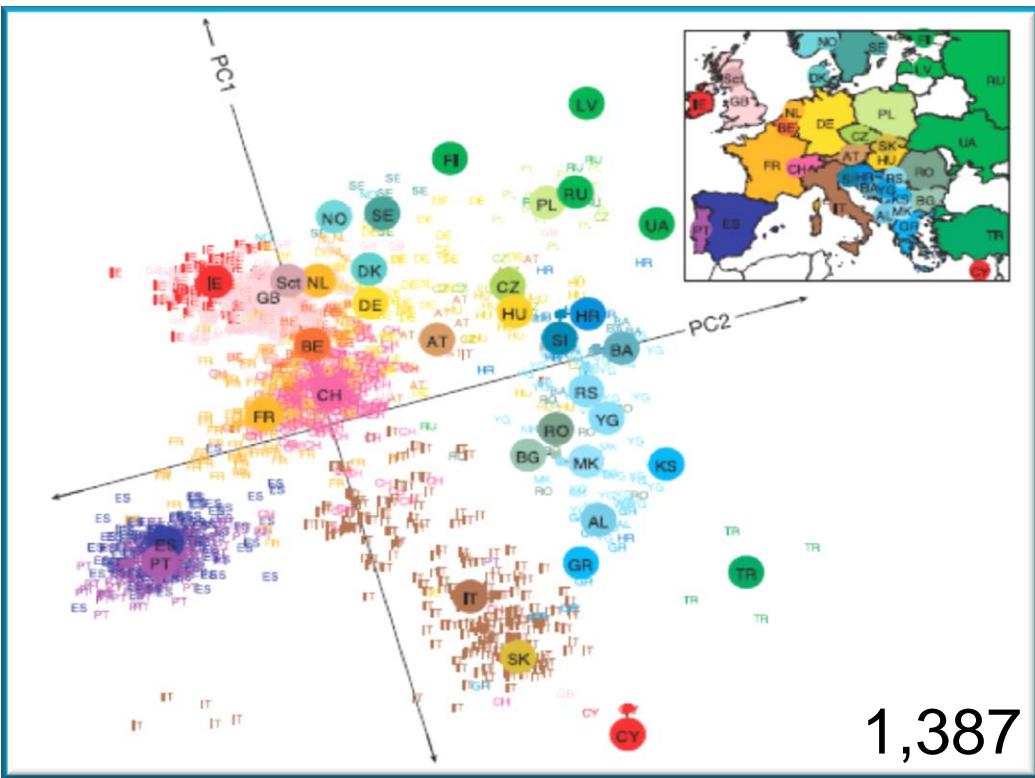


- (1) Baseiam-se em uma codificação do conjunto das soluções possíveis;
- (2) os resultados são apresentados como uma população de soluções e não como uma solução única;
- (3) não necessitam de nenhum conhecimento derivado do problema, apenas de uma forma de avaliação do resultado;
- (4) usam transições probabilísticas e não regras determinísticas

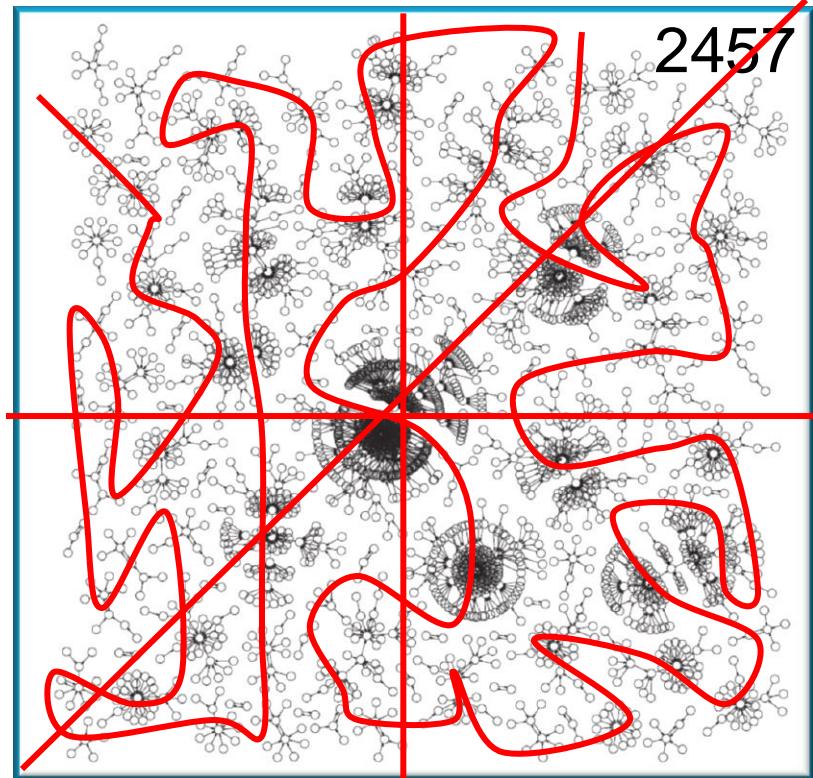
Em genômica da Nutrição é
difícil definir um grupo
controle



Facts & Challenges Genetic Diversity



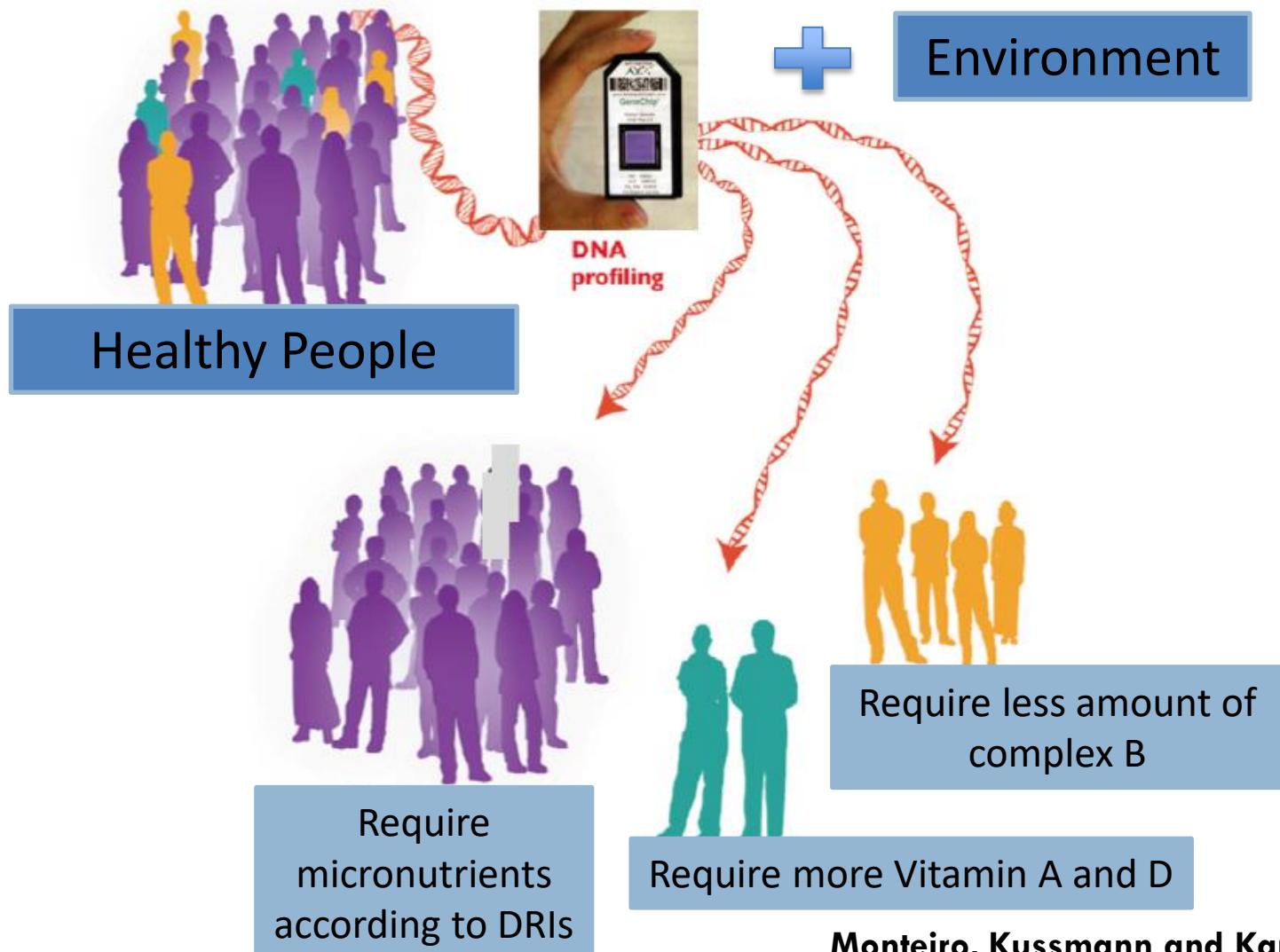
Novembre et al *Nature* 456, 98 (2008)



Lu et al *EJHG* 17, 967 (2009)

HOW TO SEPARATE CASES AND CONTROLS?

The conceptual basis of nutritional genomics is inter-individual variability in nutrient requirements

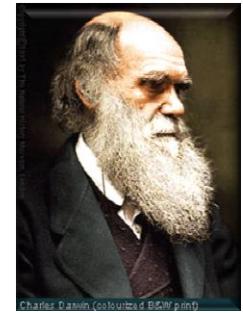


Basis of Nutrigenomics

A different effect of a *genotype* on disease
in persons with different *environmental* exposures



Genotype X Environment Interactions



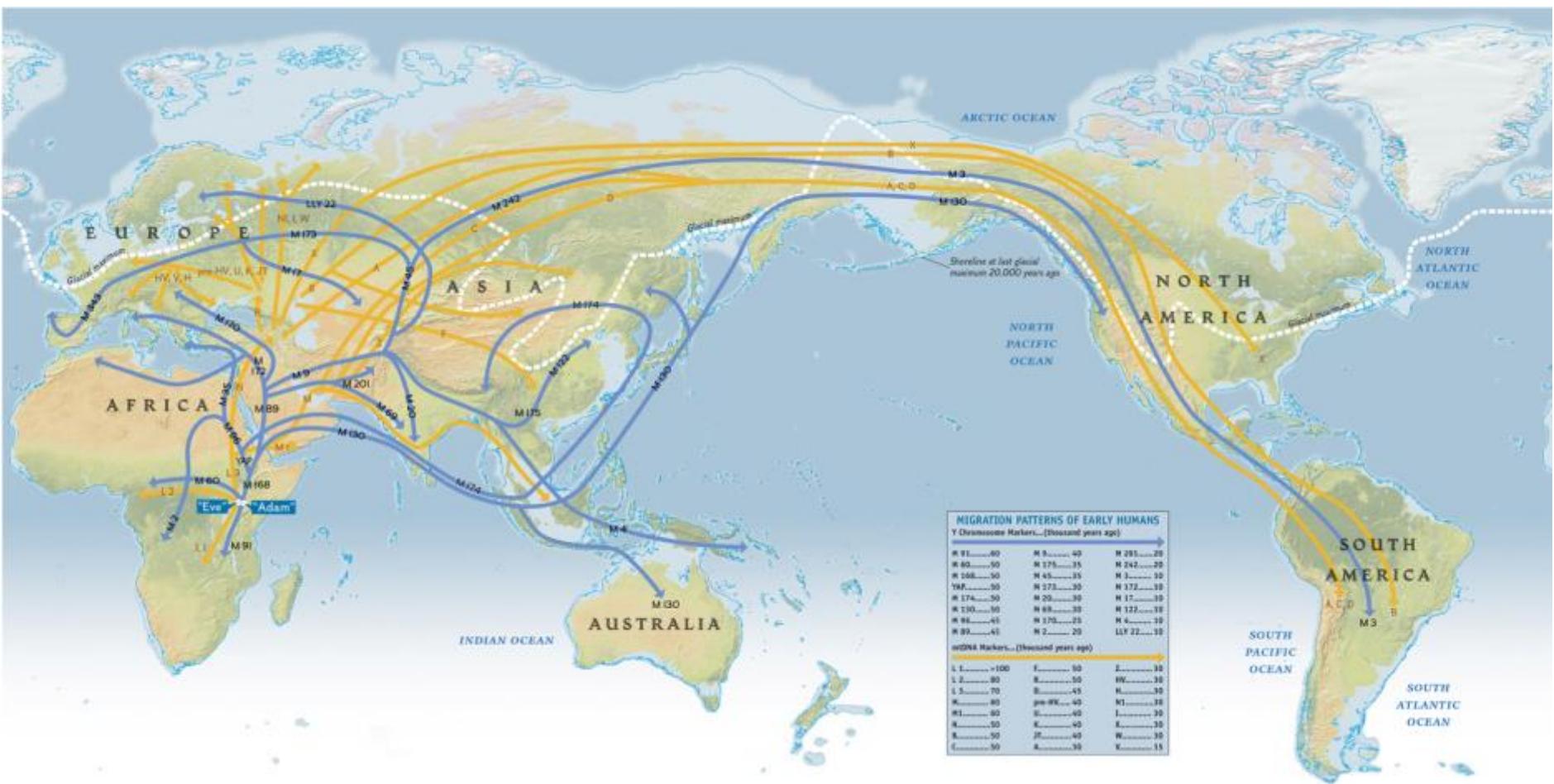
A different effect of an *environmental* exposure on
disease risk in persons with different *genotypes*

Ottman, *Prev. Med* 25, 764 (1996)

Statistical Parlance

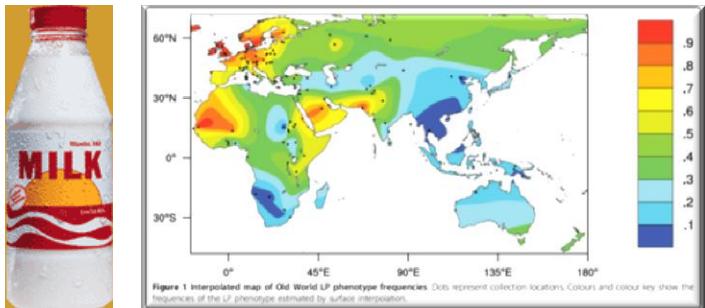
The *main effect(s)* may be
genotype x environment interaction(s)
for chronic diseases and modifying effects

Human Migrations - ancestry

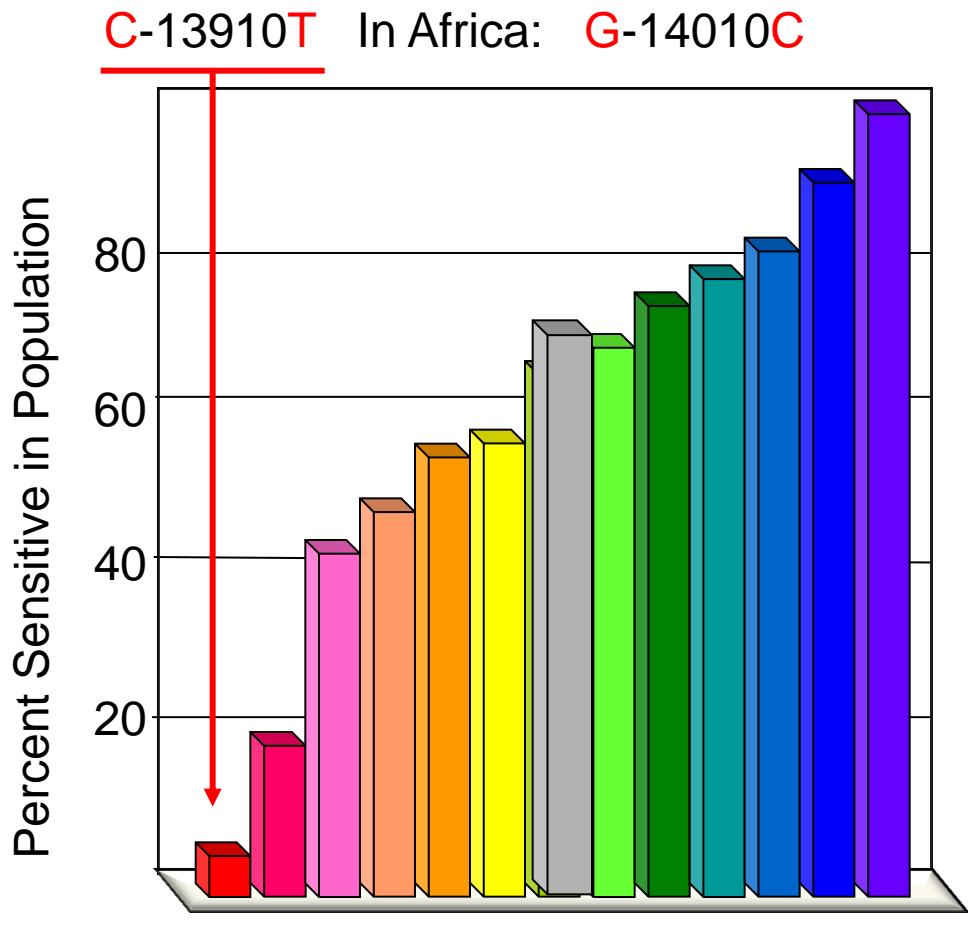


Hypolactasia

N. European Indian children
Afr American kids Indian adults
Mex American - adult Cretans
Cypriots N. American Jews
Mexicans - rural SE Asians
Eskimo Afr American - adult
Asian Americans

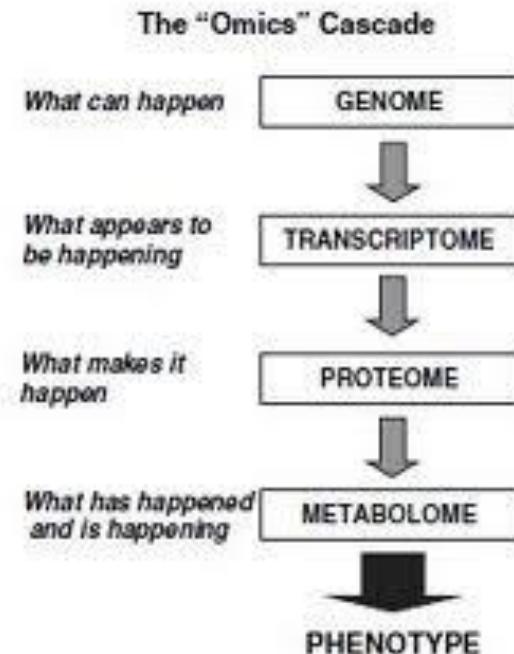
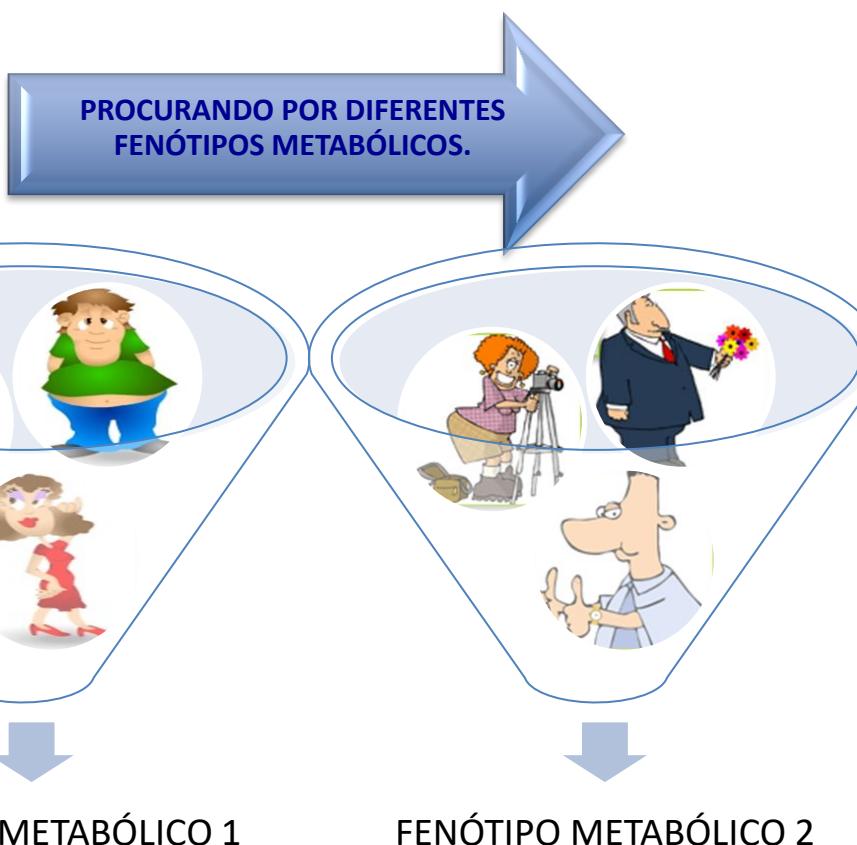


Itan et al. BMC Evolutionary Biology 2010, 10:36
<http://www.biomedcentral.com/1471-2148/10/36>

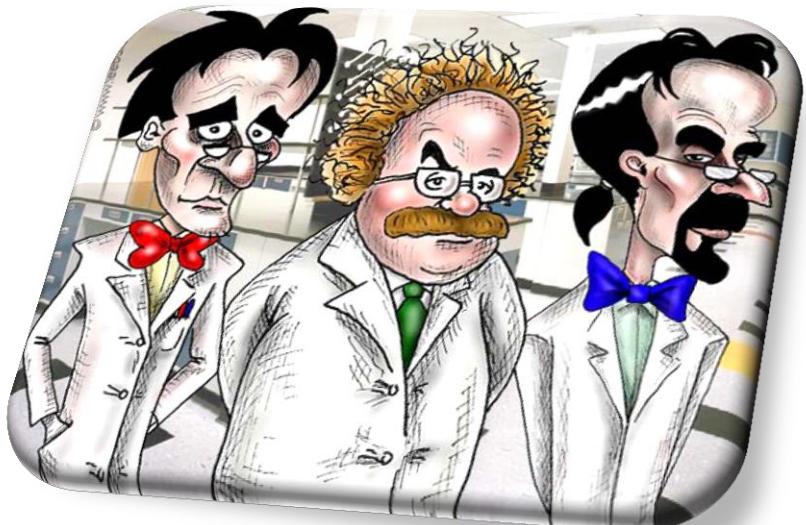


Kaput and Rodriguez, *Physiological Genomics* 16, 166 (2004)

COMO PODEMOS MEDIR A MANEIRA COMO ELES RESPONDEM?



Vamos padronizar
nossos protocolos de
pesquisa em diferentes
populações mantendo
a idéia original de
procurar por diferentes
FENÓTIPOS
METABÓLICOS



N-of-1 Trials in the Medical Literature

A Systematic Review

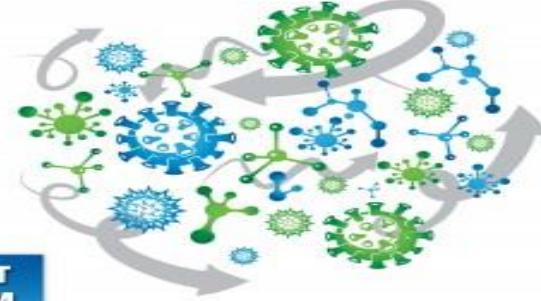
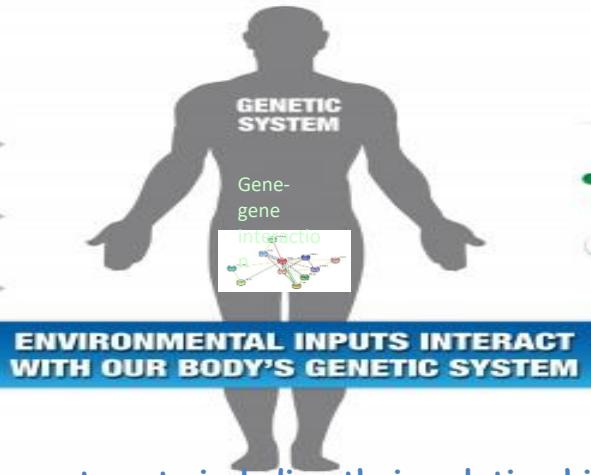
Nicole B. Gabler, PhD, MHA, Naihua Duan, PhD, †‡
Sunita Vohra, MD, FRCPC, MSc,§ and Richard L. Kravitz, MD, MSPH||*

Precisamos de mais estudos que considerem a resposta do INDIVÍDUO e, então, o classifique em grupos metabólicos semelhantes.

Os tradicionais ensaios clínicos randomizados resultam em uma política de “um tamanho serve para todos” em que o mesmo tratamento é aplicado a grupos heterogêniost.



ENVIRONMENTAL INPUTS
Exposures, Nutrition, Lifestyle



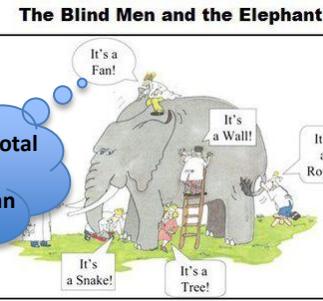
METABOLIC RESPONSE
Cancer Susceptibility Risk Factors and Other Health Outcomes

Systems thinking = a context in which components act, including their relationships and interactions in a non-static way

Prevent NCDs

Nutritional Systems Biology

What We Know About Diet, Genes, and Phenotype: Is There Potential for Translation?



Omics Technologies
(genomics,
transcriptomics,
proteomics,
metabolomics,
bioinformatics)

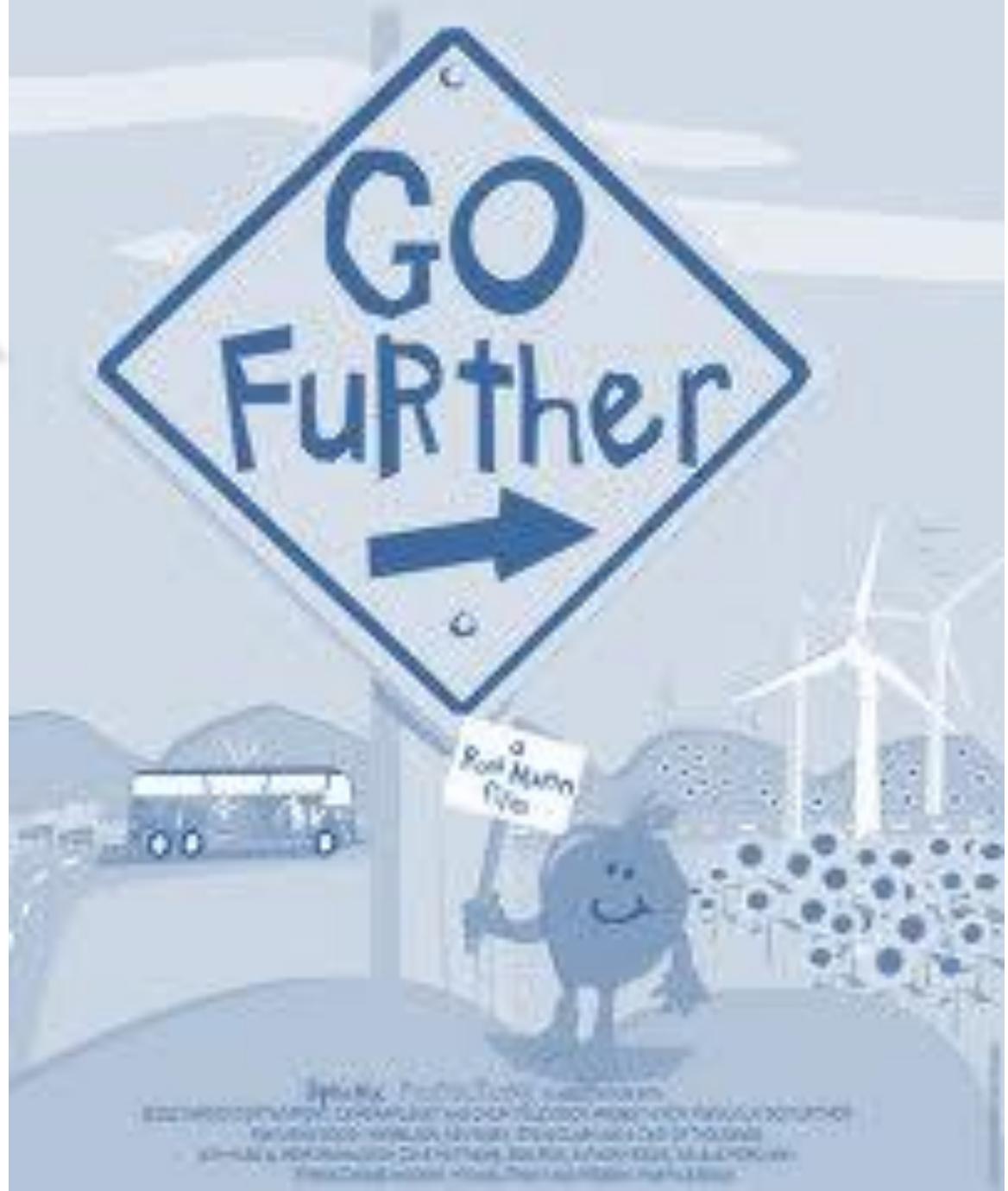
To integrate all aspects of metabolism and gene response to nutrients

To generate knowledge about the normal range of metabolism

New biomarkers and metabolic profiles to characterize predisease phenotypes

Dietary recommendations customized at a sub-population level

Procurando por grupos metabólicos

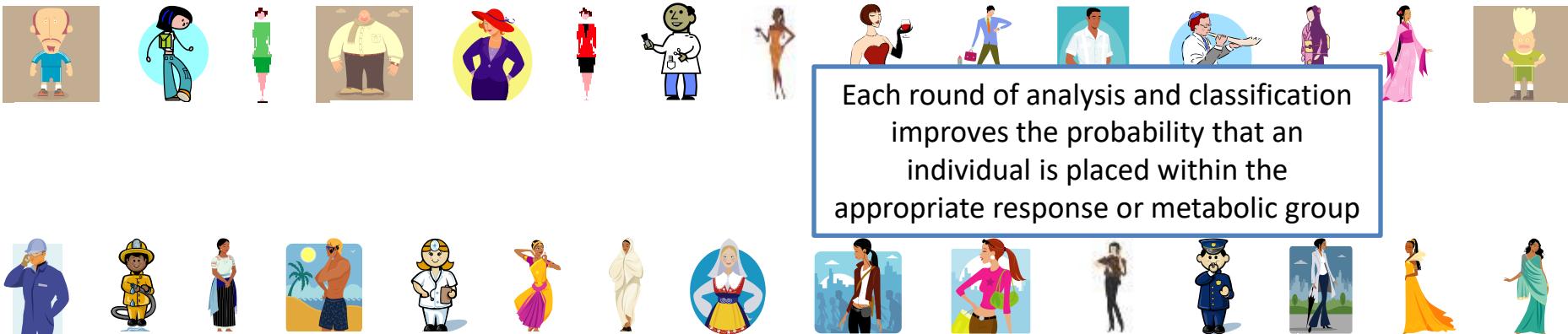




Como fazemos
esse tipo de
pesquisa usando
as ferramentas
ômicas?

Experimental Design Concept n-of-1 to group level

N-of-1 trial = Detailed intervention study of one individual over time and in response to environment



Each round of analysis and classification improves the probability that an individual is placed within the appropriate response or metabolic group

Classification Algorithms

Nutritional status; Physical activity; Social, economic and behavior status; Genome, proteome, metabolome

Phillips County Arkansas: Marvell and Elaine Obesity Prevention Summer Day Camp: USDA + FDA



Summer Day Camp
at the Boys, Girls,
and Adults
Community
Development
Center



Blood (genotyping & metabolite analyses)

- @ beginning
- @ the end (5 weeks)
- @ one month following the end of summer camp



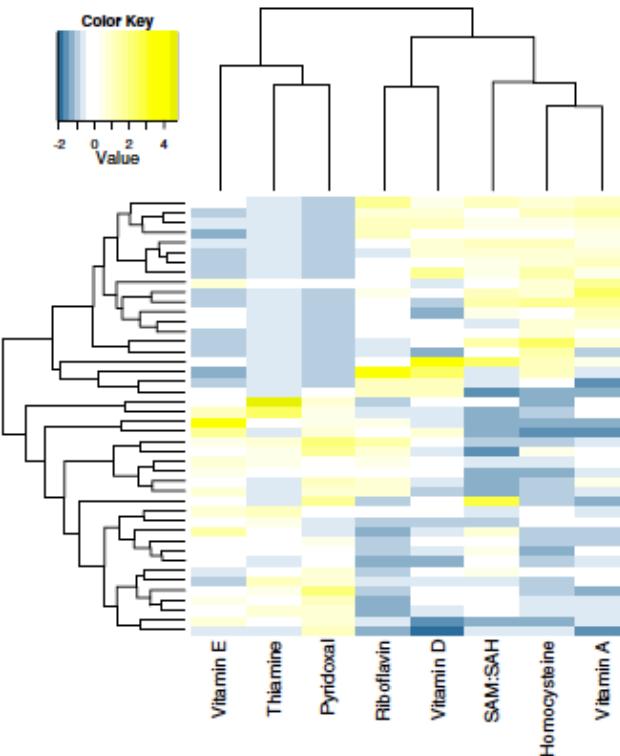
Breakfast, lunch, snack (Lowfat milk , fruits, vegetables)

- Three 24h recall and Health Eating Index
- Anthropometry

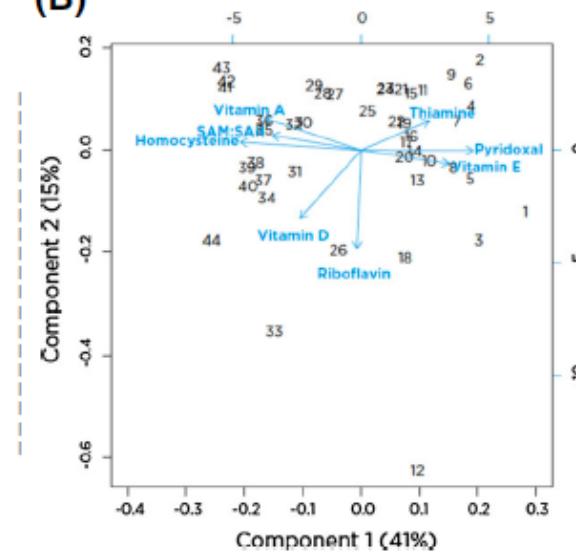
This study did not use a case-control design (105 individuals)
6 – 14 years old – 42% overweight

Individuals (represented in rows) with higher SAM/SAH tended to have higher plasma levels of fat-soluble vitamins A and D and medium or low plasma levels of vitamin E, thiamine, and pyridoxal. Individuals with low SAM/SAH tended to have the opposite patterns of these metabolites

(A)



(B)



(C)

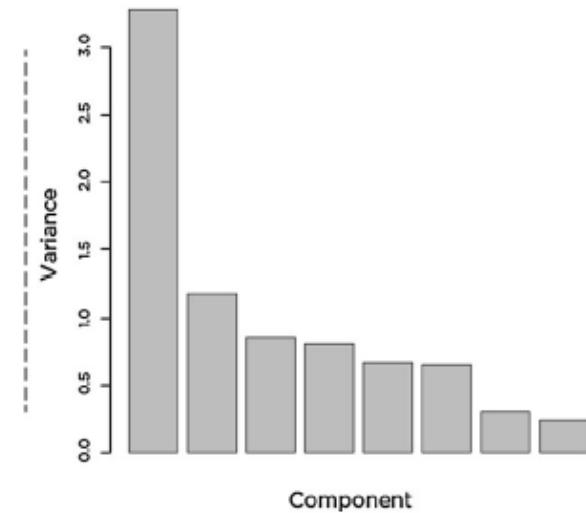
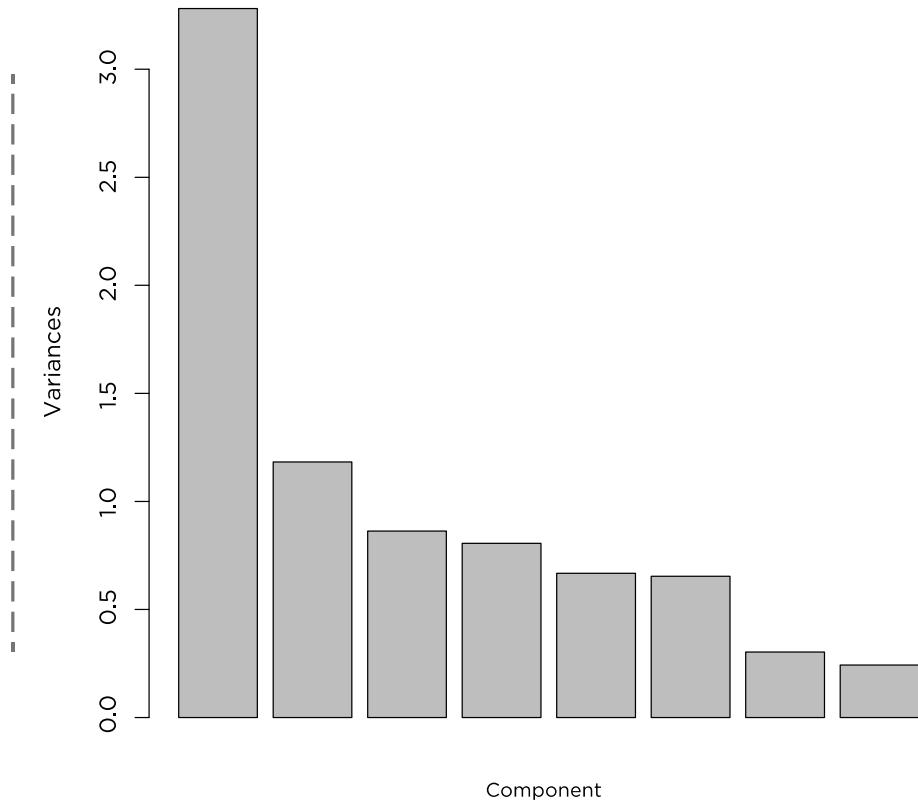
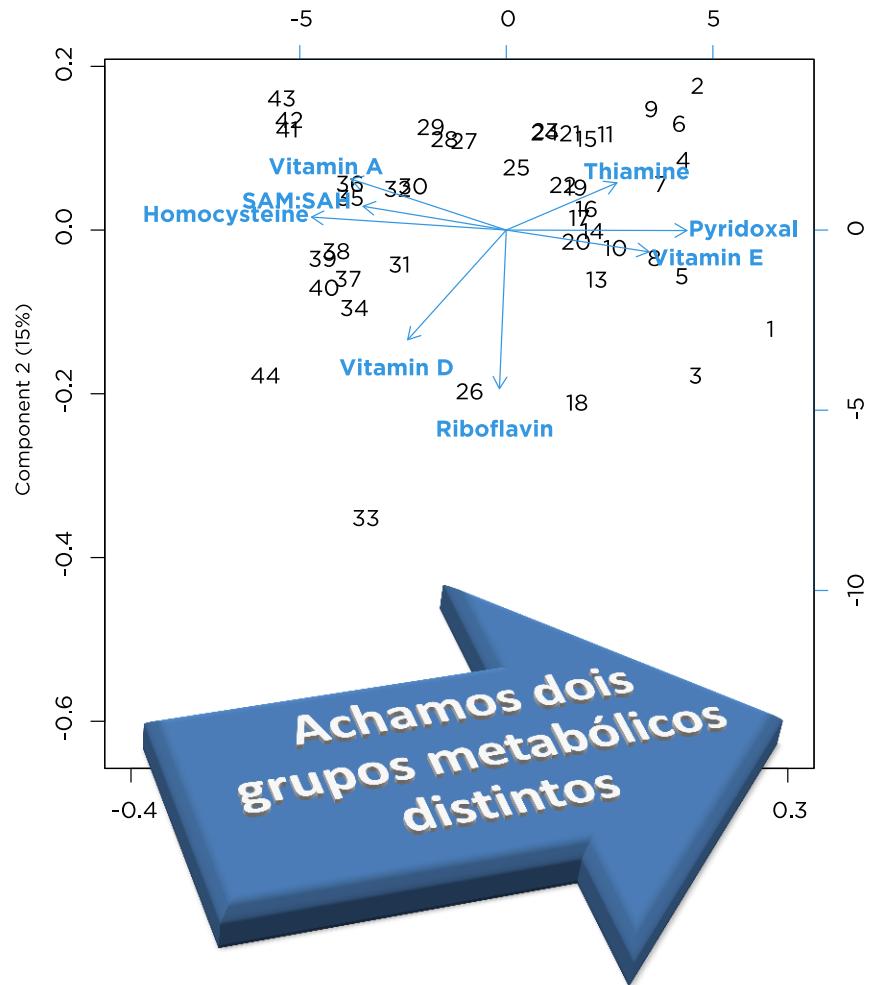


Fig. 1 Metabolite-level heat map and principal component analysis of vitamin levels. **a** Metabolite heat map where individuals are represented in the *rows*, and mean value of metabolite levels from three blood samplings is in the *columns*. **b** Principal component

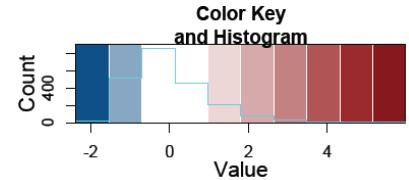
analysis of mean values of vitamin or metabolites. *Numbers* indicate values for individuals (c). Variances in each principal component (see “Materials and methods” section for details)

MICRONUTRIENT PROFILE - PCA

Plasma Metabolites



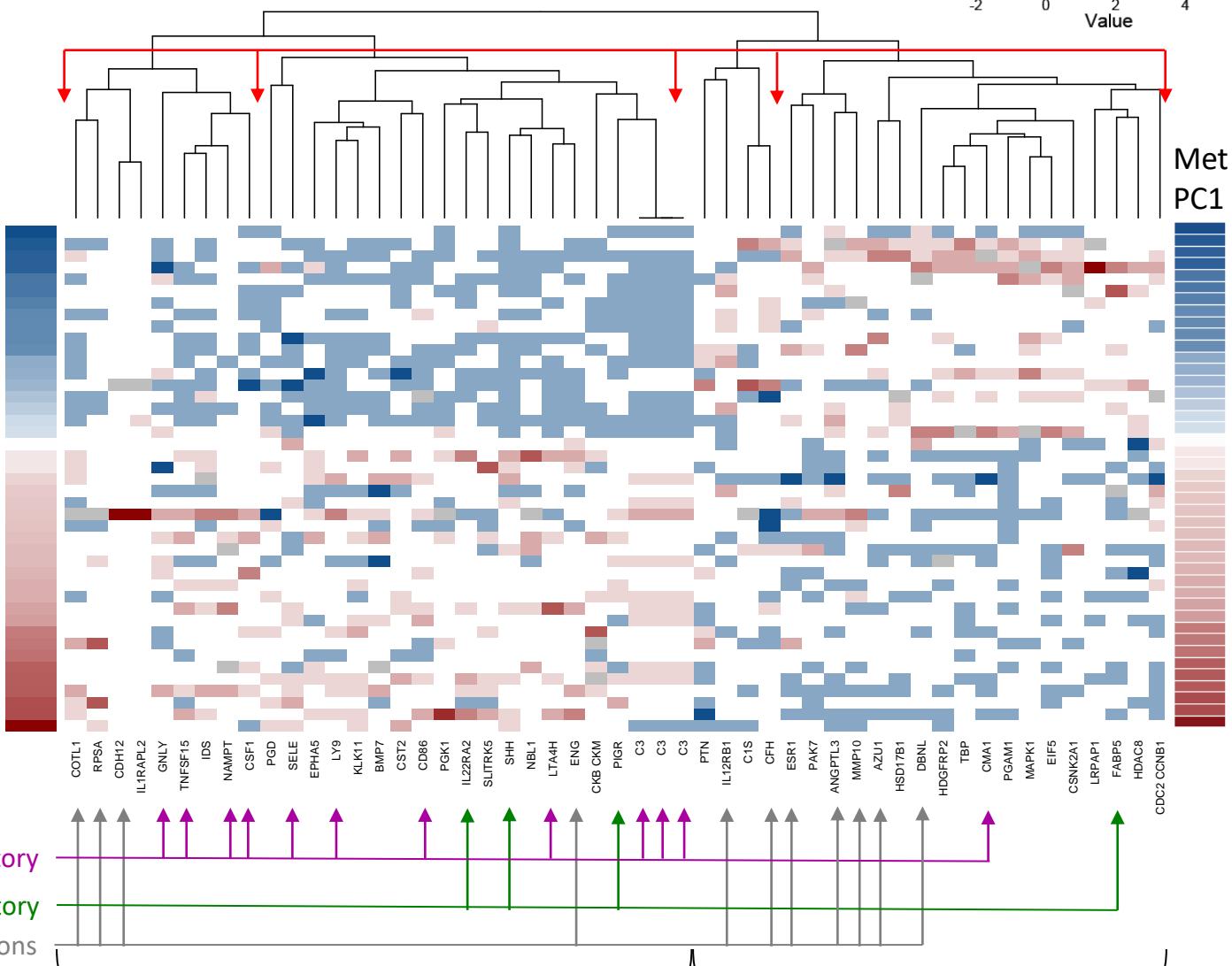
Proteomic data showed 51 proteins significantly associated with MET_PC1 variable



Functional analysis of branches

Vitamin A
SAM:SAH
Homocysteine

Pyridoxal
Thiamine
Vitamin E



24/27 = 88.9%

3/27 = 11.1%

5/12 = 41.6%

7/12 = 58.4%

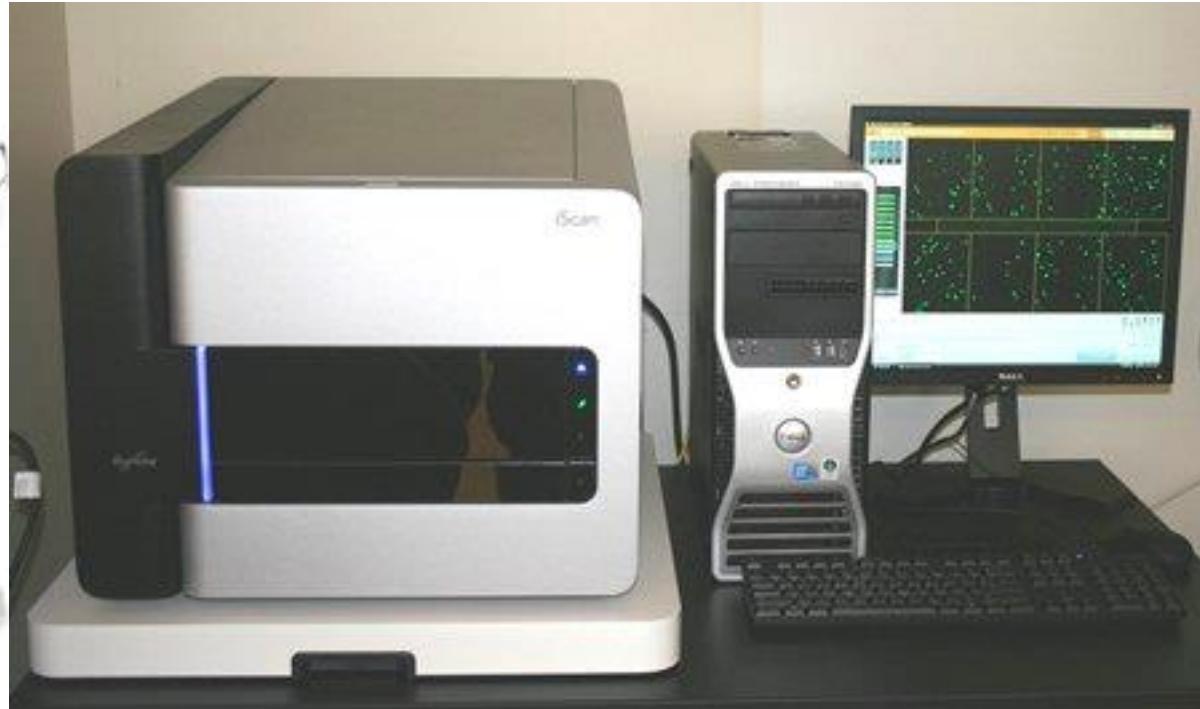
What are the SNPs and genes related to those 2 metabolic groups?

RAW SNP
data

GENOTYPING

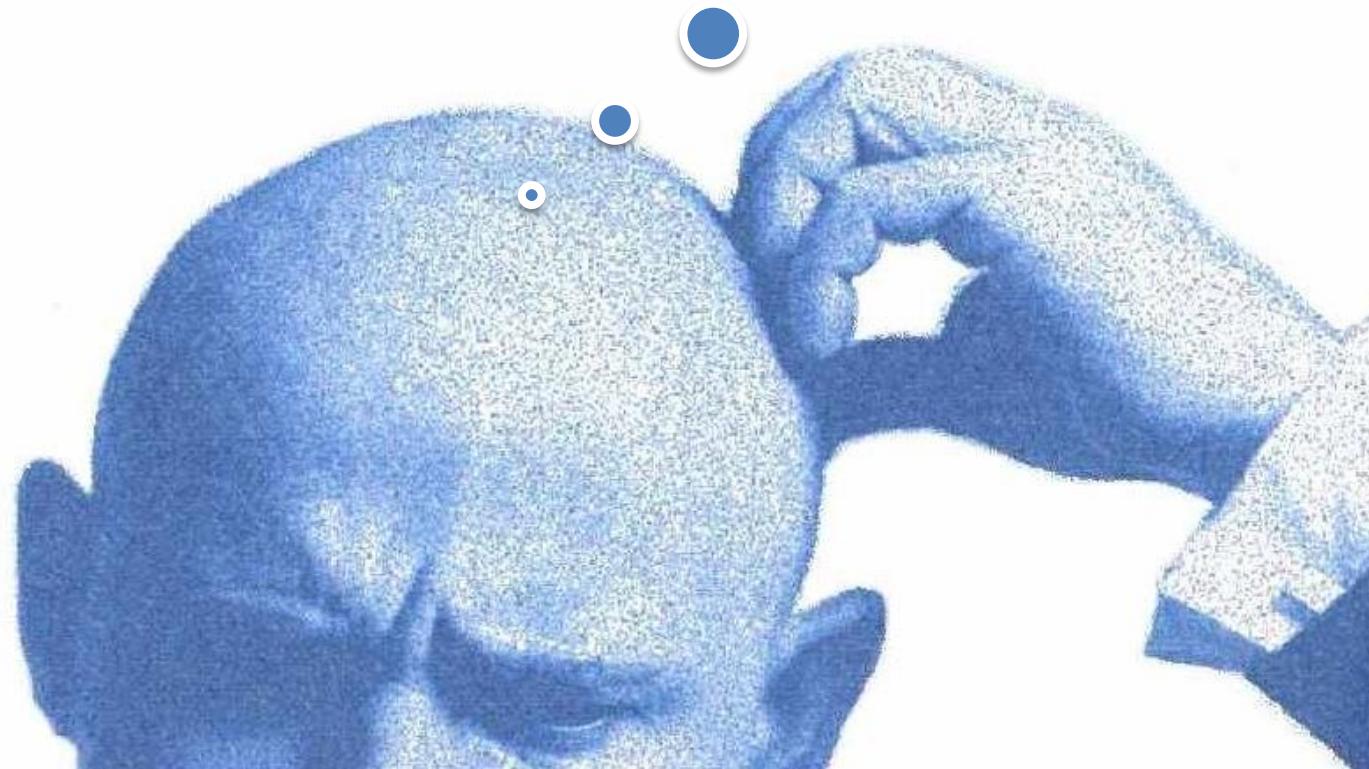
BeadChip 1 million SNPs

125959
SNPs



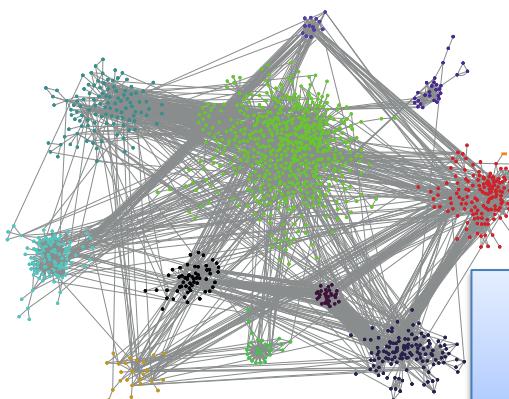
A pergunta que não quer calar...

Como relacionamos o perfil genético com estes resultados?



ATCCGAACTCGT
CGACCTAGACCT
AGTATTAACGGCA

125959 SNPs



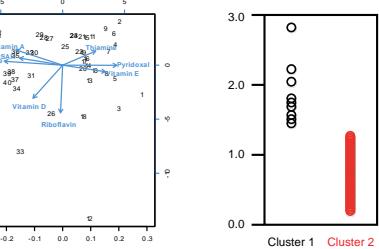
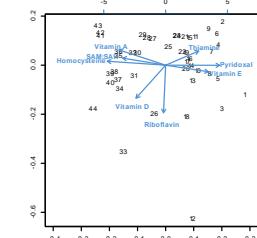
TOPOLOGICAL MODULES
 58 modules: 116210 interactions between 13705 genes

Generalized Estimating Equation

GENOTYPE DATA

MICRONUTRIENT PROFILE DATA

GEE



To connect 125959 SNPs with PCA1 (metabolic groups)

MICRONUTRIENT CORRELATED SNPS

VEGAS

ATCCGAACTCGT
CGACCTAGACCT
AGTATTAACGGCA

3200 SNPs

MICRONUTRIENT CORRELATED GENES

HYPERGEOMETRIC TEST

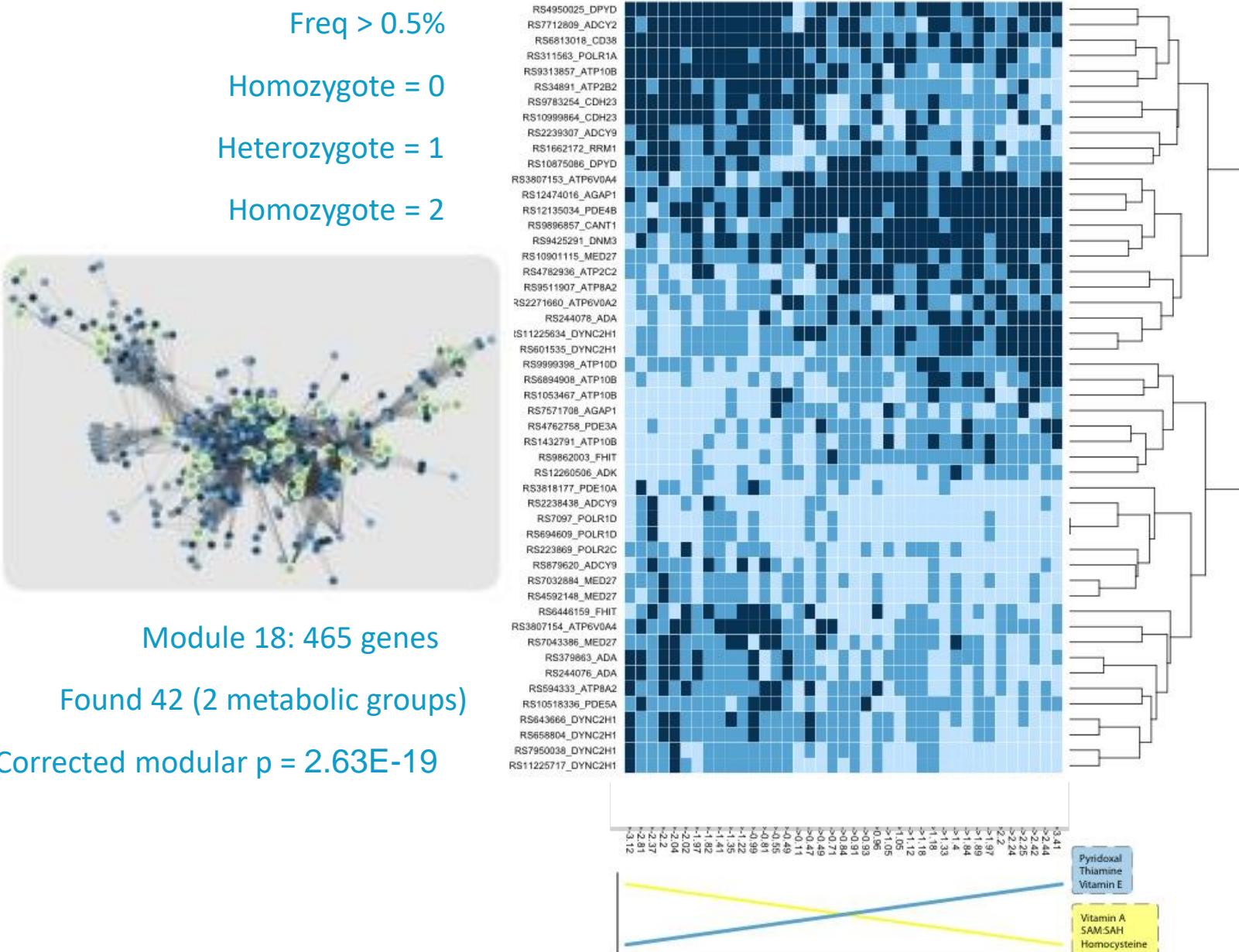
1392 genes

MICRONUTRIENT CORRELATED MODULES

To reasonably represent the System Biology ,statisticians got a global networking using two manually curated protein-protein interaction database

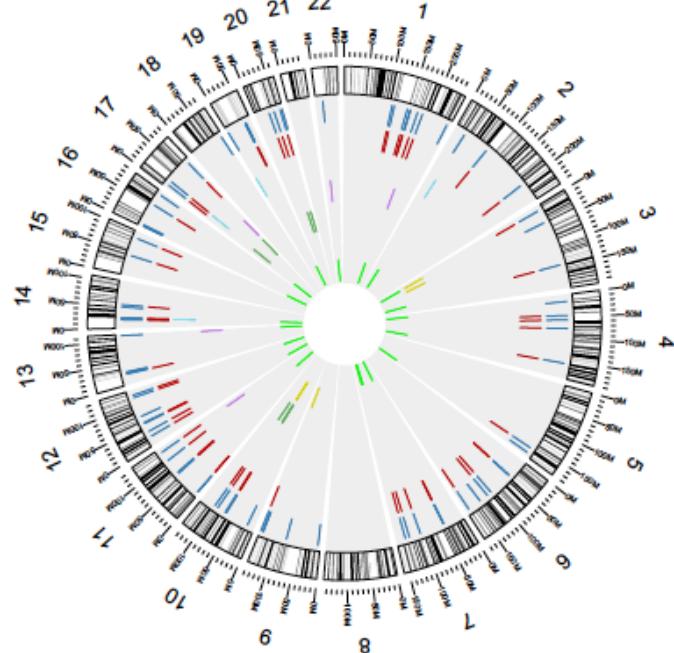
4 modules (18, 52, 45, 2)

Middle Out Enriched module – Genotype



Micronutrient module genes map to phenotype loci

MODULE 18

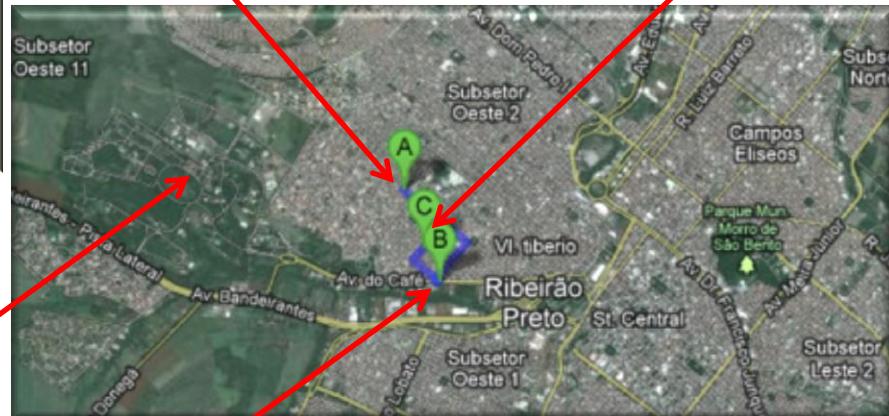
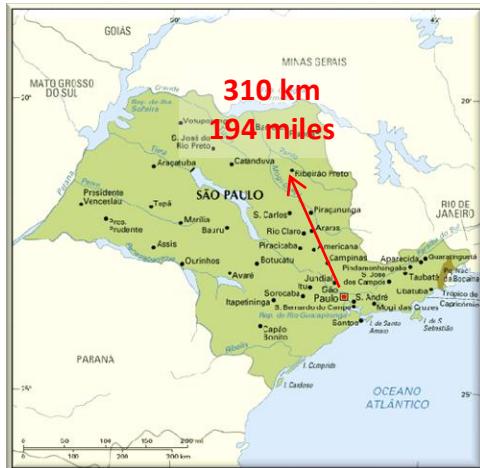


- Significantly correlated with PC1
- body weight QTL
- leptin QTL
- glucose QTL
- fibrinogen QTL
- gwasdb - plasma metabolites
- secretion/absorption genes

42 DOS NOSSOS GENES ESTAVAM EM
REGIÕES CROMOSSÔMICAS (QTL/LOCI)
QUE CODIFICAM GENES ASSOCIADOS AO
PESO CORPORAL, À LEPTINA, AO
METABOLISMO DA GLICOSE



Location Ribeirão Preto, São Paulo, Brazil



Brazil Micronutrient Project



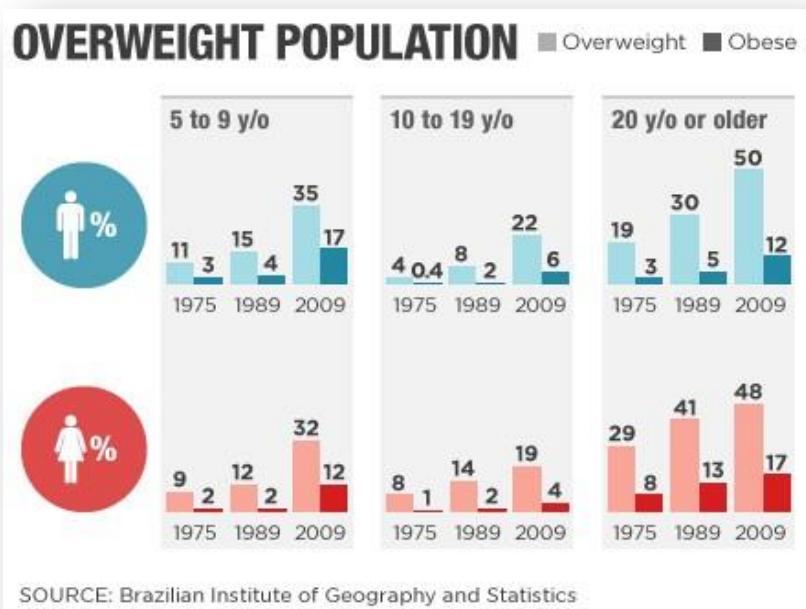
Nestlē Institute of **Health** Sciences



As amostras de sangue serão enviadas para análise no laboratório de pesquisa do Instituto de Pesquisa em Saúde da Nestlé (NIHS) na cidade de *Lausanne*, na

Brazil Micronutrient Intervention Study

OVERWEIGHT POPULATION



33.5% children are overweight in Brazil
(IBGE 2014)

Increased metabolic syndrome in children
eg. *Dyslipidemia and glucose intolerance*
(Harris et al. 2006)

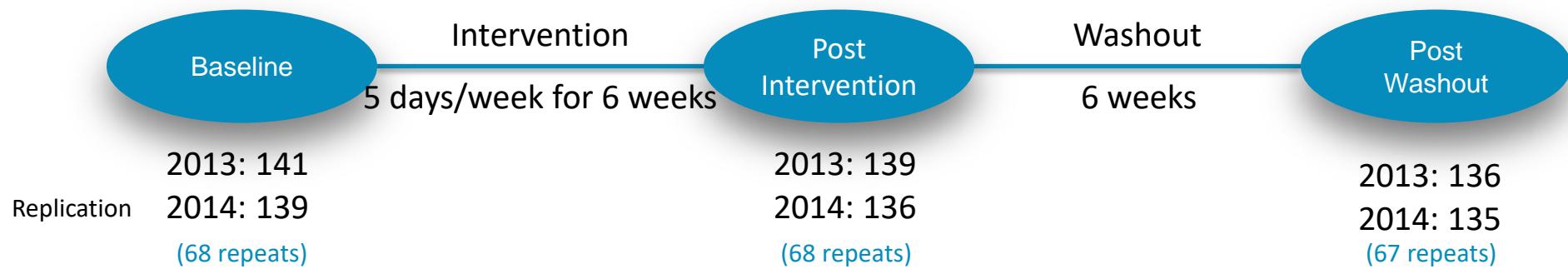
Obesity and metabolic syndrome are related to micronutrients deficiencies

Objectives

- Primary** Identify *responders & nonresponders* defined by glucose, LDL cholesterol, total cholesterol to *multiple micronutrients*
- Secondary** Develop methods to target appropriate combinations of micronutrients to individuals to improve metabolic health

Clinical Trial Design

2 tablets for 9, 10, 11 & 3 tablets for 12 & 13



Milk Bar Composition Per 3 Tablets

	Amount	% RD for 3 tablets
Vitamin A	801 µg	133.3%
Vitamin D	5.1 µg	50%
Vitamin E	9.9 mg	90%
Vitamin C	60 mg	133.3%
Vitamin B1	1.4 mg	155.5%
Vitamin B2	1.76 mg	178%
Niacin	18 mg	150%
Vitamin B6	2 mg	200%
Folate	200 µg	50%
Vitamin B12	1.1 µg	55.5%
Biotin	150 µg	750%
Pantothenate	6 mg	150%
Calcium	287 mg	22%
Phosphorous	217 mg	17.3%
Iron	6.5 mg	81.2%
Magnesium	125 mg	52%
Zinc	6 mg	75%

Measurements

Anthropometric

Clinical chemistry & CBC

DNA damage

1,129 plasma proteins

~200 plasma metabolites

5M SNP plus whole exome

Plus other

Body Mass Index



Selected Study Population Data

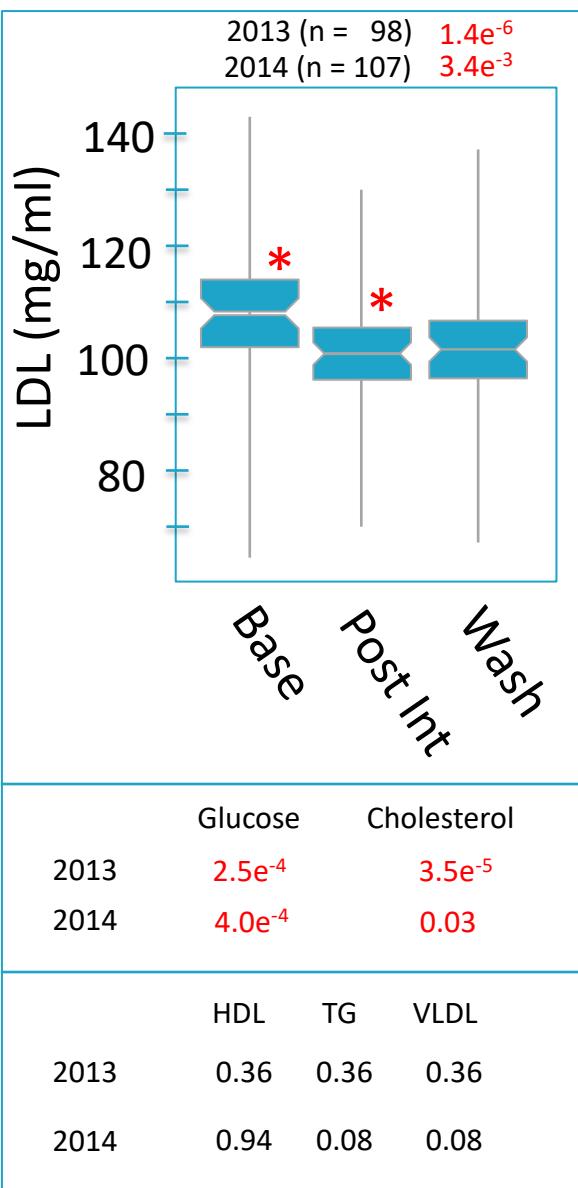
	2013	2014	2013 + 2014	2014 Validation	2014 Replication
Participants	141 → 136	139 → 135	280	69 → 65	70 → 70
Female	56.7%	54.0%	55.35%	44.9%	62.9%
Age (years)	11.4 ± 1.1	11.9 ± 1.0	11.6 ± 1.1	11.6 ± 1.1	12.2 ± 0.9
Mean weight - kg	48.8 ± 16.7	50.0 ± 14.6	49.4 ± 15.7	48.3 ± 11.8	51.7 ± 16.7
Mean BMI	20.6 ± 5.3	20.5 ± 4.9	20.5 ± 5.1	20.0 ± 4.1	21.0 ± 5.6
Overweight/Obese	48.9%	37.4%	43.2%	34.8%	40.0%

Vitamin insufficiency	Vitamin B12 insufficiency: 0%	Folate insufficiency: 5.2%	Riboflavin insufficiency: 19%	Beta-carotene: insufficiency: 44%	Retinol insufficiency: 48%
-----------------------	-------------------------------	----------------------------	-------------------------------	-----------------------------------	----------------------------

Validation = new recruits in 2014

Replication = returnees

Main Results Difference between Intervention & Baseline



	Responders			Non -Responders		
	2013	#	Ave. Decrease	2013	#	Ave. Increase
Glucose		77	$4.7 \text{ mg/dl} - 5\%$		31	$3.9 \text{ mg/dl} - 4\%$
LDL		78	$13.4 \text{ mg/dl} - 11\%$		24	$8.5 \text{ mg/dl} - 5.2\%$
Cholesterol		62	$17.8 \text{ mg/dl} - 13\%$		29	$9.1 \text{ mg/dl} - 8.8\%$

Statistical tests demonstrate that the fold change is due to the intervention

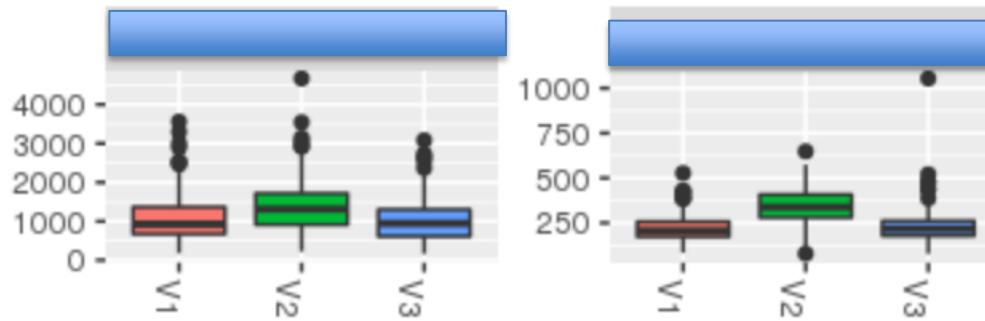
Conclusion

Multiple micronutrients alter lipid/glucose profile
Response is clinically relevant

*T test p values corrected for multiple testing (Benjamini-Hochberg)

Plasma Vitamin & Clinical Variables changed by Intervention

Examples



Subset of variables changed by intervention

	# changed	Total
Micronutrients	14	17
Clinical	3	6

Bodybugg at the same time...

Three 24 hour recall (last week prior blood drawn and FFQ application)

Energy expenditure

- Skin temperature
- Galvanic skin response

Energy expenditure

- Flux sensors
- Resting energy expenditure

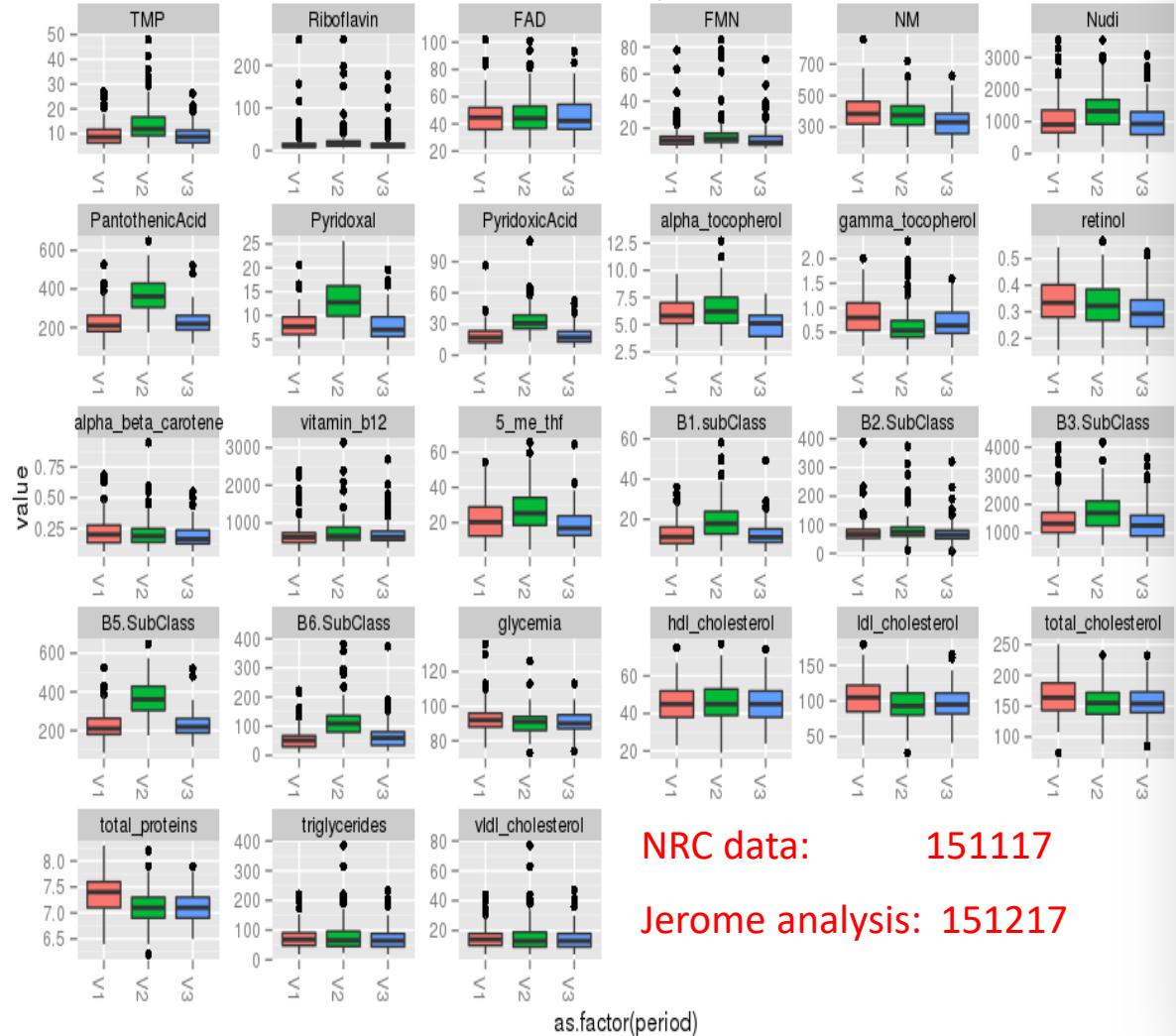
Physical activity

- Number of steps
- Movement detector



Plasma Vitamin & Clinical Variables

Vitamins and clinical var levels at baseline, after intervention and after washout



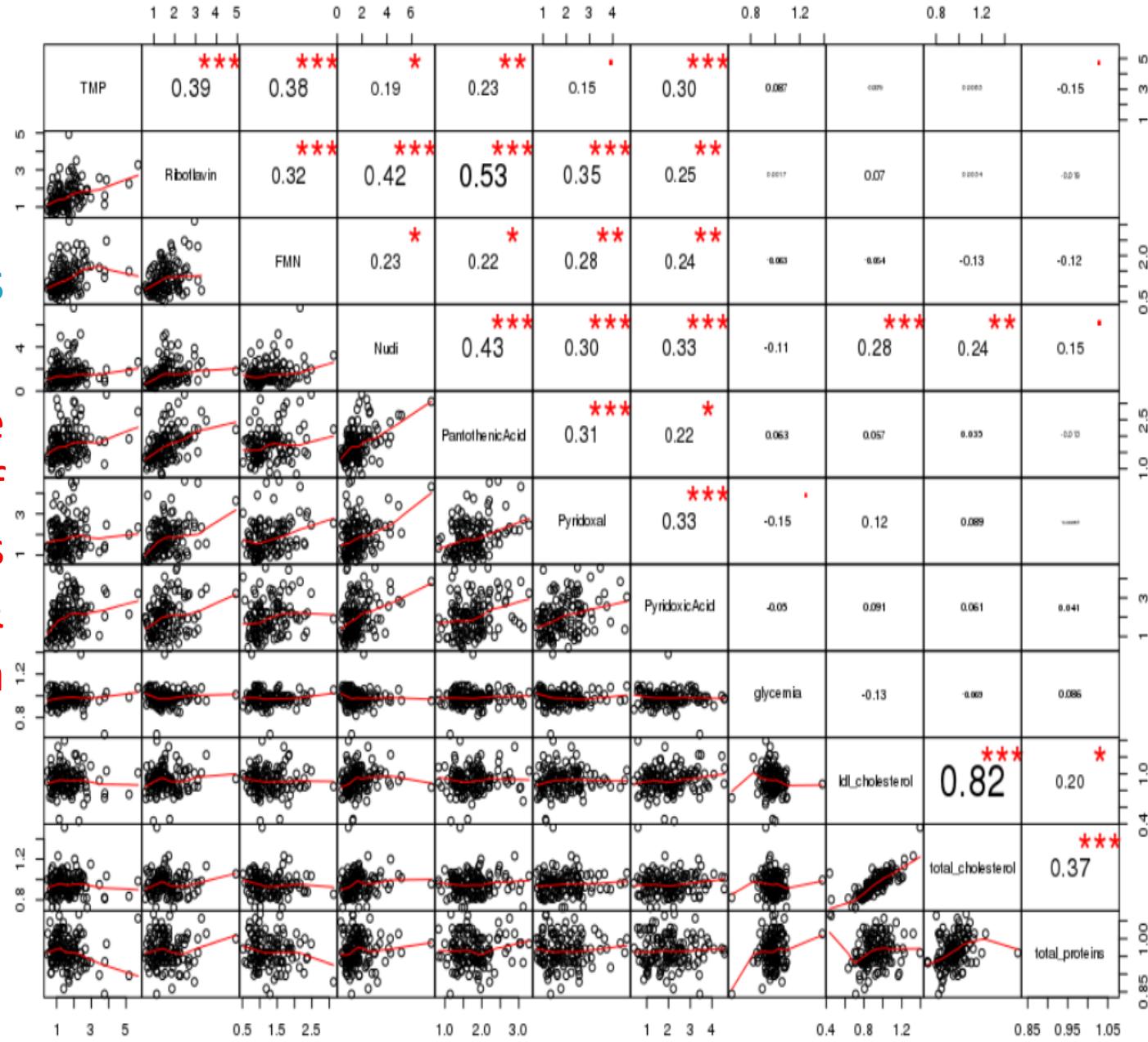
NRC data: 151117
Jerome analysis: 151217

✓ Statistically
Significant for V1 to V2

Vitamins	Pvalue	Pcorrected
✓ TMP	1.2e-11	3.6e-11
✓ Riboflavin	8.9e-15	3.4e-14
FAD	7.6e-01	0.76
✓ FMN	2.7e-05	4.6e-05
NM	2.1e-01	0.26
✓ Nudi	9.2e-08	1.8e-07
PantothenicAcid	2.2e-23	3e-22
✓ Pyridoxal	3.1e-20	2.1e-19
✓ PyridoxicAcid	1.1e-18	5.9e-18
✓ alpha_tocopherol	8.0e-03	0.011
✓ gamma_tocopherol	1.1e-09	2.7e-09
retinol	8.2e-02	0.11
alpha_beta_carotene	3.6e-01	0.41
✓ vitamin_b12	1.5e-03	0.0021
✓ 5_me_thf	2.2e-08	4.9e-08
B1.subClass	5.5e-15	2.5e-14
✓ B2.SubClass	3.8e-05	6e-05
B3.SubClass	1.0e-06	1.8e-06
✓ B5.SubClass	2.2e-23	3e-22
✓ B6.SubClass	2.2e-20	2e-19
glycemia	2.5e-04	0.00038
hdl_cholesterol	2.7e-01	0.32
✓ ldl_cholesterol	1.1e-10	3e-10
✓ total_cholesterol	6.0e-08	1.2e-07
total_proteins	1.7e-14	5.7e-14
triglycerides	6.3e-01	0.68
vldl_cholesterol	7.6e-01	0.76

Correlations

Fold Change of Vitamins & Clinical Data



Jerome: 151217

Statistical Tests of intervention

COSBI: 160117

Permutation

Procedure Pooled V2 & V1, randomly divided the data into two equal groups

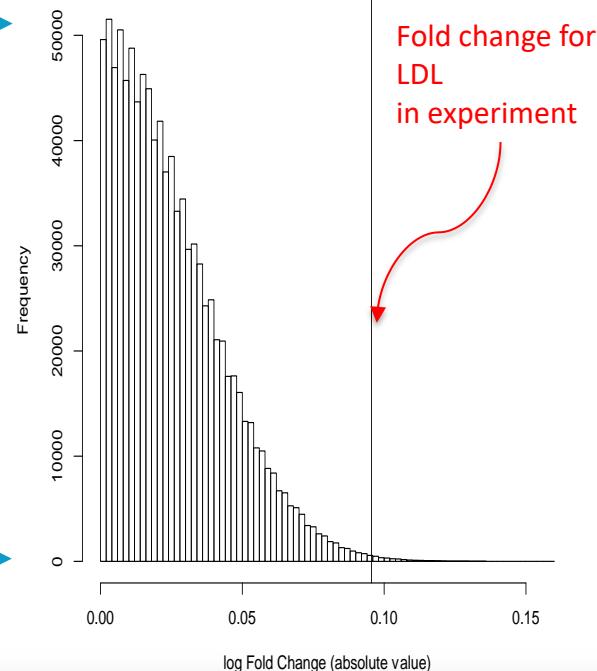
Evaluated the significance of the response (V1 vs V2 with Student t-test)

Repeated 1,000,000 times

Results In 5% of permutations significant differences between both time points

Conclusions The LDL-C response to intervention was rarely (< 5%) observed by chance

The observed intervention effect on LDL-C was not driven by outliers



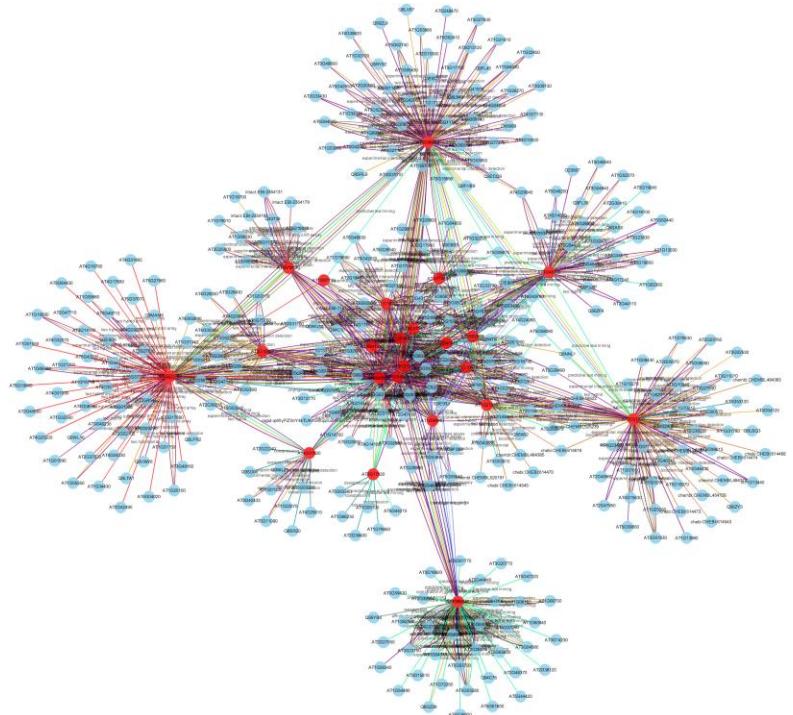
Regression to the mean

Variable	Effect	Down-Down				Down-Up				Up-Down				Up-Up			
		treatment	p-value	washout	p-value												
LDL	-	12.	1E-	1E-	07	14.	5E-	13	5E-	2E-	-	3E-	0.0	7.	0.01	7	1
	0	0	07	-8.2	07	7	11.4	15	8.9	06	12.8	05	8.3	0.0	7	0.01	7

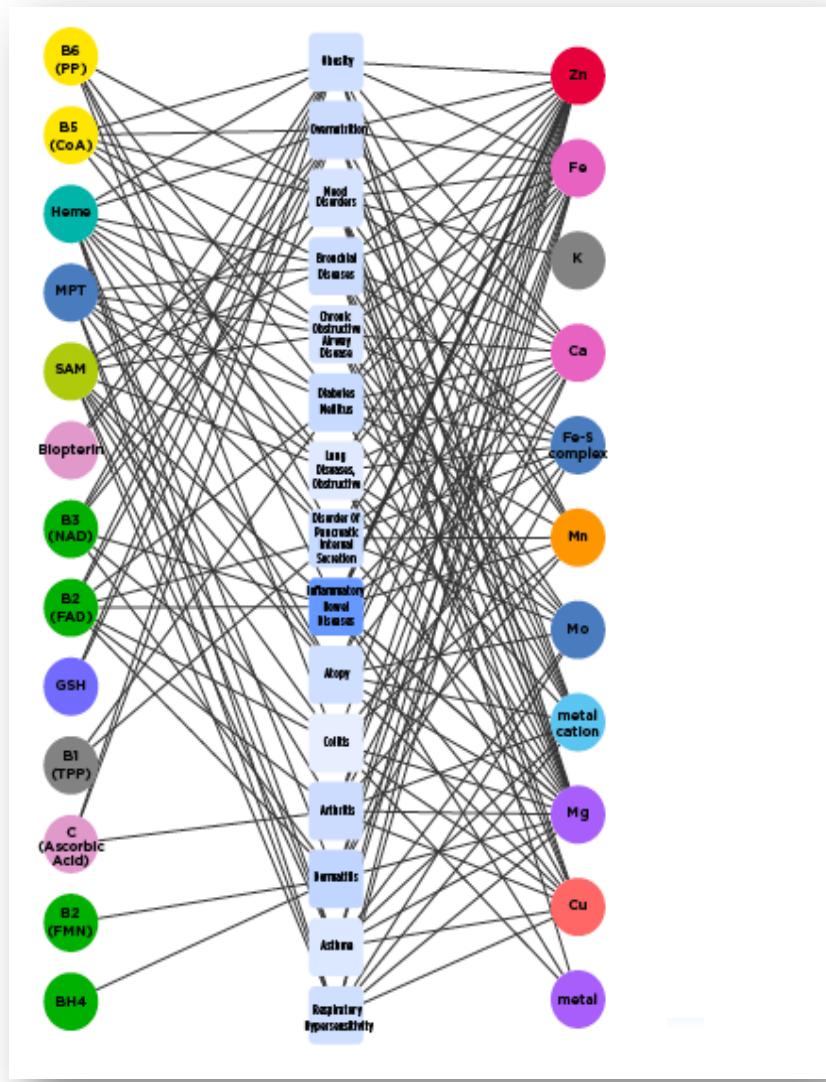
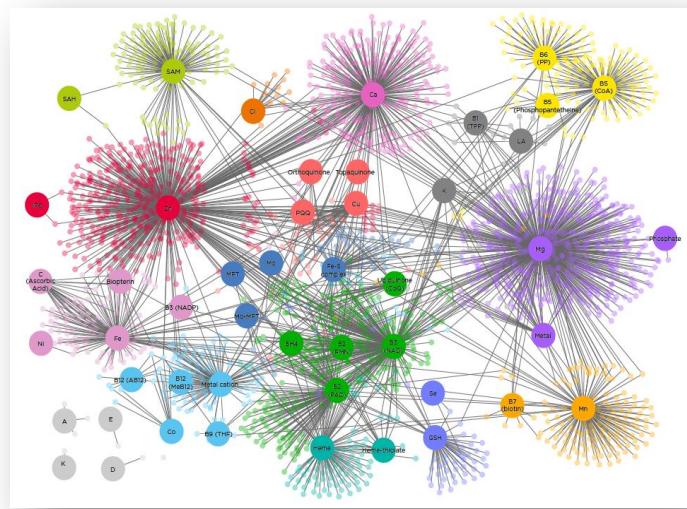
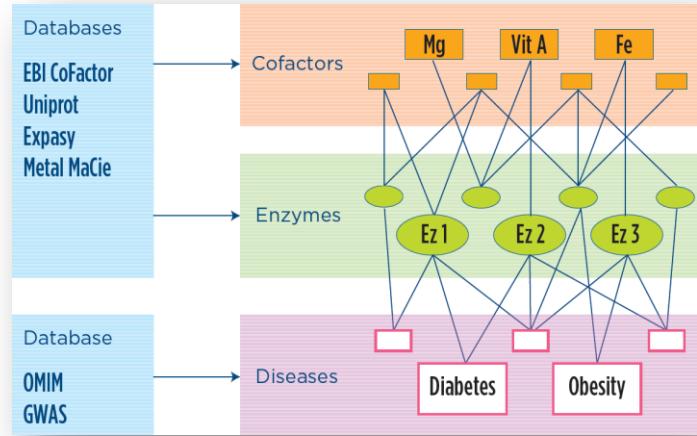
Conclusion RTM & PM analysis indicate that the fold change is due to the intervention, not RTM or random chance

Systems modeling using protein-protein interaction

Modeling of metabolic networks is one powerful approach to allow a better understanding of nutrient behavior in cells both in normal and in pathogenic states



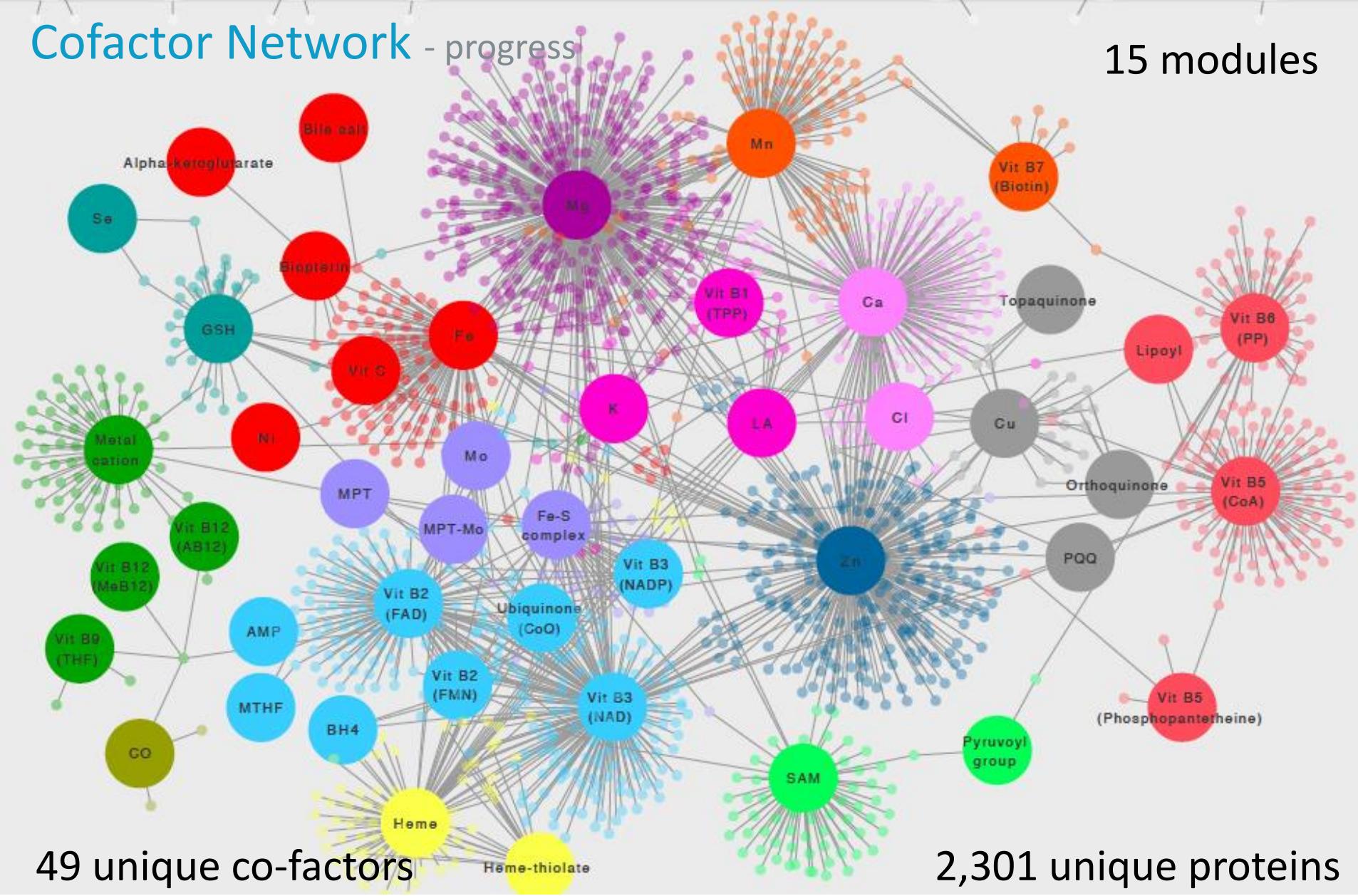
Cofactor-Protein Database



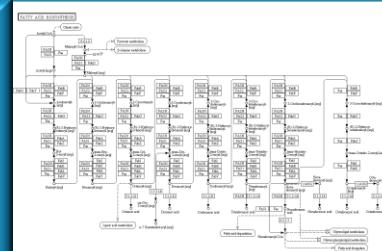
Global effect of micronutrient: To associate genes identified by data mining methods with nutrients through cofactor network

Cofactor Network - progress

15 modules



Cofactor Database Provenance



Gene - pathway

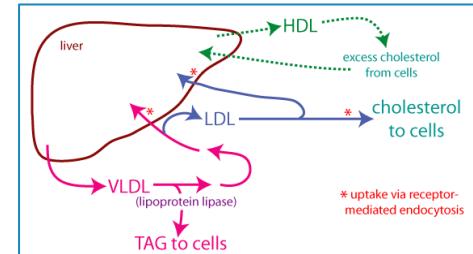
Proteins that bind inorganic and organic (includes in vivo produced) cofactors identified in 4 databases (below)

Genes mapped PPMI network, gene ontology & functional pathways to link processes to cofactors

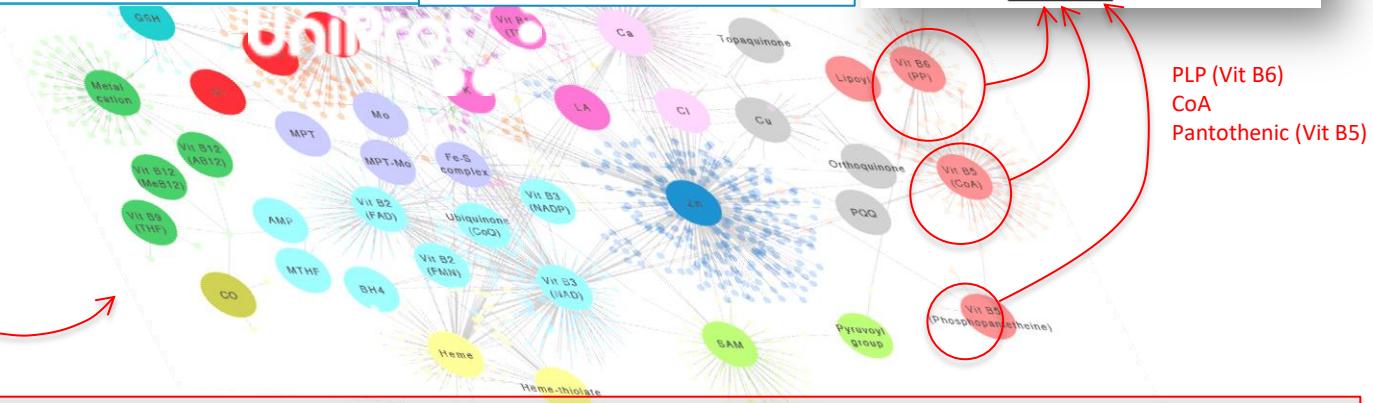
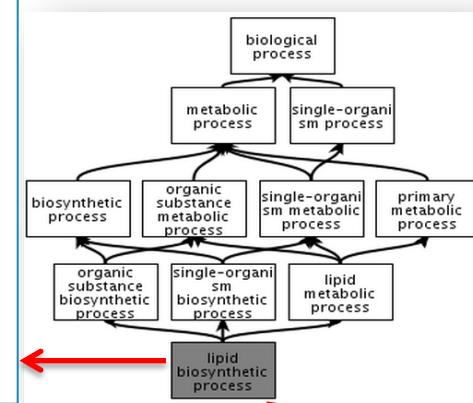
Genes linked with disease and GWAS to associate cofactors to disease and phenotype

Marie Pier Scott-Boyer
Sebastien Lacroix

Genetic Variation & Phenotype Associations



Gene - phenotype

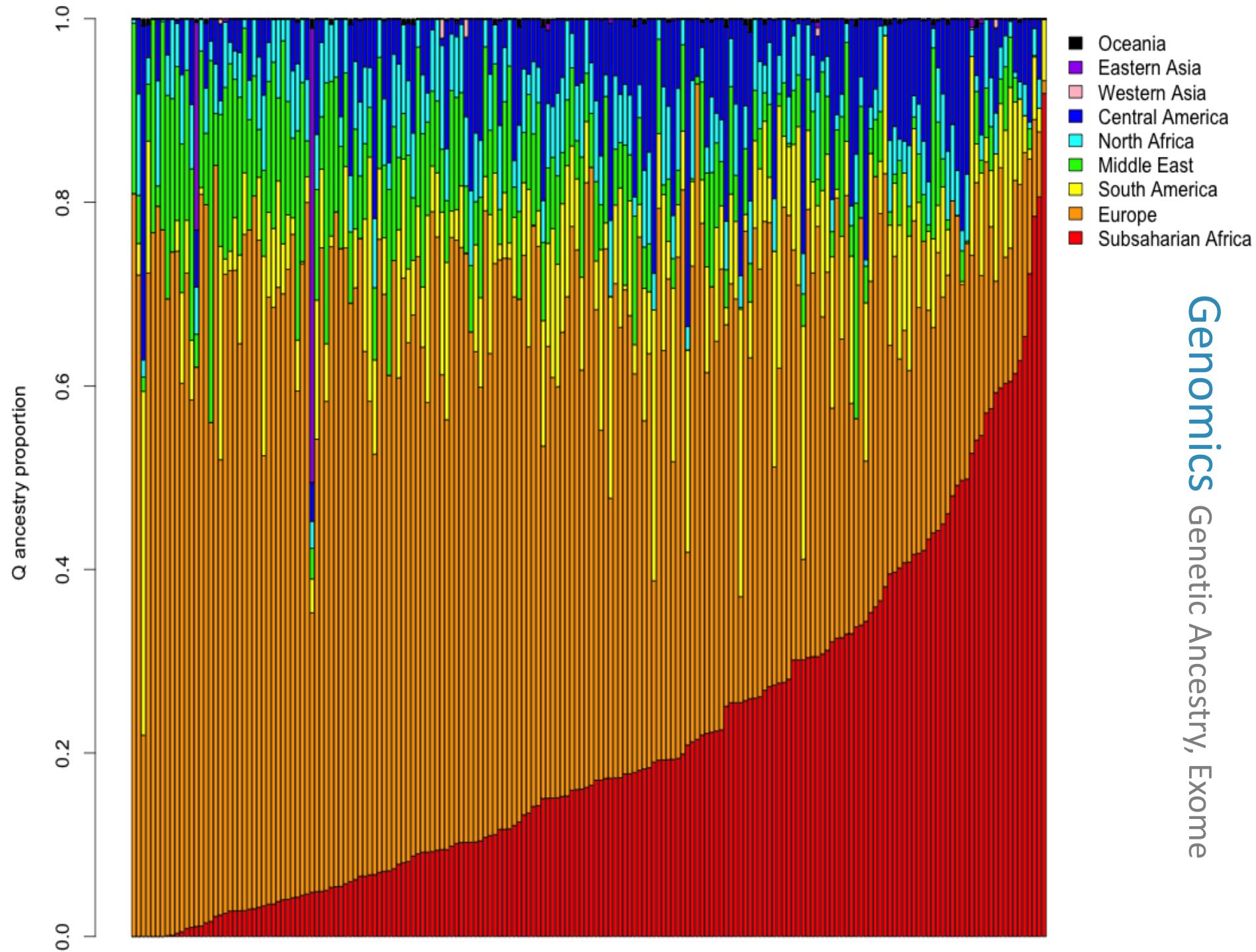


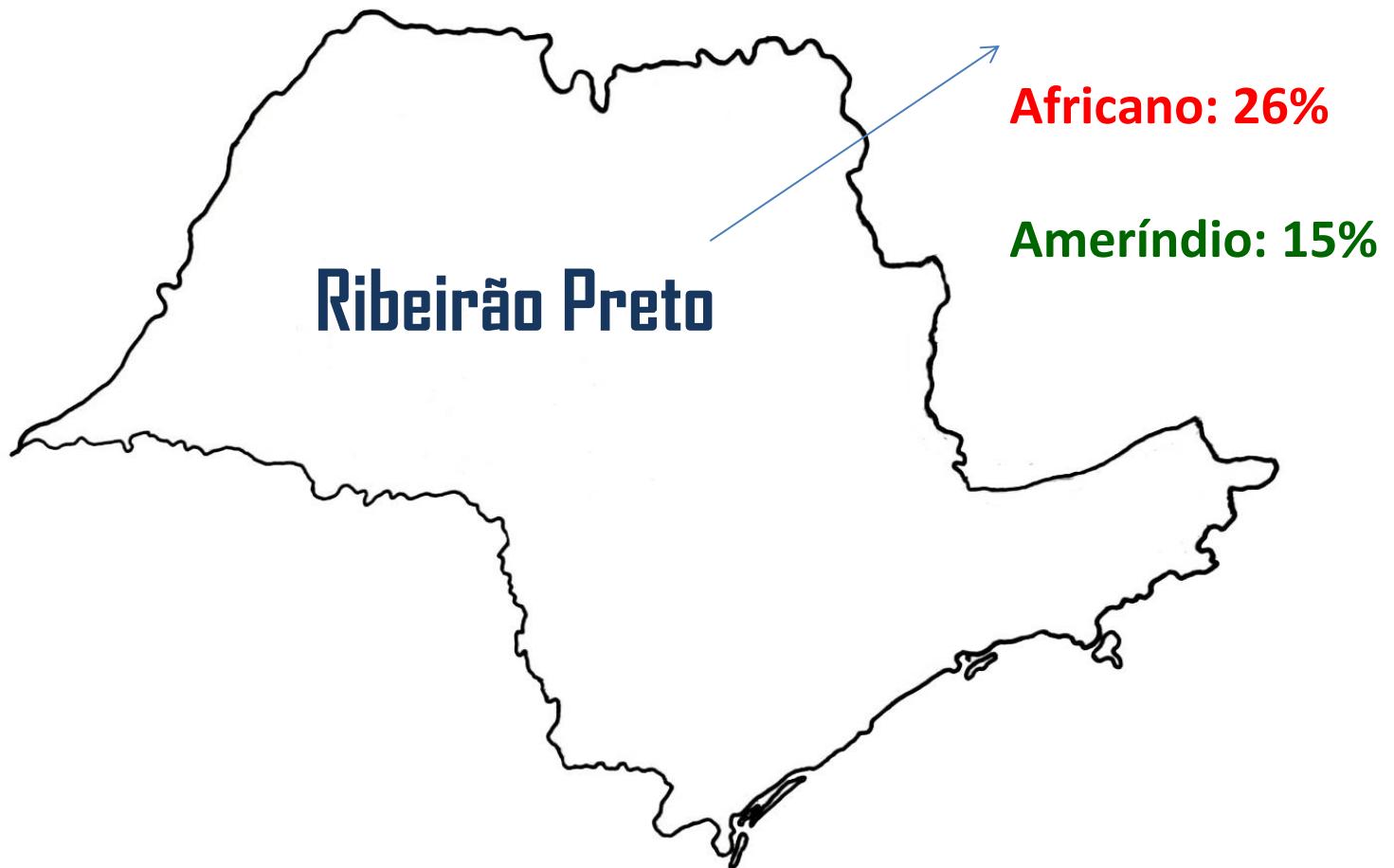
Metal MACiE: the database of catalytic metal ions



 ExPASy Bioinformatics Resource Portal

Genomics Genetic Ancestry, Exome





Africa Subsaariana: 0-92%

Norte da África: 0-11%

Oriente Médio: 0-39%

Oeste da Ásia: 0-2%

Leste da Ásia: 0-50%

Oceania: 0-1%

Europa: 1-82%

América Central: 0-36%

América do Sul: 0-37%

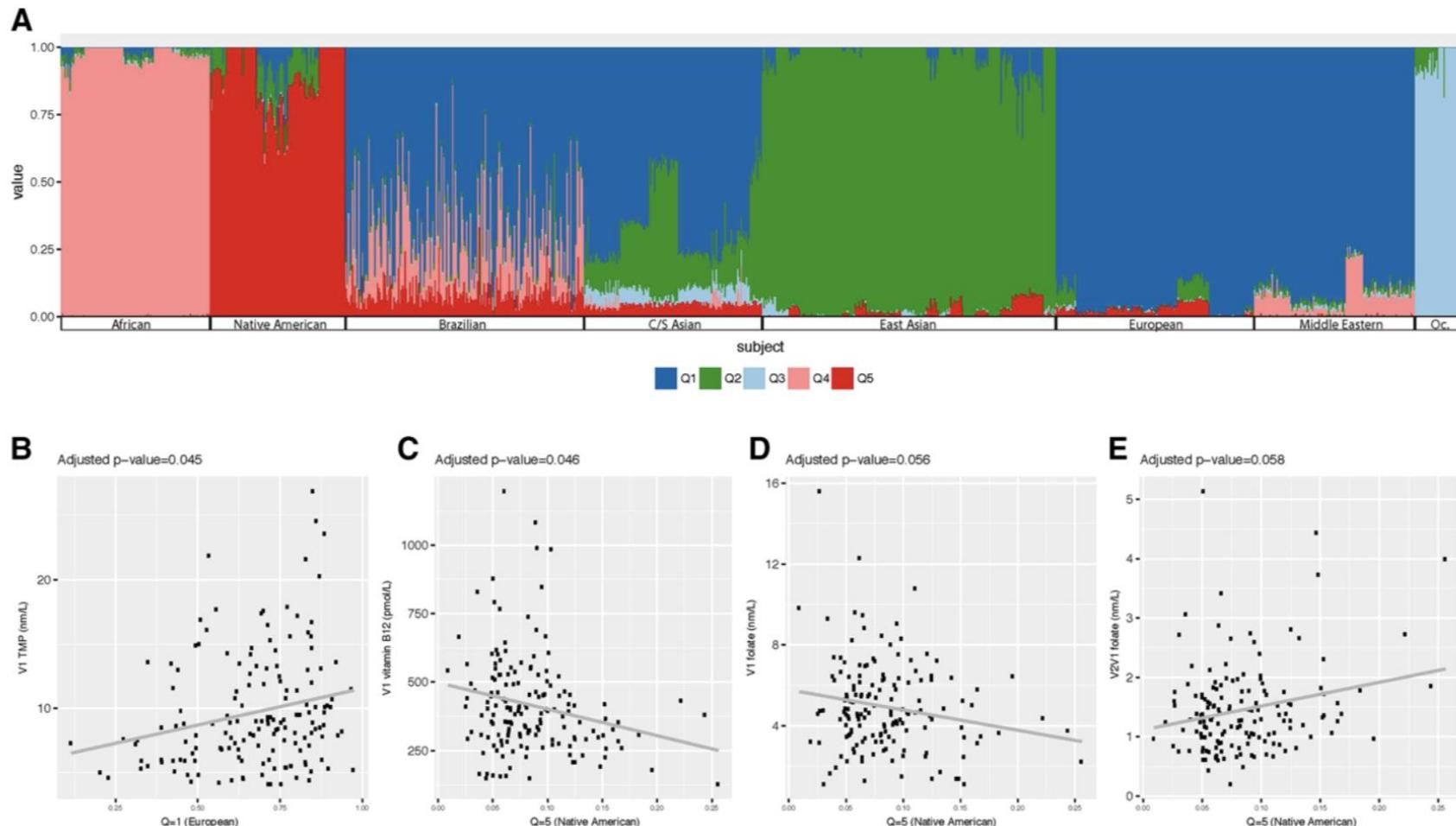


Figure 2. Admixture analysis. Influence of genetic ancestry on baseline vitamin levels. Ancestry markers from the Human Genome Diversity Project (HGDP) reference populations were used A) to identify admixture in data from unrelated participants from both years as per methods. To test whether linear regression between the ancestral components and baseline vitamin levels existed, a $k = 5$ model was used to the following covariates: trial year, sex, age, fat mass, and tanner score. Adjusted p -value of 0.05 was used as significance threshold. B) Baseline TMP and Q1 (Europe) with estimate of regression coefficient (ERC) 4.57, C) baseline vitamin B12 and Q5 (Native American) ERC = 186.53, D) baseline folate and Q5 (Native American) ERC = 2.13, and E) folate response as ratio of V2/V1 and k5 (Native American) with ERC = 0.77.

Brazil Micronutrient Project

**Food history and micronutrient profile and their relation to DNA damage
in children in Brazil**



Tamiris Trevisan de Barros ;Vinícius Venâncio; Lívia Cristina Hernandes; Lusânia Maria Greggi

jacque@fmrp.usp.br

Background

Dietary pattern of children and adolescents:

↑ High energy density food ↓ Fruits and vegetables
→ Insufficient intake of vitamins and minerals

Micronutrients → cellular protection as antioxidants

Repair DNA damage

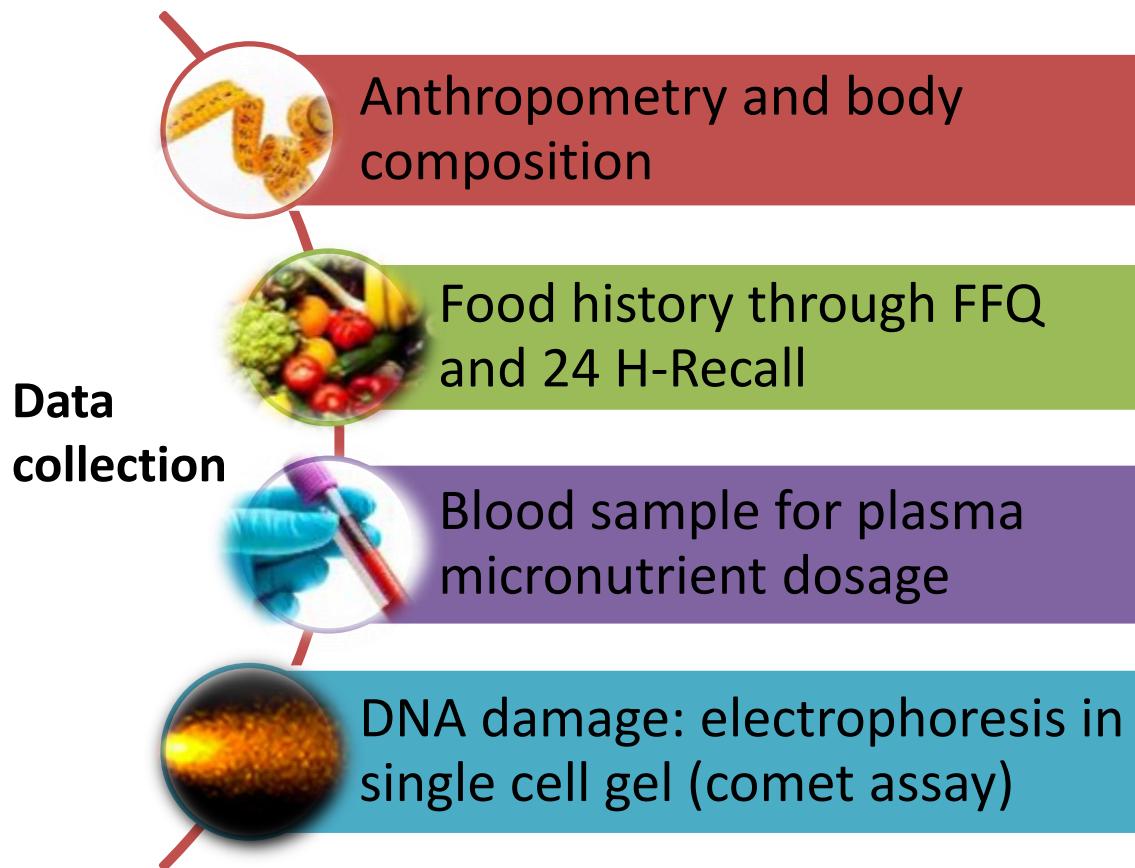
Unrepaired DNA damage can lead to the development of carcinogenic or mutagenic changes in cells



Objective

To investigate the association between DNA damage and nutritional status in 9 to 13 years old children and adolescents

Methods

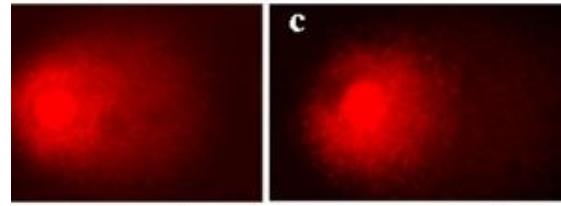
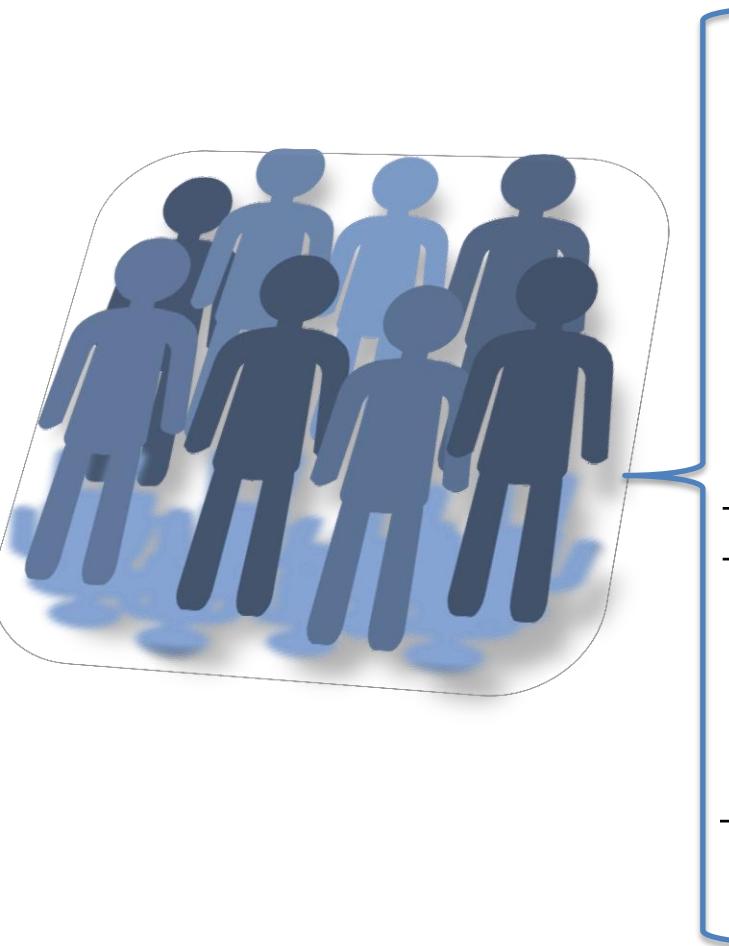


**9 to 13 years old healthy children
Total of 141 subjects**

After exclusion of under and over diet reports: 120 subjects

Software SPSS 20.0 for Statistical Analysis

Results – Population data

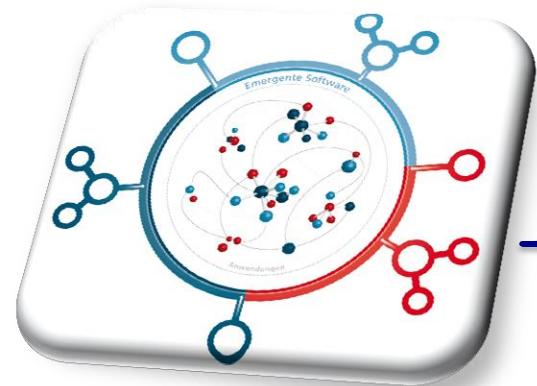


Tail intensity: $10.32\% \pm 4.35$
Tail moment: 4.78 ± 2.46
(no differences by sex and
pubertal status)

Body Mass Index/Age*		Frequency (n / %)
< percentil 3	Very thin	4 (3.3%)
percentil 3 - percentil 15	Slimness	9 (7.5%)
percentil 15 - percentil 85	Eutrophic	51 (42.5%)
percentil 85 - percentil 97	Overweight	27 (22.5%)
> percentil 97	Obesity	29 (24.2%)

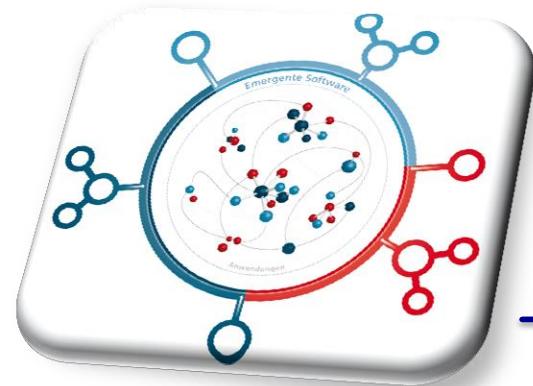
Body Mass Index according to OMS 2007 5 to 19 years

Results – Cluster Analysis (Tail intensity/tail moment)



Variables	Cluster 1 n = 73	Cluster 2 n = 47	p value
Age (years)	11.49 ± 1.04	11.28 ± 1.16	0.29
Sex (% M/F)	43.8/56.2	46.8/53.2	0.75
Fat mass (% body weight)	24.77 ± 6.72	24.37 ± 7.69	0.76
Tail intensity (%)	7.08 ± 2.24	15.35 ± 2.40	< 0.001
Tail moment	3.38 ± 1.23	6.97 ± 2.30	< 0.001

Results – Cluster Analysis (Tail intensity/tail moment)

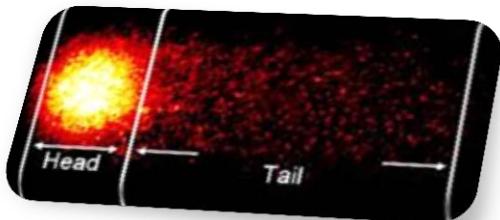


Variables	Cluster 1 n = 73	Cluster 2 n = 47	p value
Total vegetables	3.13 ± 2.04	2.36 ± 1.93	0.041
Green, yellow, orange and red vegetables	3.47 ± 2.10	2.67 ± 2.19	0.047
Milk and dairy	4.92 ± 3.62	6.63 ± 3.02	0.008
Meat	$10.0 (10.0 - 10.0)$	$10.0 (8.8 - 10.0)$	0.022
Healthy Eating Index	56.7 ± 10.0	52.7 ± 9.2	0.03
Plasma riboflavin ($\mu\text{mol/L}$)	4.17 ± 3.11	2.68 ± 1.83	0.03

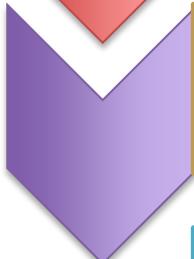
Moser et al 2011
Collins, 1998.
Konopacka, 2000

Separation into 2 groups according DNA damage

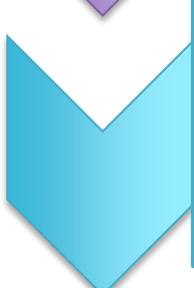
(Wollowski et al. 1999; Giovannelli et al 2002)



- **Comet assay:** fragments of damaged DNA are dragged in electrophoresis, forming a tail



- Tail intensity values:
→ Measures % of DNA in tail (damaged DNA)

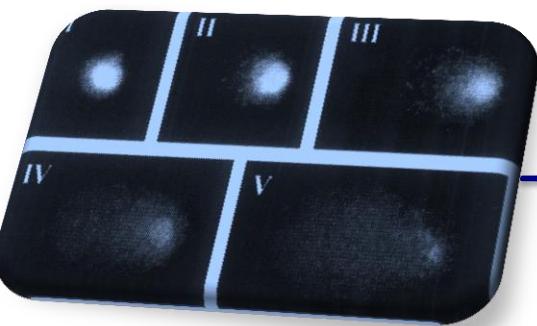


- Classification proposed by Wollowski et al (1999)
- **Group 1:** 0 to 17% of damage (n=108)
- **Group 2:** $\geq 17,1\%$ of damage (n=12)

class I: 0–6%; class II: 6.1–17%;
class III: 17.1–35%; class IV:
35.1–60%; class V: 60.1–100%

Results – Cluster Analysis (Wollowski et al. 1999; Giovannelli et al 2002)

COLLINS et al, 1998
 MANTHEY et al, 2006
 MINNET et al, 2011
 KONOPACKA et al, 2001
 MORIN et al, 2007



Tail intensity

Variables	Cluster 1 n = 108	Cluster 2 n = 12	p value
Age (years)	11.43 ± 1.09	11.25 ± 1.14	0.60
Sex (%), M/F	46.3/53.7	33.3/66.6	0.40
Tail intensity (%)	9.39 ± 3.91	18.68 ± 0.93	< 0.001
Fat mass (%)	25.02 ± 7.05	20.97 ± 6.56	0.06
Overweight (%)	50.6	8.3	0.047
Plasma retinol ($\mu\text{mol/L}$)	0.35 ± 0.08	0.27 ± 0.09	0.01
Plasma – β carotene ($\mu\text{mol/L}$)	0.22 ± 0.13	0.15 ± 0.10	0.02
Plasma riboflavin ($\mu\text{mol/L}$)	$3.10 (1.57 - 5.07)$	$1.57 (1.13 - 3.00)$	0.04

class I: 0–6%; class II: 6.1–17%;
 class III: 17.1–35%; class IV:
 35.1–60%; class V: 60.1–100%

Nutrient intake patterns

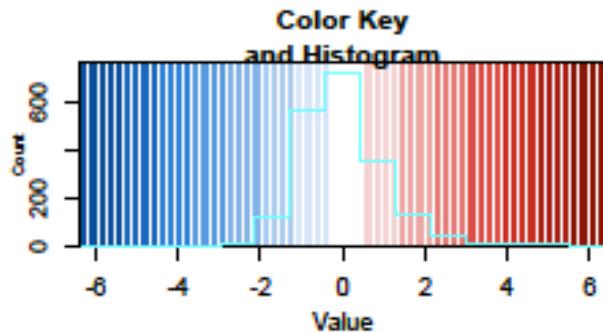
Robust Sparse K-means clustering

Intake of amino acids and some micronutrients

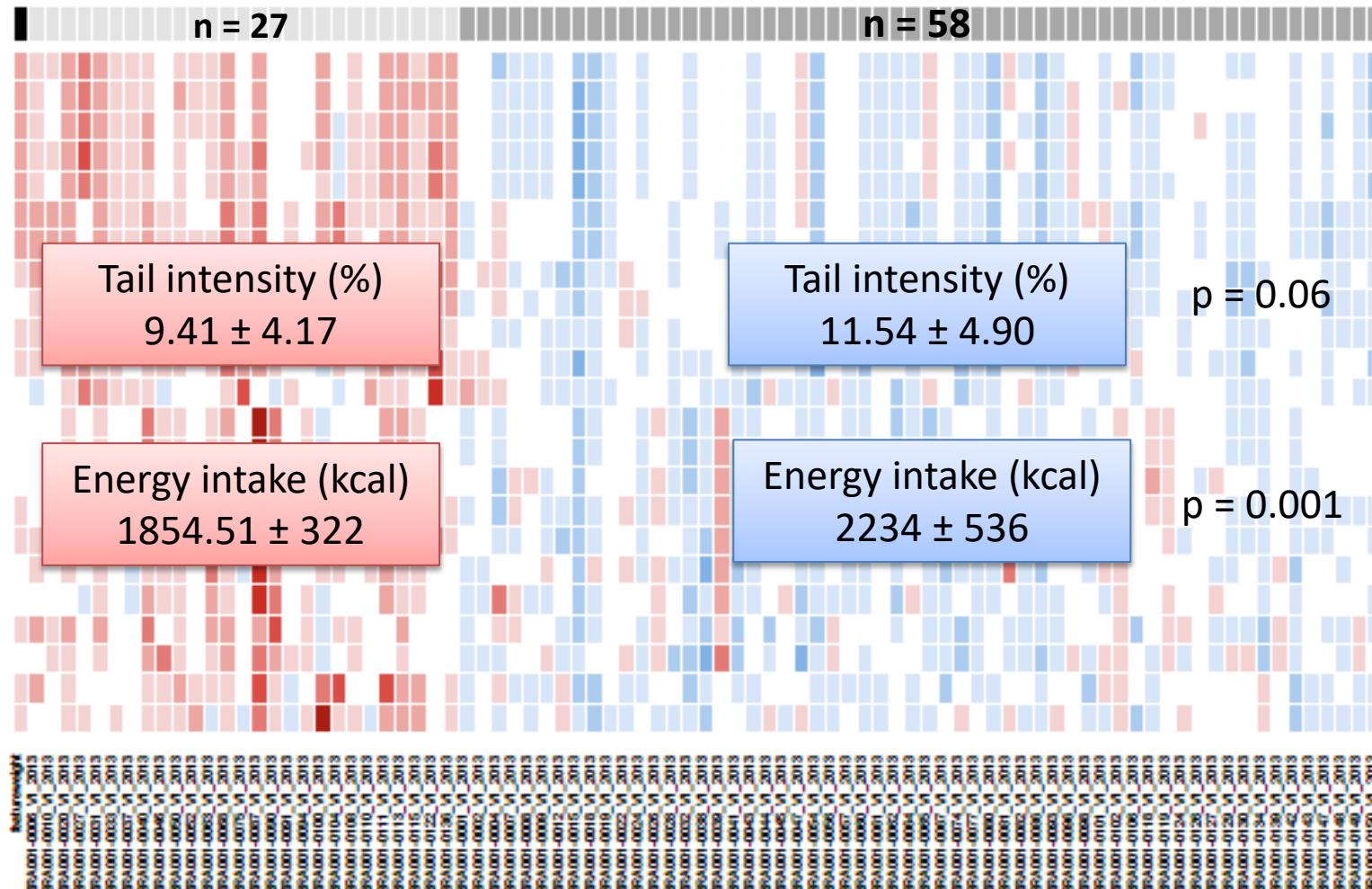
Aromatic amino acids and branched amino acids, niacin, phosphorus, pantothenic acid, cyanocobalamin, purines, chrome, manganese, zinc, copper, magnesium, inositol and choline

Cluster 1 (n = 27)
higher intake

Cluster 2 (n = 58)
lower intake



Heatmap: separation of the accurate FFQ reporters into 2 dietary patterns

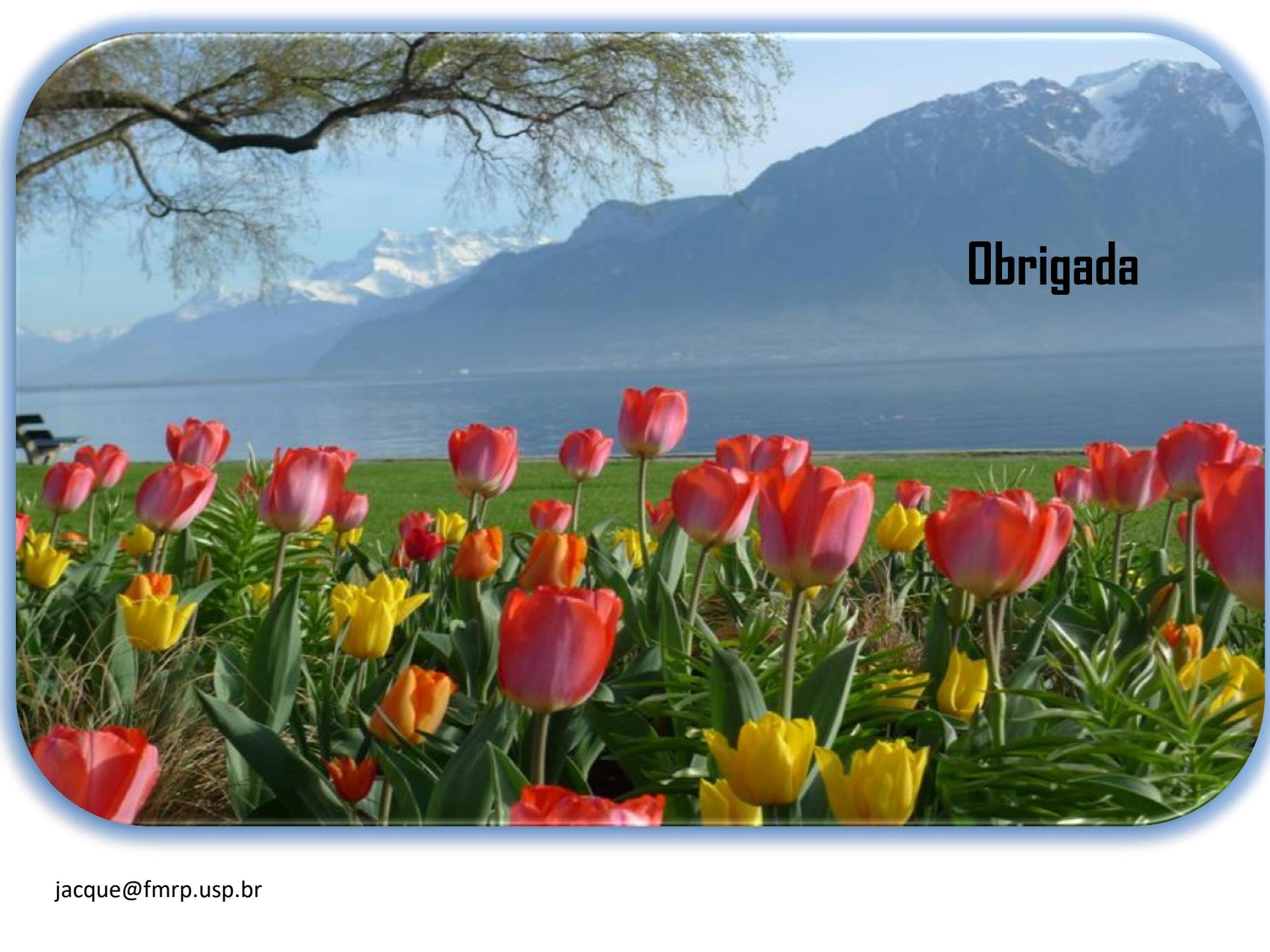




This study confirms the protective effect of micronutrients against DNA damage



Children are increasing energy density food intake lacking in micronutrients

A scenic landscape featuring a variety of tulips in the foreground, including red, pink, yellow, and orange varieties. Beyond the flowers is a calm body of water, likely a lake, with snow-capped mountains in the background under a clear blue sky.

Obrigada