Nutrigenomics Organization (NuGO)

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JPI-HDHL National consultation workshop
MIUR - February 24, 2012

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2004

www.nugo.org

2012

2004-10 EU-funded Network of Excellence "The European Nutrigenomics Organisation: linking genomics, nutrition and health research"

Aims:

- Train European scientists to use post-genomic technologies in nutrition research
- Develop and integrate genomic technologies for the benefit of European nutritional science
- Facilitate the application of these technologies in nutritional research world-wide
- Create the world-leading virtual centre of excellence in nutrigenomics

Presently an Association of Member Institutions from EU and non-EU countries

Nutritional effects on health are subtle and multi-factorial

Nutrients usually do not have acute effects on health

Several confounders (genetics, metabolic flexibility, hormonal effects, food intake, physical activity, inaccurate “phenotypic descriptions)

Inter-individual variation in biomarker values is often larger than the effect related to the intervention

how can we quantify the exposure –> status -> health effect relationship?

COMPLEXITY

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Systems biology approaches

Parallel analysis of mRNA, proteins & metabolites from complex samples

Identification of “Biomarker profiles” of disease

Translation of co-variant sets of mRNA, proteins and metabolites (biomarker profiles) into disease pathways and systems knowledge

Nutrition can exert effects exclusively at early disease onset, prognostic biomarkers are therefore essential

Phase 1 NuGO activities

To elucidate pathways essential for definition of -omic biomarker profiles of health/disease

Develop Standardized Operating Procedures (SOPs)

Genotype

Food intake

-omics analysis

Develop Infrastructures (technological/food/health)

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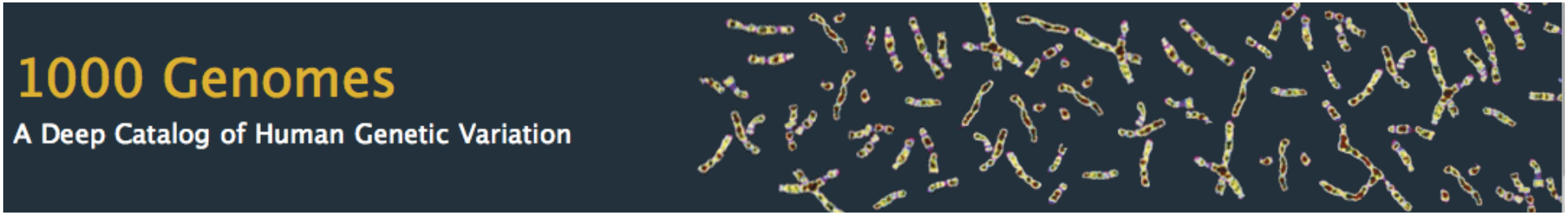
Human genetic variation
Genotype-phenotype translation?

Hap Map Project released 3 million SNPs (0.1 % Human Genome)

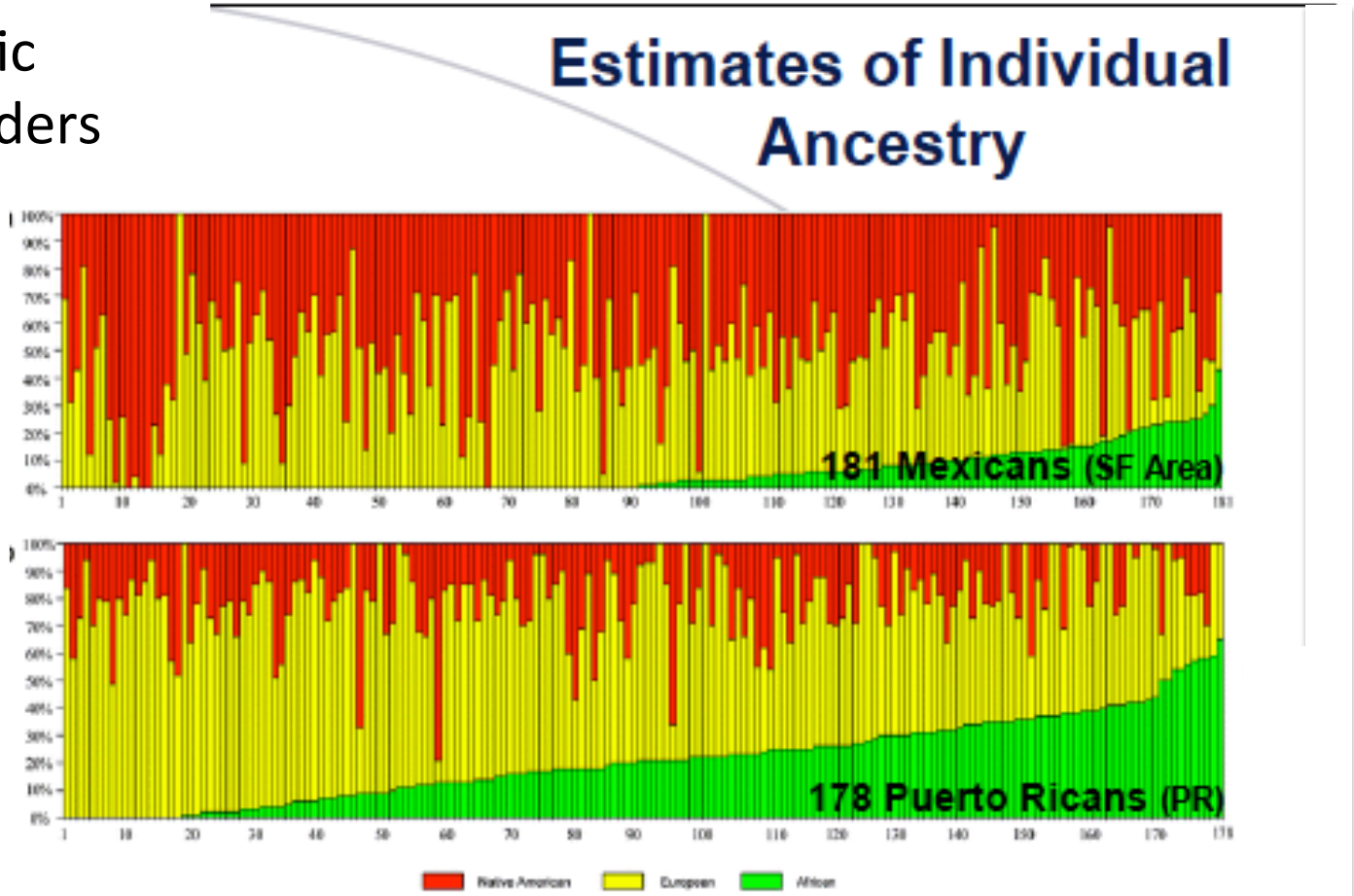
Nature 473, 1241 – Oct 27, 2005

1000 Genomes Pilot Project released 15 million SNP (≈ 50% non-synonymous). Each individual: 250-300 loss-of-function variants in annotated genes, 50-100 variants previously implicated in inherited disorders
Estimated rate of *de novo* germline base substitution mutations: approximately 1028/bp/generation

Nature 467, 1061 – Oct 28, 2010



Genetic Confounders



Choudhry S et al. Human Genetics. 2006

Stratification before or after intervention?

Healthy subjects: remarkable capacity to maintain homeostasis (metabolic regulation, metabolic compensation of unhealthy dietary input, defence and repair mechanisms in oxidative and inflammatory stress)

Processes involved in homeostasis ≠ processes involved in early onset of diet-related diseases

Targeting the step of homeostatic response should allow to identify biomarker profiles of health/disease states that are not significantly affected by genetic variation.

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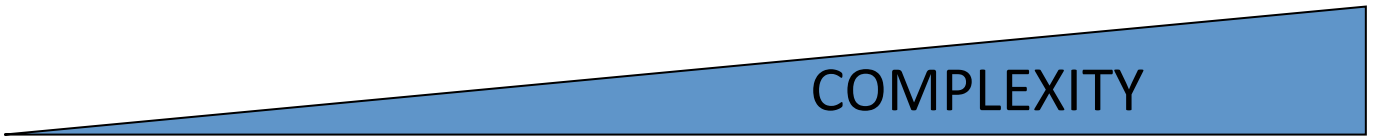
Phase 2 NuGO activities

New generation of biomarkers resulting from multidisciplinary (systems biology) approaches

Inclusion of “extensive phenotyping” in mechanistic research, intervention studies and observational cohorts

Better understanding and exploitation of personalized aspects

These developments need an infrastructural sustainment Food & Health RI



Research Labs

Research Networks

NUTRITIONAL PHENOTYPE DATABASE

Genes Nutr (2010) 5:189–203
DOI 10.1007/s12263-010-0167-9

REVIEW

Challenges of molecular nutrition research 6: the nutritional phenotype database to store, share and evaluate nutritional systems biology studies

Ben van Ommen · Jildau Bouwman · Lars O. Dragsted · Christian A. Drevon · Ruan Elliott · Philip de Groot · Jim Kaput · John C. Mathers · Michael Müller · Fre Pepping · Jahn Saito · Augustin Scalbert · Marijana Radonjic · Philippe Rocca-Serra · Anthony Travis · Suzan Wopereis · Chris T. Evelo

Genes Nutr (2011) 6:81–87
DOI 10.1007/s12263-010-0190-x

ORIGINAL PAPER

Answering biological questions: querying a systems biology database for nutrigenomics

Chris T. Evelo · Kees van Bochove · Jahn-Takeshi Saito

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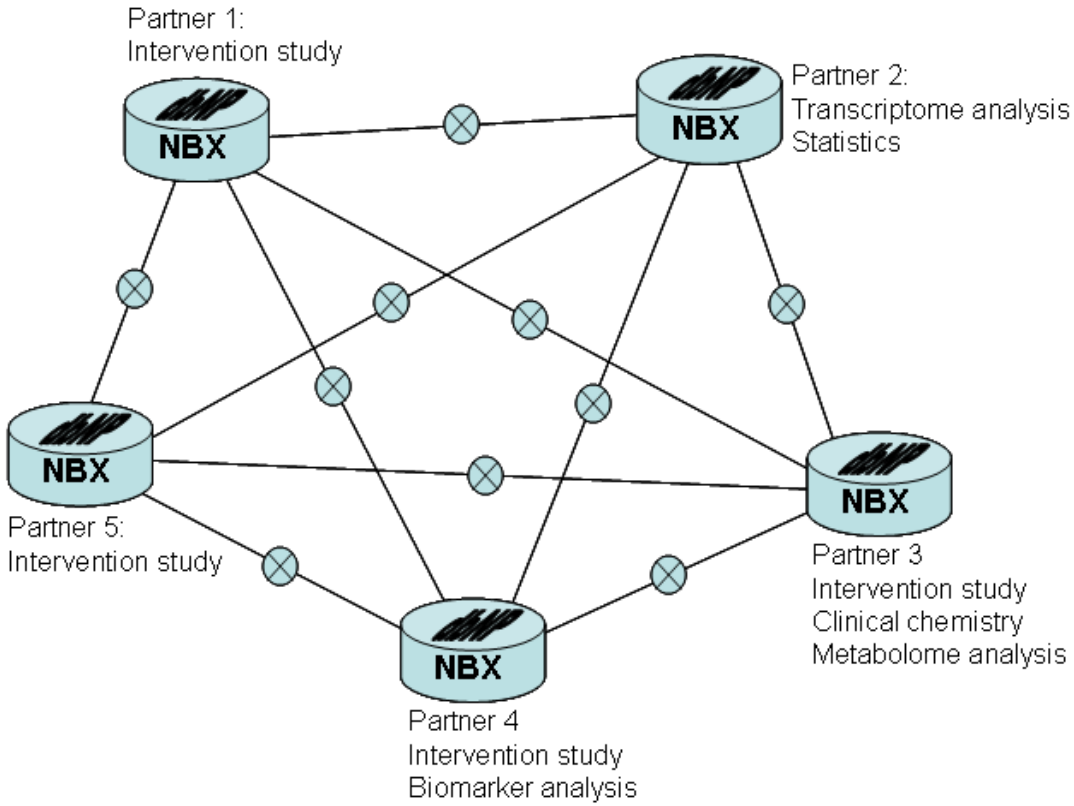
The Data-Grid

The research infrastructure side of NuGO develops into a bridge between generic infrastructure (NCBI, EBI) and the nutrition research community



van Ommen et al (2010) Genes Nutr 5,189–203

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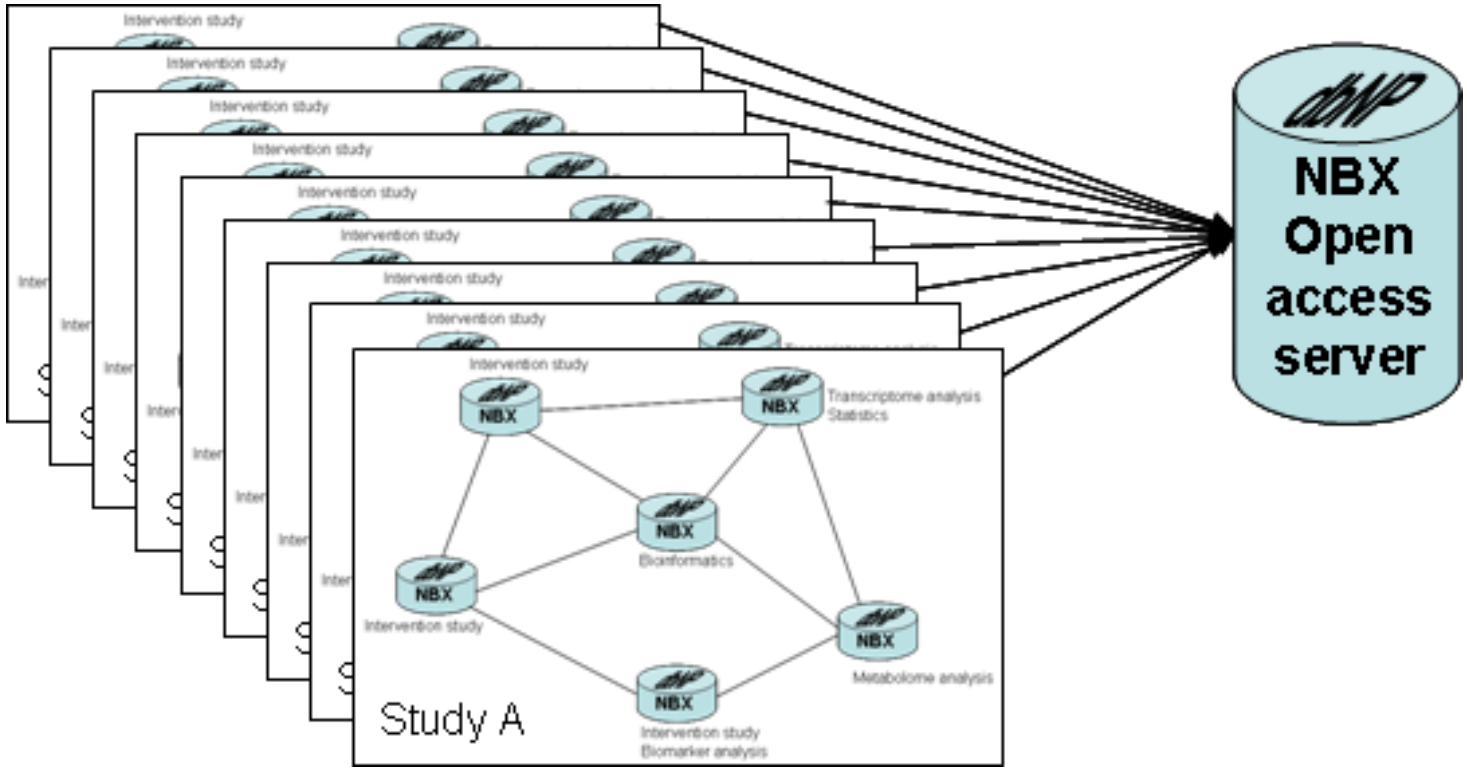
Integration of data grids



Genotype
Food intake
Biomarker profile
-omics analysis
Modelling

van Ommen et al (2010)
Genes Nutr 5,189–203

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MICRONUTRIENT GENOMICS PROJECT

MICRONUTRIENT GENOMICS PROJECT

Genes Nutr (2010) 5:285–296
DOI 10.1007/s12263-010-0192-8

REVIEW

The Micronutrient Genomics Project: a community-driven knowledge base for micronutrient research

Ben van Ommen · Ahmed El-Sohemy · John Hesketh · Jim Kaput · Michael Fenech · Chris T. Evelo · Harry J. McArdle · Jildau Bouwman · Georg Lietz · John C. Mathers · Sue Fairweather-Tait · Henk van Kranen · Ruan Elliott · Suzan Wopereis · Lynnette R. Ferguson · Catherine Méplan · Giuditta Perozzi · Lindsay Allen · Damariz Rivero · The Micronutrient Genomics Project Working Group

THE HUMAN VARIOME PROJECT

International Consortium Global initiative to collect, curate and share data on human genetic variation affecting human disease

Genes Nutr (2010) 5:275–283
DOI 10.1007/s12263-010-0186-6

COMMENTARY

Connecting the Human Variome Project to nutrigenomics

Jim Kaput · Chris T. Evelo · Giuditta Perozzi · Ben van Ommen · Richard Cotton

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MICRONUTRIENT GENOMICS PROJECT

- Micronutrients are essential regulators of metabolic and physiological processes in humans
- Complex, often overlapping biological actions
- Micronutrient deficiencies cause specific metabolic dysfunctions
- Increasing evidence that sub-optimal intakes may contribute to the development and severity of chronic diseases.
- High micronutrient doses (i.e. supplements intake) often lead to toxicity

Re-assessment of dietary requirements and upper safety limits for micronutrients is ongoing worldwide in the context of public health nutrition, especially for specific subgroups (elderly, children, pregnant women).

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MICRONUTRIENT GENOMICS PROJECT

- Molecular studies have accumulated a wealth of data on gene/protein-micronutrient interactions
- Systems biology and genomics technologies (-omic approaches) allow to assess the effects of specific micronutrients on multiple metabolic pathways, including interactions with other nutrients.
- Genetic variations affecting such interactions partly known but health impact difficult to assess
- Information often disconnected/heterogeneous

Difficult translation into biomarkers/safe limits

MICRONUTRIENT GENOMICS PROJECT

Challenge of the Micronutrient Genomics Project (MGP):

•To catalogue the inventory of all relevant gene-micronutrient interactions and map the inter-related pathways

•To determine the genetic markers that affect and predict responsiveness to micronutrients

A biological network for each micronutrient, allowing to:

•visualize all transcriptome, proteome, metabolome changes observed in plasma, cells and tissues (in vivo, in vitro, models);

•access all relevant genetic variations

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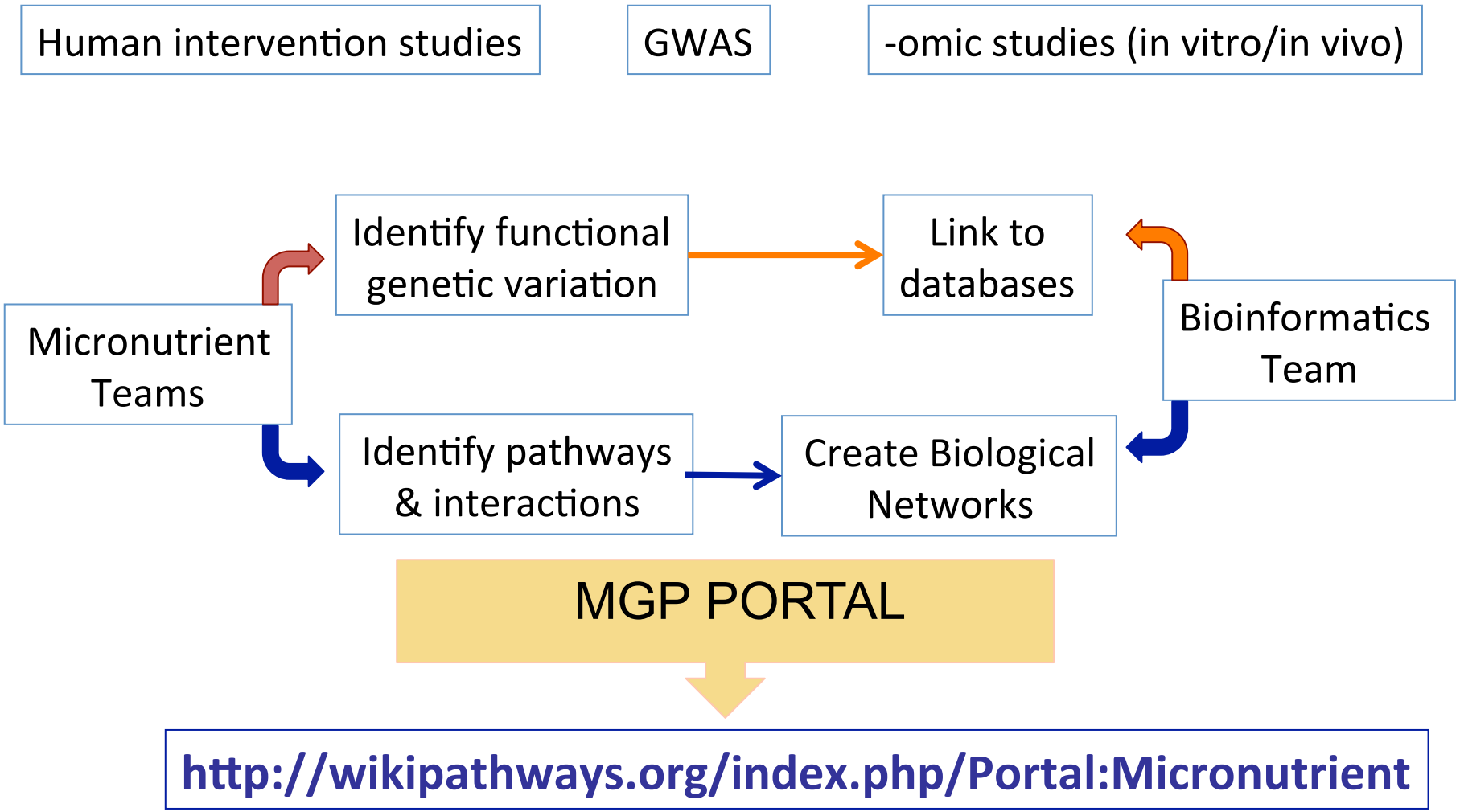
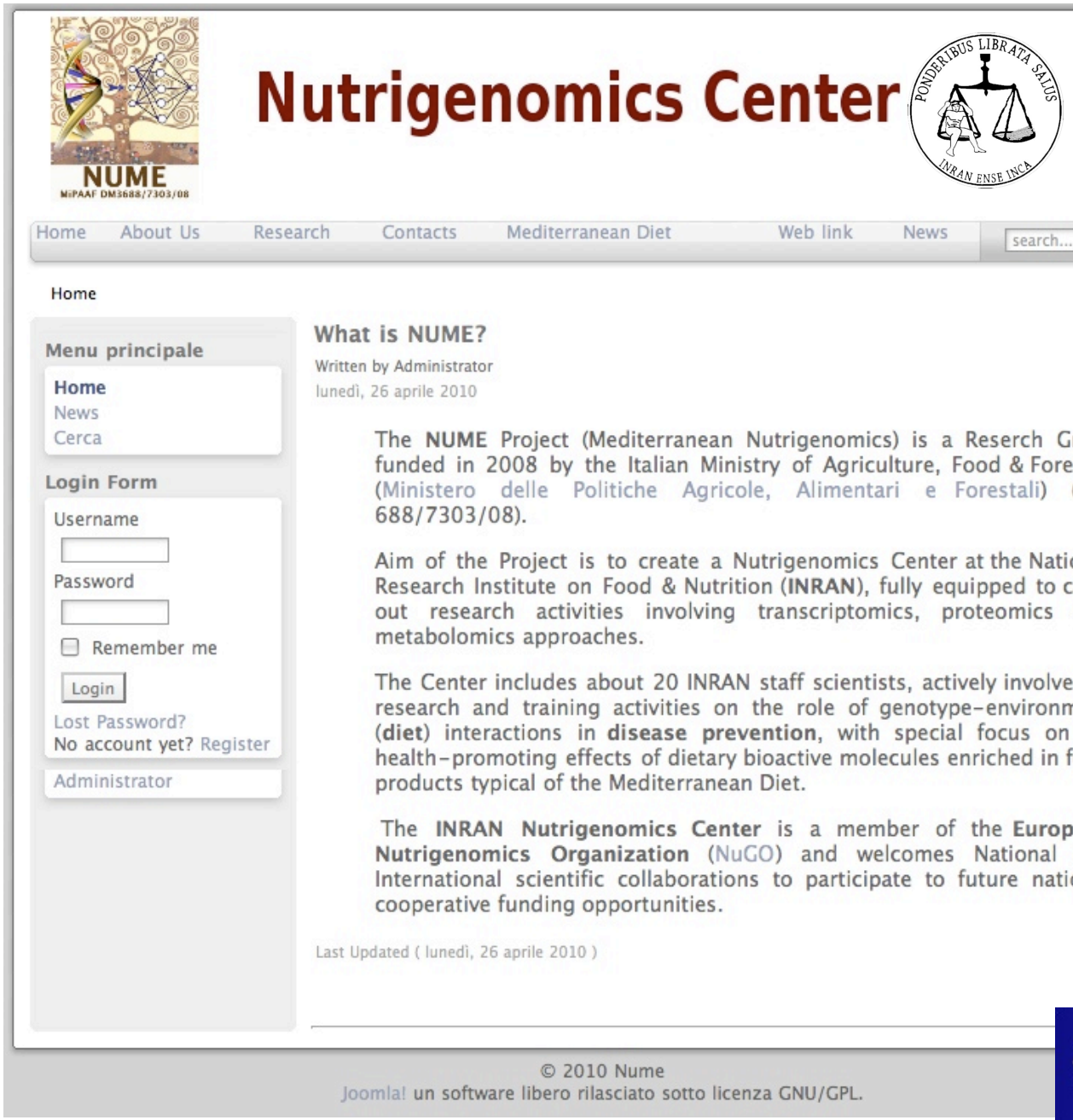
MICRONUTRIENT GENOMICS PROJECT

Initial MGP RoadMap

(Van Ommen et al, Genes Nutr 2010)

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No account yet? Register
Administrator
What is NUME?
Written by Administrator
lunedì, 26 aprile 2010
The NUME Project (Mediterranean Nutrigenomics) is a Reserch Grant funded in 2008 by the Italian Ministry of Agriculture, Food & Forestry (Ministero delle Politiche Agricole, Alimentari e Forestali) (DM 688/7303/08).
Aim of the Project is to create a Nutrigenomics Center at the National Research Institute on Food & Nutrition (INRAN), fully equipped to carry out research activities involving transcriptomics, proteomics and metabolomics approaches.
The Center includes about 20 INRAN staff scientists, actively involved in research and training activities on the role of genotype-environment (diet) interactions in disease prevention, with special focus on the health-promoting effects of dietary bioactive molecules enriched in food products typical of the Mediterranean Diet.
The INRAN Nutrigenomics Center is a member of the European Nutrigenomics Organization (NuGO) and welcomes National and International scientific collaborations to participate to future national cooperative funding opportunities.
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