

Gene Prioritization Strategies

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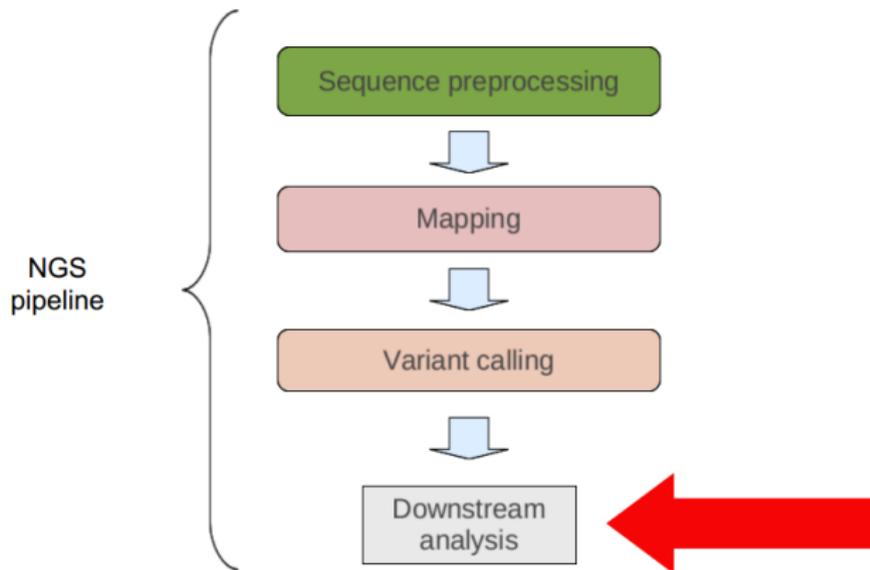
Valencia, July 2012



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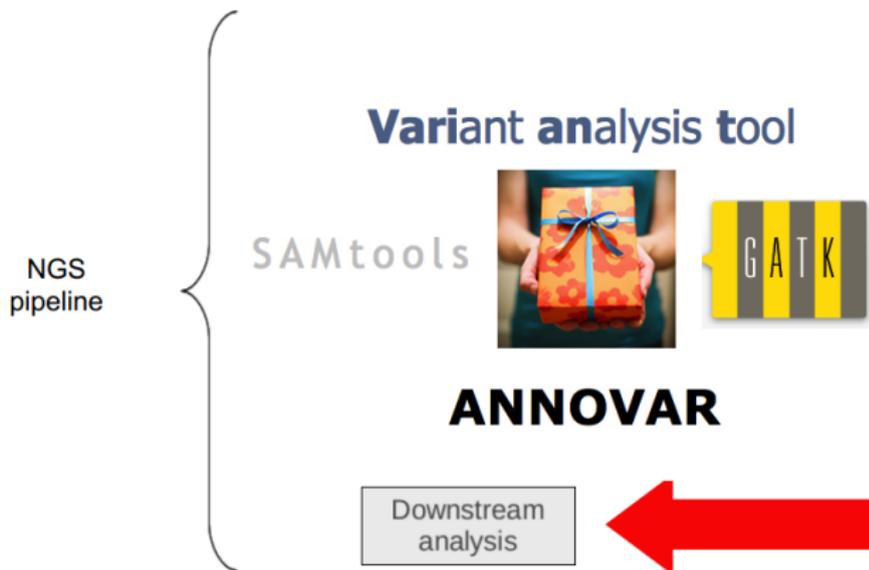
ROADMAP

OBJECTIVE: To find the variants associated to the phenotype under study



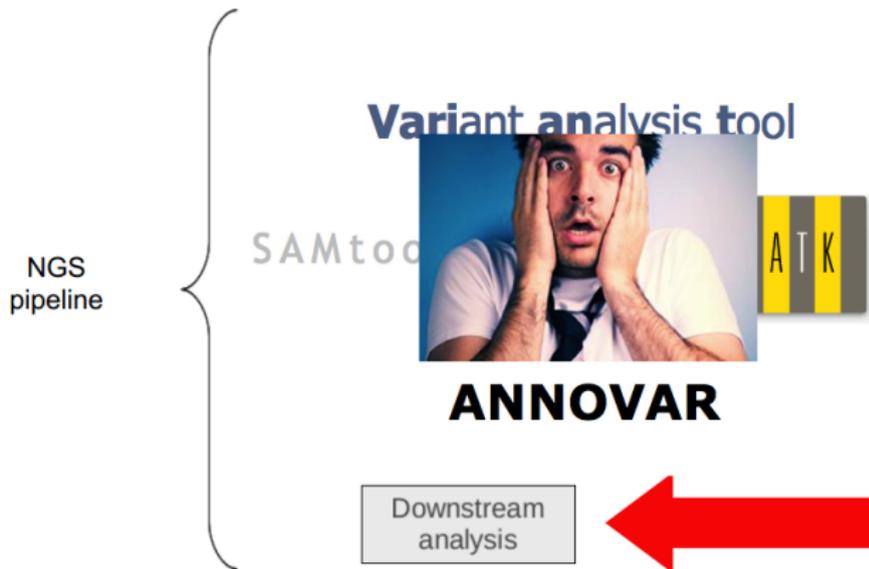
ROADMAP

OBJECTIVE: To find the variants associated to the phenotype under study



ROADMAP

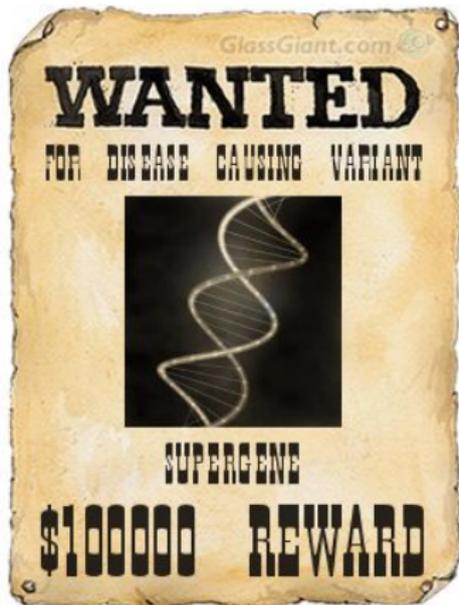
PROBLEM: Large number of candidates



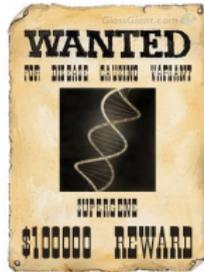
The candidate gene lists generated contain hundreds of genes among which only one or a few are of interest

PROBLEM: Large number of candidate genes/variants

An end has a start ...

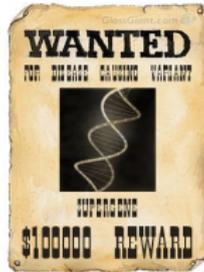


PROBLEM: Large number of candidate genes/variants



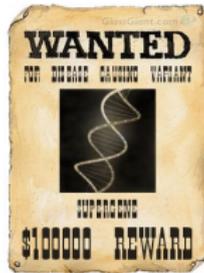
- The experimental validation of every candidate

PROBLEM: Large number of candidate genes/variants



- The experimental validation of every candidate
- **BUT** it is expensive and time consuming.

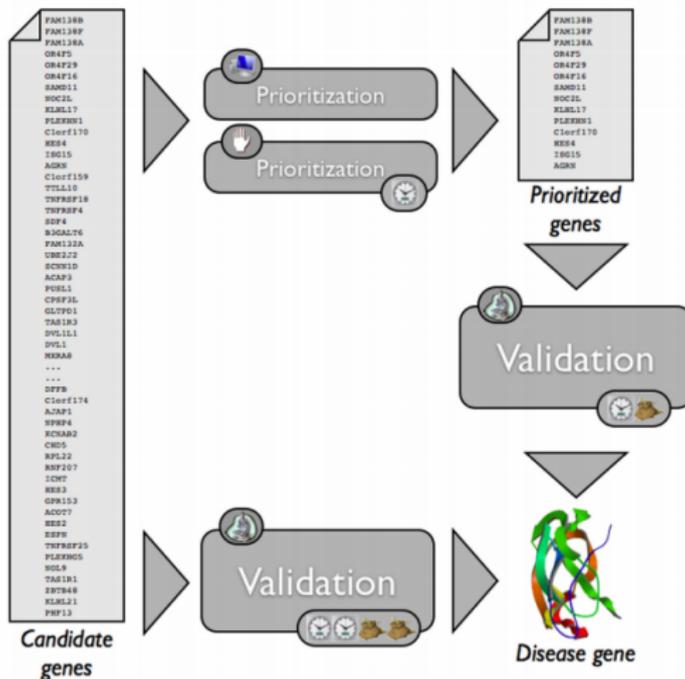
PROBLEM: Large number of candidate genes/variants



- The experimental validation of every candidate
- **BUT** it is expensive and time consuming.
- It is needed to prioritize the candidate genes using a computational approach at almost no cost and to experimentally validate only these genes.

PRIORITIZATION

The identification of **the most promising** genes among a list of candidate genes.



PRIORITIZATION

What would we expect?

Number of genes implicated

- 1 Mendelian or complex disease?
- 2 Rare alleles or multiple common variants?
- 3 Family-specific variant?
- 4 High or small effect (penetrance)?

Biological profile

- 1 Is any biological process known to be implicated?
- 2 There are known disease-associated genes?

IMPORTANT Different methods, different hypothesis tested!

Looking for ONE gene ...

ENDEAVOUR: based on how similar a candidate gene is to a profile derived from genes already known to be involved in the processes

<http://homes.esat.kuleuven.be/~bioiuser/endeavour/tool/endeavourweb.php>

Pros

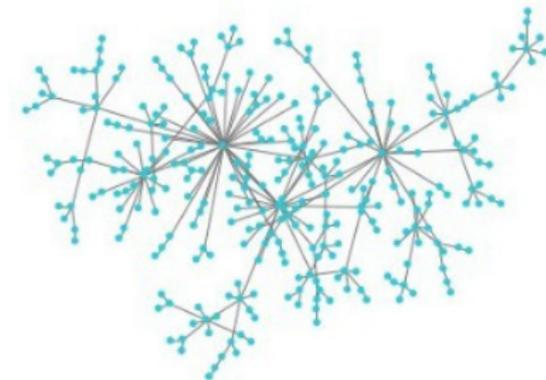
- Easy to use
- Several biological databases screened

Cons

- Reference genes needed
- Does not take into account the cell complexity
- Does not take into account collective effects of candidate genes
- The genes more annotated are more likely to have a good score

Why protein networks?

- Disease-associated variants occur more frequently in protein-coding regions than expected
- The integration of the whole set of protein interactions provides detailed map (network) about the pathways and molecular complexes and brings a safe place to work with.
- Non-random placement of disease-causing genes in the network
- A network-neighbour of a disease-causing gene is likely to cause a related phenotype



NetworkPrioritizer: based on network location similarity of candidate gene with respect to reference genes.

Pros

- Takes into account the whole cell complexity
- Several biological databases screened

Cons

- Reference genes needed
- Does not take into account collective effects between candidate genes
- The biological processes understudied are less likely to be well prioritized

Looking for SEVERAL genes ...

NetworkMiner: based on subnetwork aggregation between the candidate genes. Finds significant subnetworks of protein-protein interactions within a list of ranked genes/proteins

<http://babelomics.bioinfo.cipf.es/functional.html>

Pros

- Takes into account the whole cell complexity
- Takes into account collective effects between candidate genes
- Does not need reference genes, but they are allowed

Cons

- The biological processes understudied are less likely to be well prioritized
- Valid for complex phenotypes where several genes are expected to be associated

jFamNet: Some human diseases are known to cluster in families. That is, we can expect each family has a different affected gene but located in the network neighborhood.

Pros

- Takes into account the whole cell complexity
- Takes into account collective effects between candidate genes
- Does not need reference genes, but they are allowed

Cons

- Several families needed
- The biological processes understudied are less likely to be well prioritized

- ① Refine the previous methods
- ② Moving to a high resolution map of the cell able to work with variant level
- ③ Including genome and transcriptome regulation network
- ④ Develop new methodologies able to test new hypothesis

