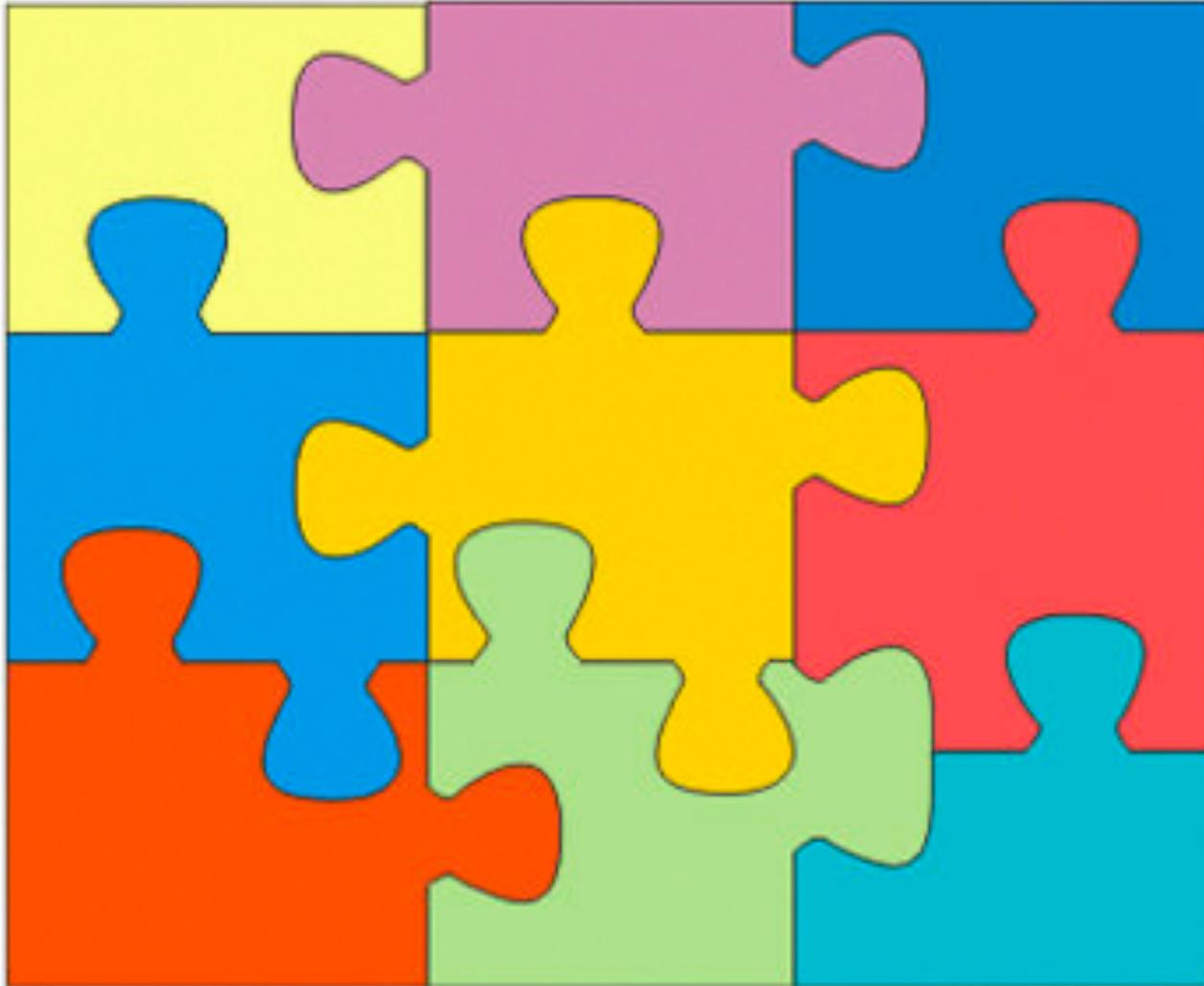


From Proteomics to Systems Biology



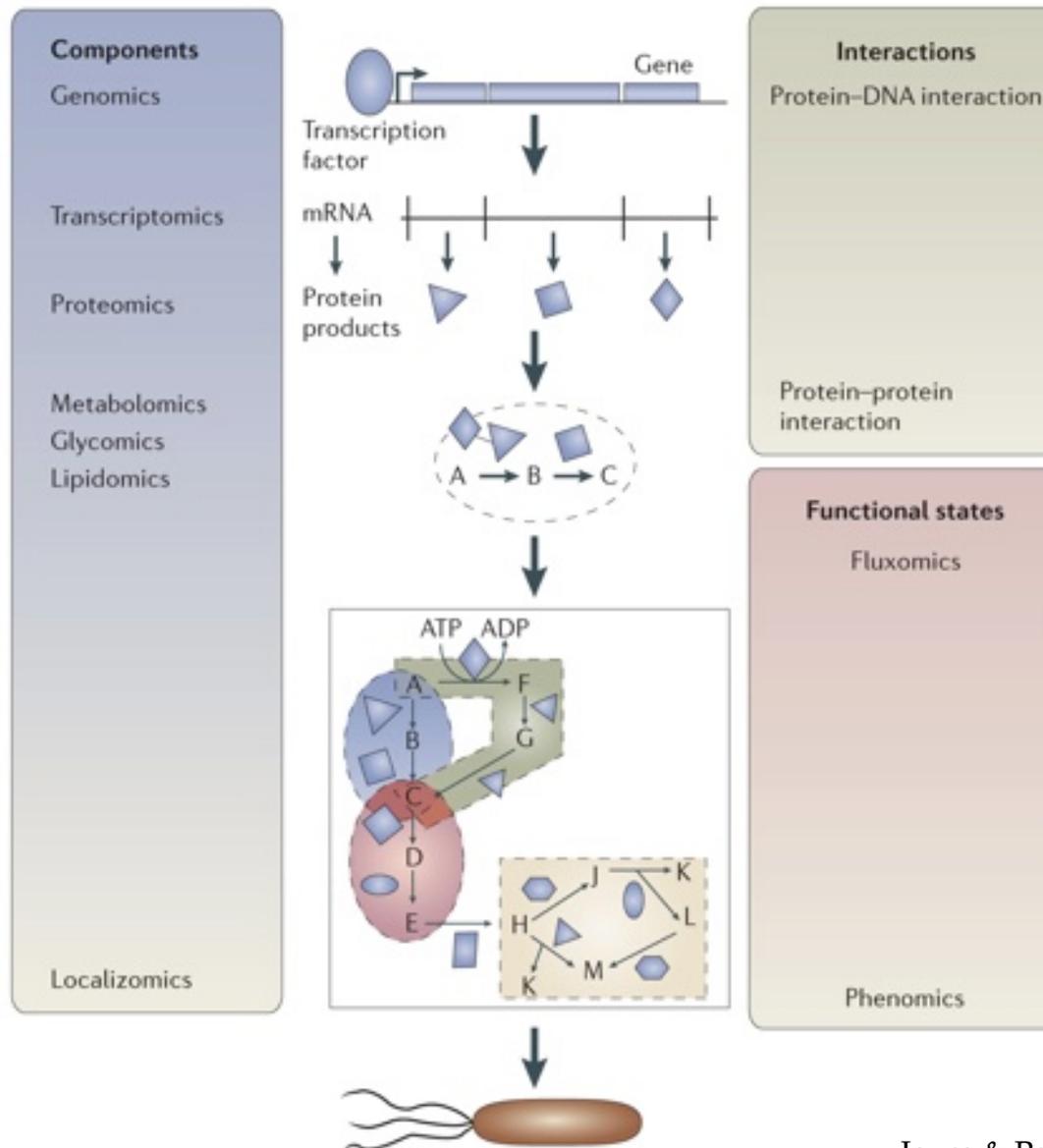
Integration of “omics”- information

Outline and learning objectives

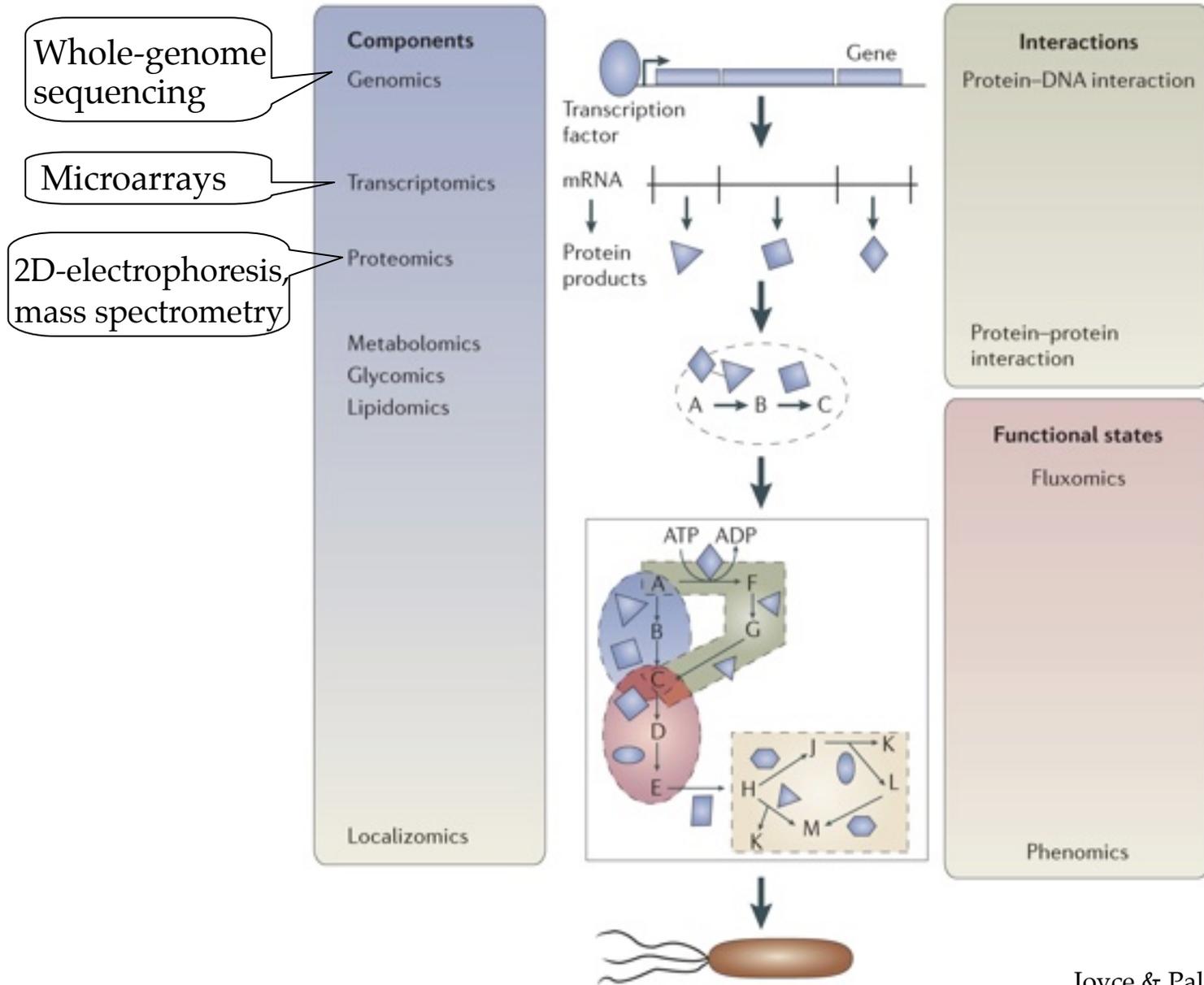
“Omics” science provides global analysis tools to study entire systems

- How to obtain omics - data
- What can we learn? Limitations?
- Integration of omics - data
- In-class practice:
Omics-data visualization

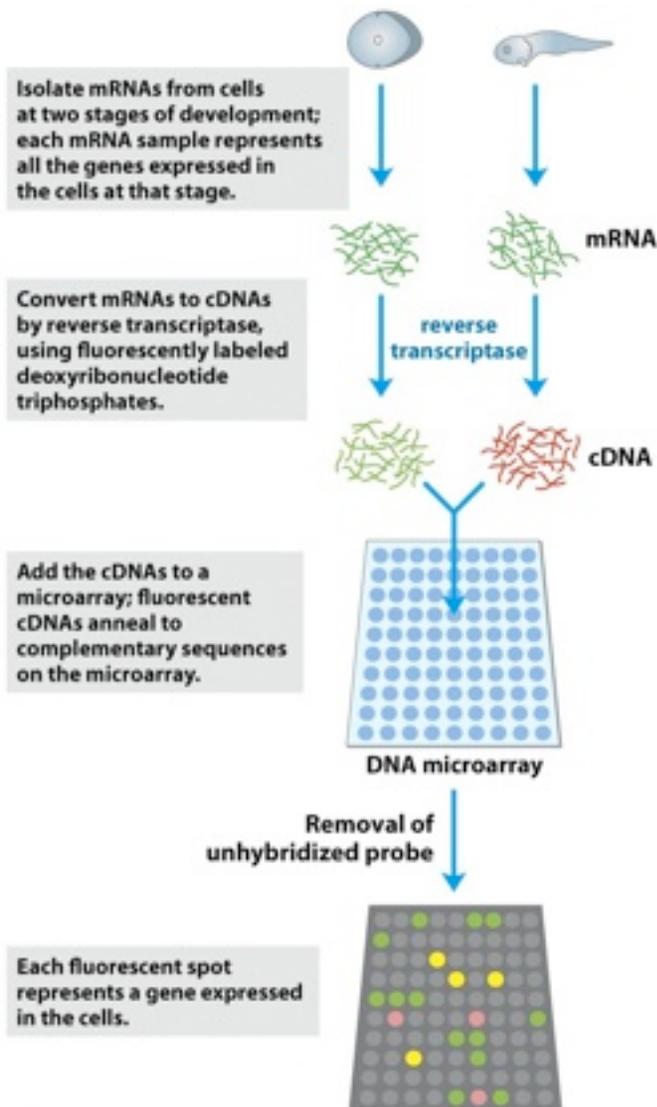
Omics - data provide systems-level information



Omics - data provide systems-level information



Transcriptomics (indirectly) tells about RNA-transcript abundances



⇒ primary genomic readout

Strengths:

- very good genome-wide coverage
- variety of commercial products

Drawback:

No protein-level info!!

-> RNA degradation

-> Post-translational modifications

⇒ validation by e.g. RT-PCR

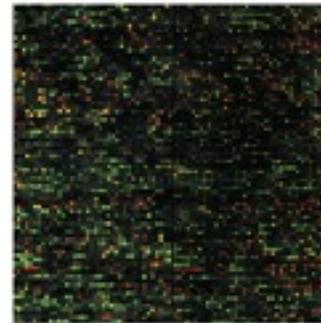
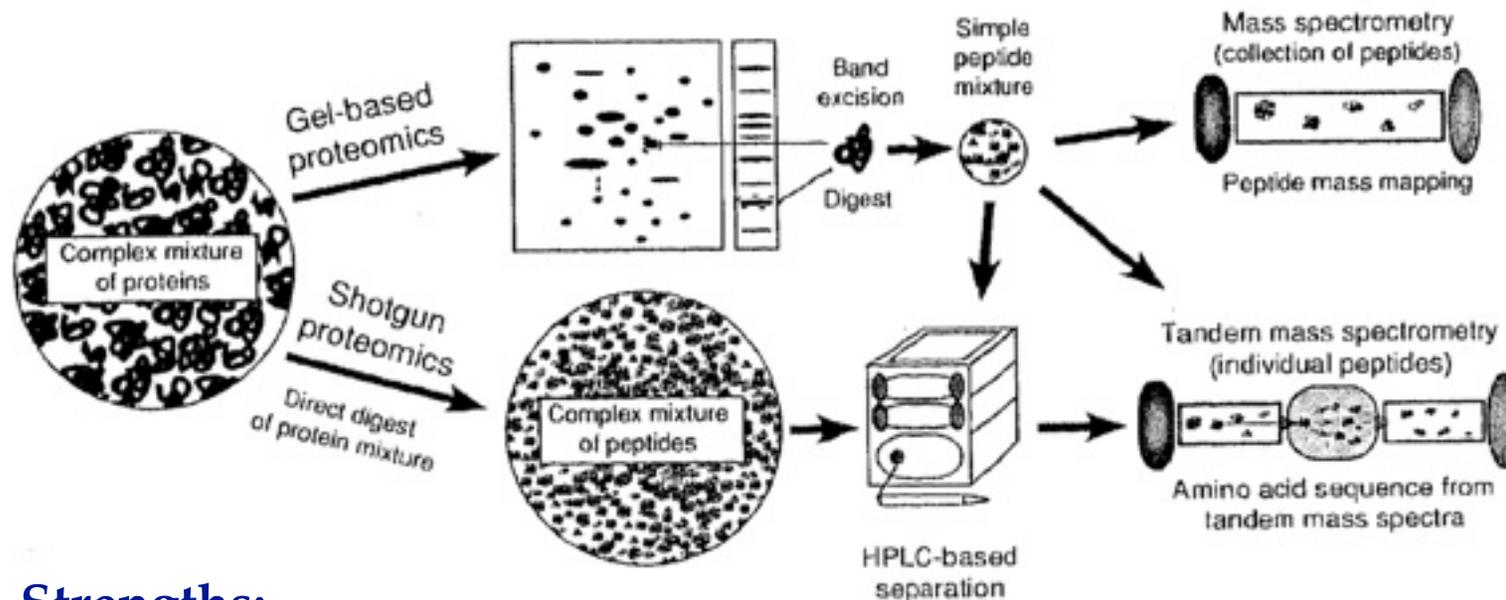


Figure 9-22

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Proteomics aims to detect and quantify a system's entire protein content



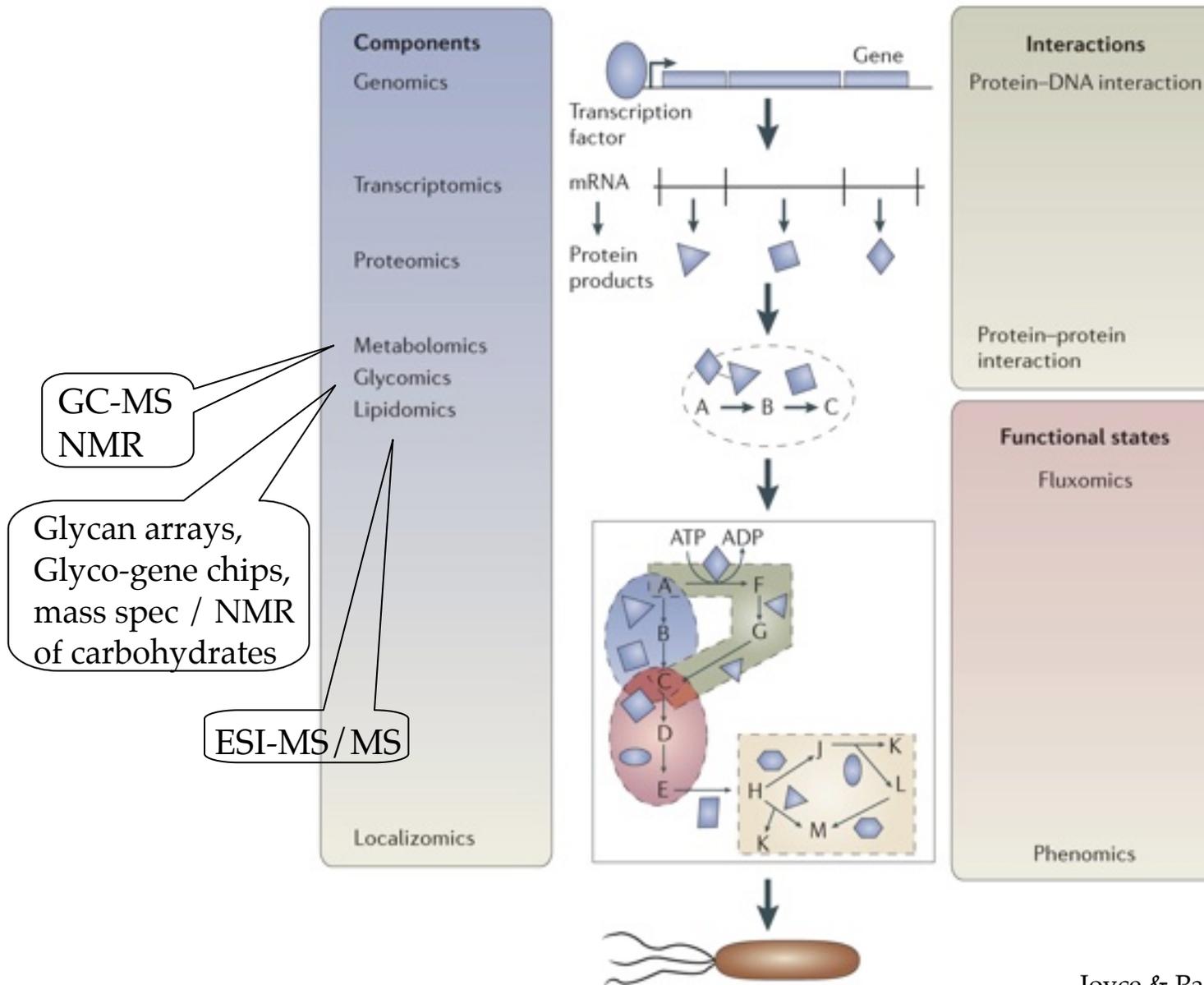
Strengths:

- > info about post-translational modifications
- > high throughput possible due to increasing quality and cycle speed of mass spec instrumentation

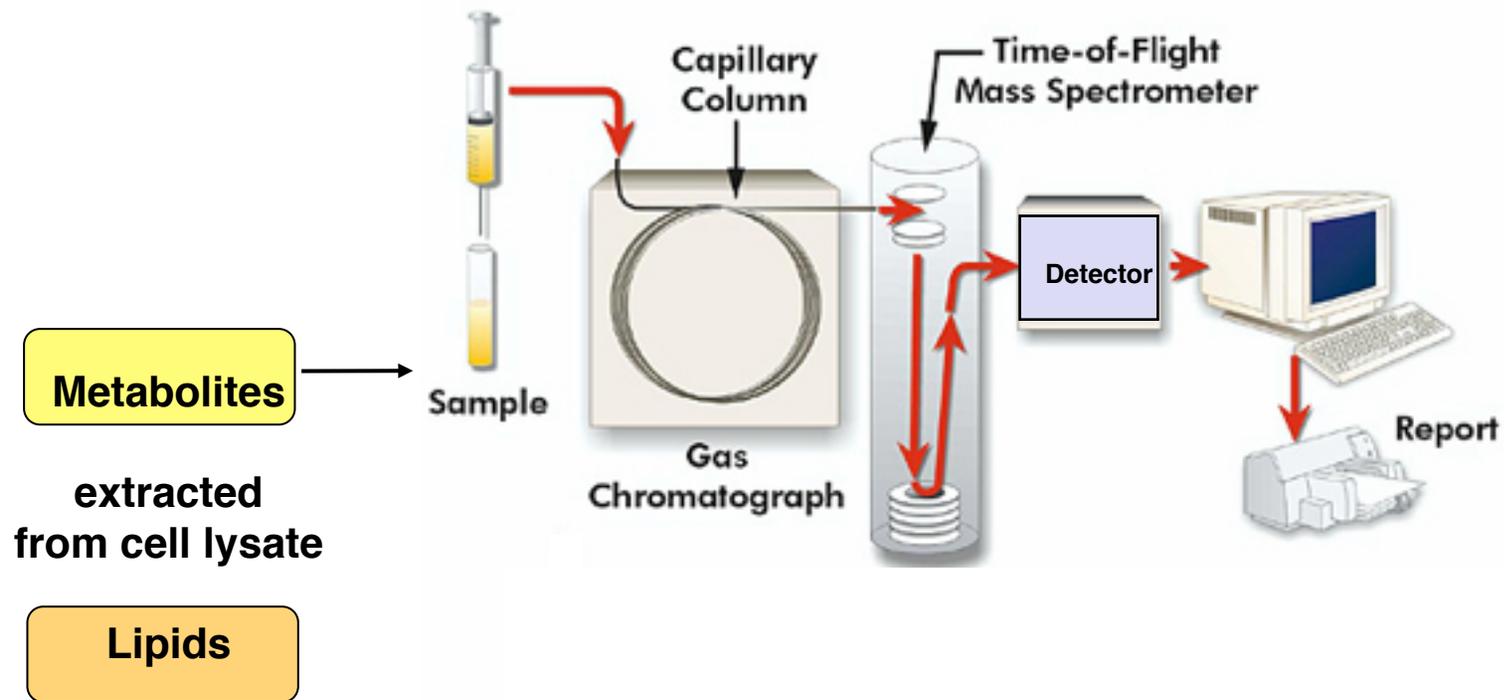
Limitations:

- coverage dependent on sample, preparation & separation method
- bias towards most highly abundant proteins

Omics - data provide systems-level information



Metabolomics and Lipidomics



Metabolomics and Lipidomics

Metabolomics:

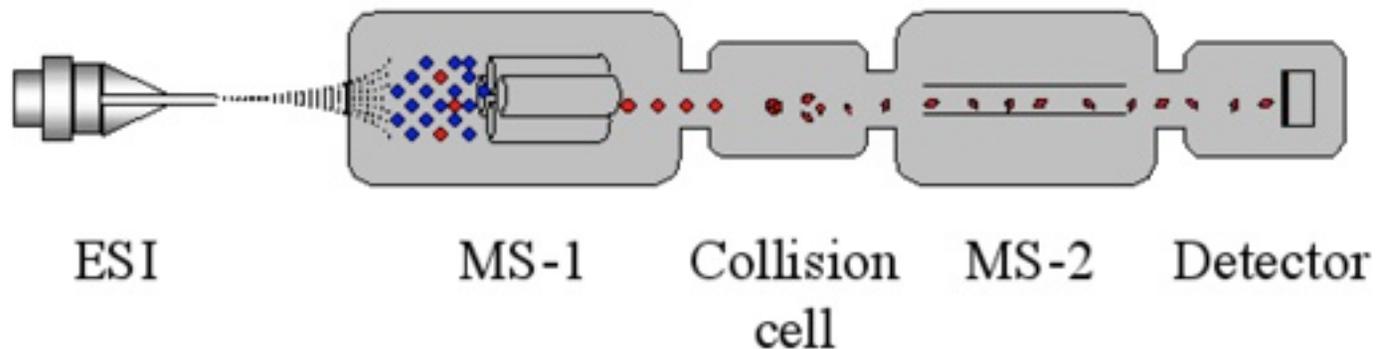
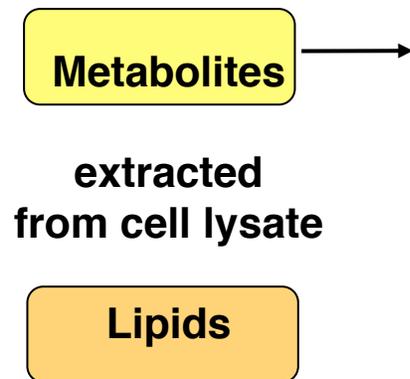
Large-scale measurement of cellular metabolites and their levels

-> combined with proteome:

functional readout of a cellular state

Limitations / challenges:

- often low reproducibility of sample preparations
- highly diverse set of metabolites
- large dynamic range



Metabolomics and Lipidomics

Metabolomics:

Large-scale measurement of cellular metabolites and their levels

-> combined with proteome:

functional readout of a cellular state

Limitations / challenges:

- often low reproducibility of sample preparations
- highly diverse set of metabolites
- large dynamic range

Lipidomics aim:

To identify & classify cellular inventory of lipids and lipid interacting factors

-> pathobiological impact

Limitations:

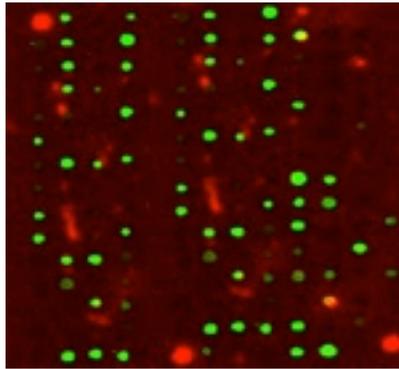
- low to medium throughput
- reproducibility difficult

Metabolites

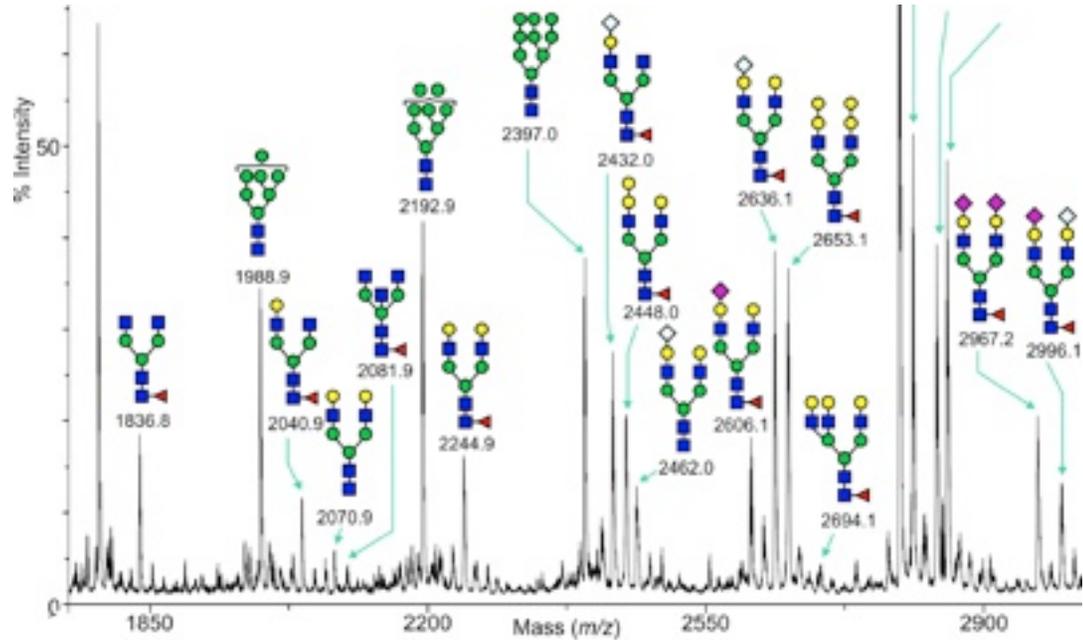
extracted
from cell lysate

Lipids

Glycomics identifies cellular glycan components and glycan-interacting factors



Glycan-array
-> glycan-recognition proteins

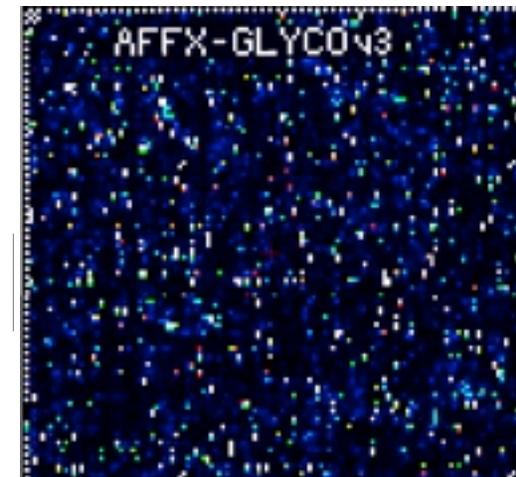


Impact:

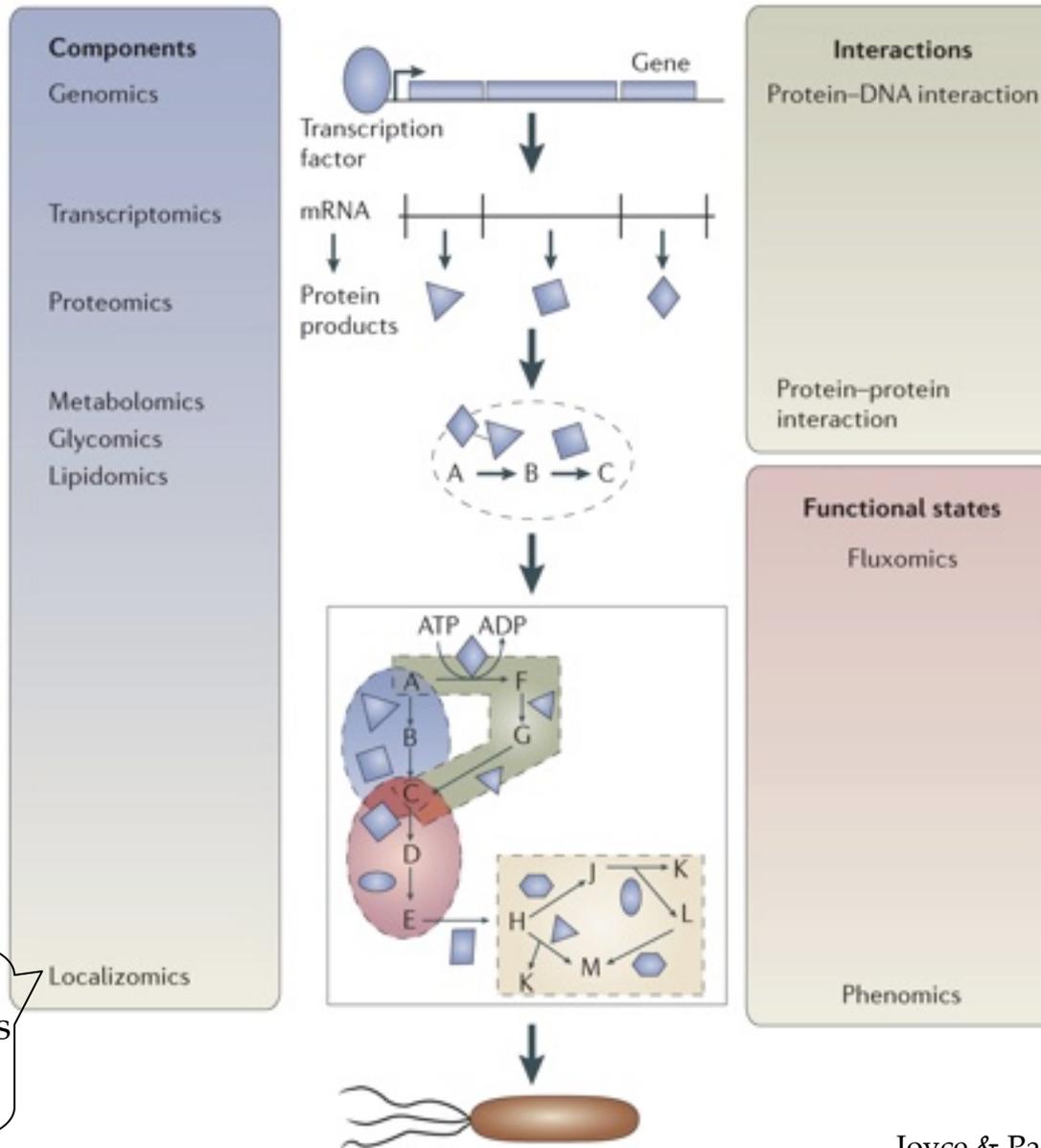
- antigen recognition
- cell adhesion
- cancer biology

Limitations:

Methods still under development



Omics - data provide systems-level information



In silico predictions,
organelle proteomics
histocytomics,

'Localizomics' tells about sub-cellular locations

Bioinformatics

TargetP

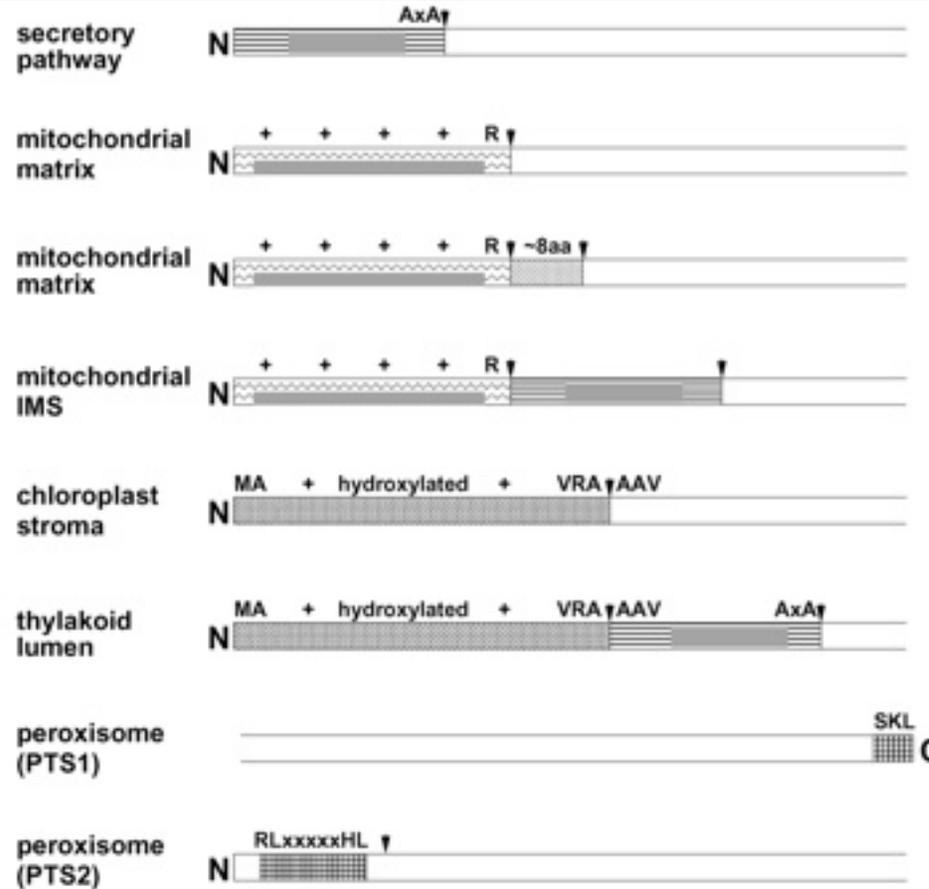
<http://www.cbs.dtu.dk/services/TargetP/>

PSORT

<http://www.psort.org/>

Expasy

-> Topology Prediction
<http://www.expasy.ch/tools/#proteome>



Eukaryotic protein sorting signals



'Localizomics' tells about sub-cellular locations

Bioinformatics

TargetP

<http://www.cbs.dtu.dk/services/TargetP/>

PSORT

<http://www.psort.org/>

Expasy

-> Topology Prediction
<http://www.expasy.ch/tools/#proteome>

Microscopy techniques

- > tagging (GFP)
- > antibody detection



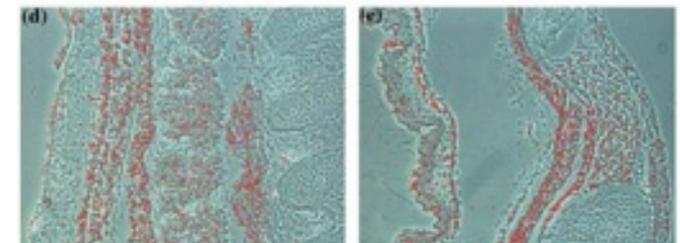
Spalding *et al.*, 2010

Organelle proteomics

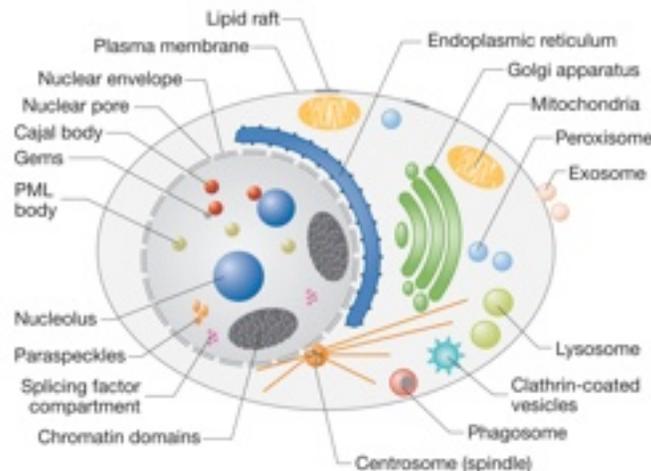
Preparation / digestion
-> 2DE & MS

Histocytomics

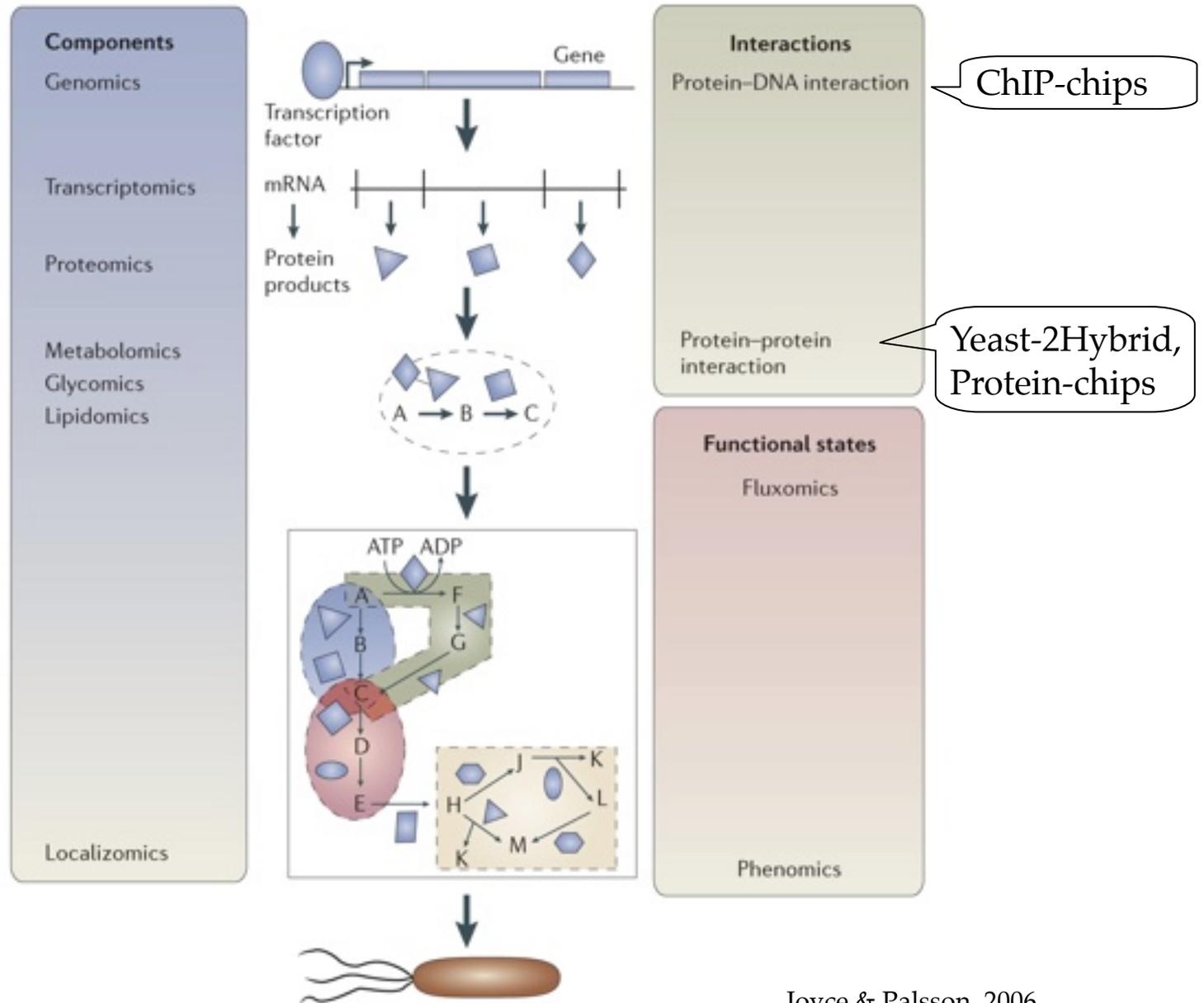
e.g. LSC (Laser Scanning Cytometry)
or LES (Layered Expression Screening)



Coulton, 2004



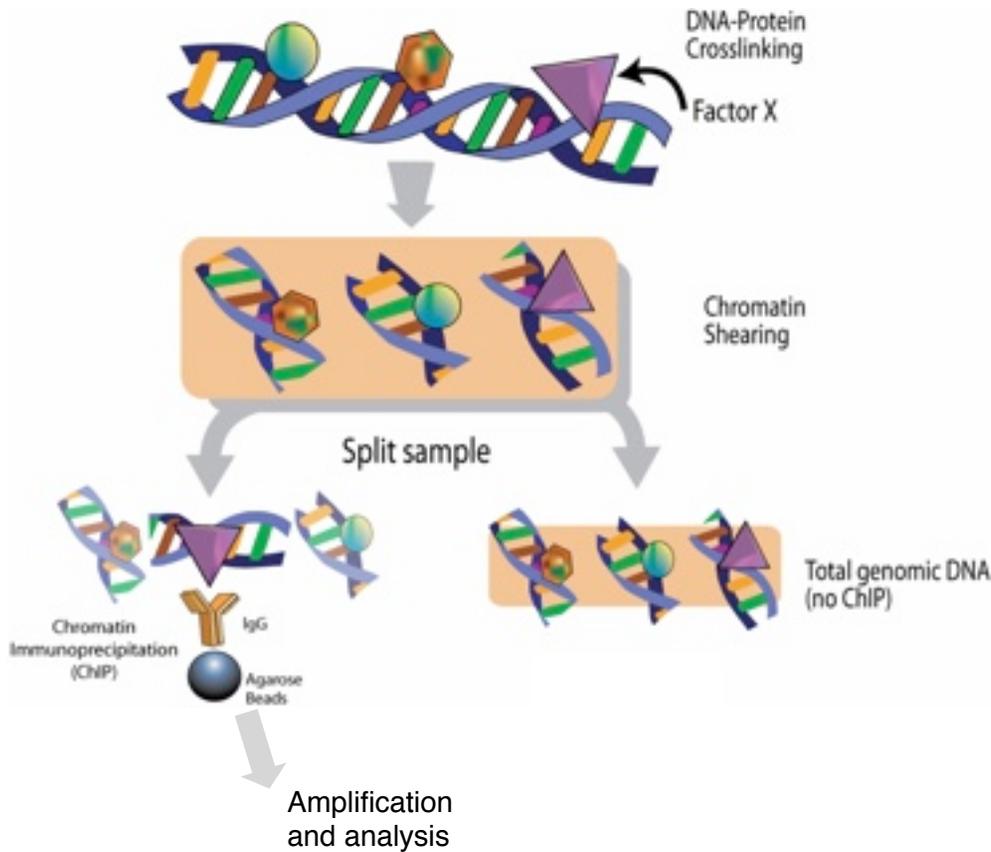
Omics - data provide systems-level information



Interactomics

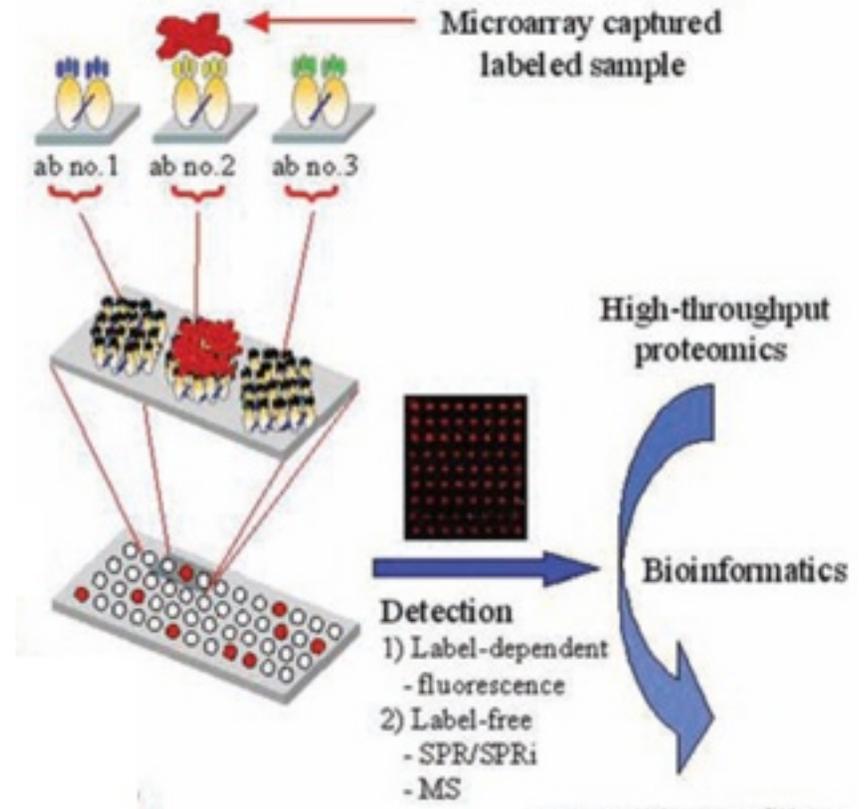
Protein-DNA interactions

-> e.g. ChIP on chips



Protein-Protein interactions

-> e.g. Antibody-based protein arrays



Interactomics

Protein-Protein interactions

-> Yeast two-hybrid screens

All interactomics data need to be validated!!!
=> often false positives!!!

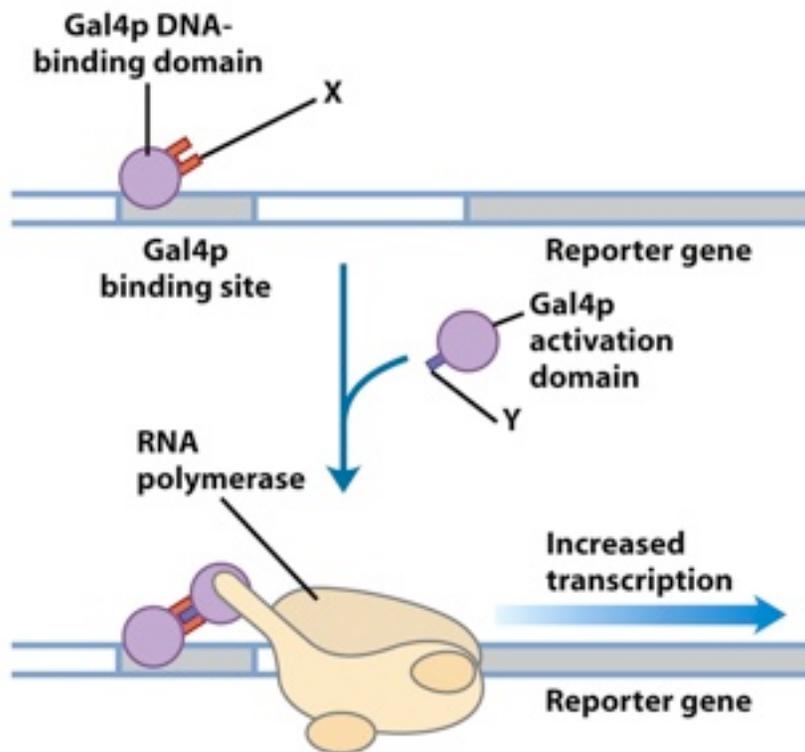


Figure 9-25a
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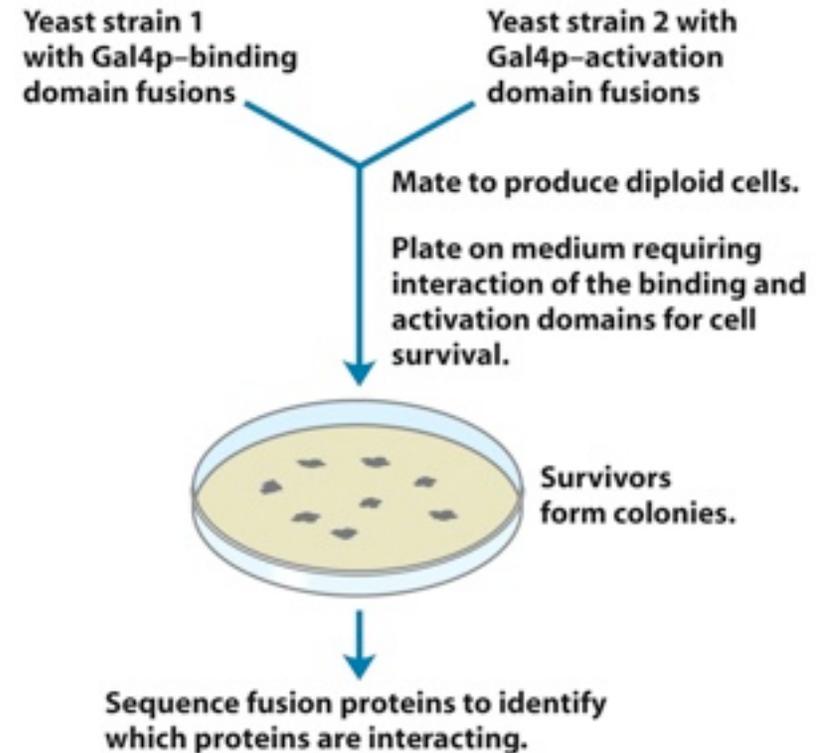
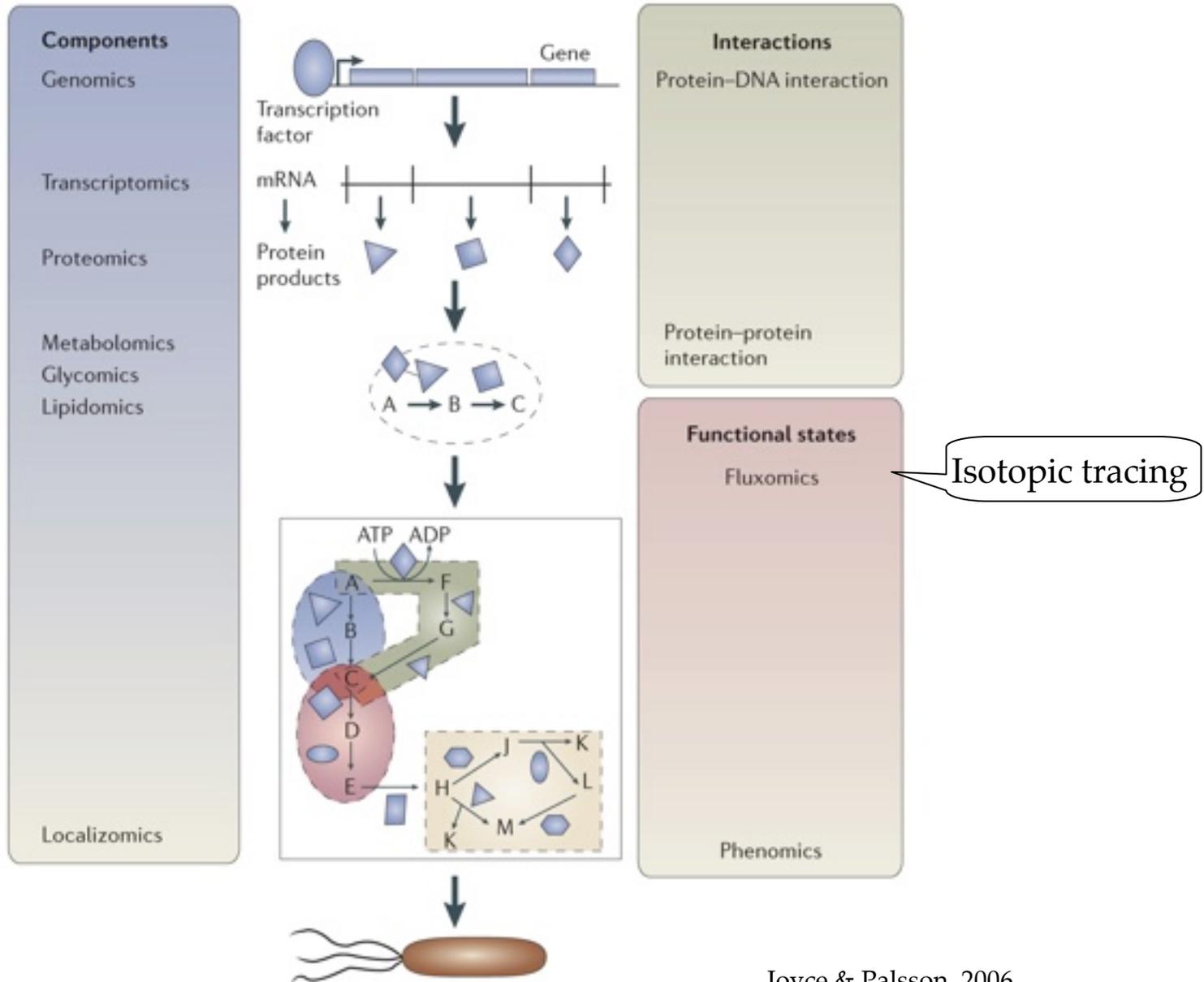


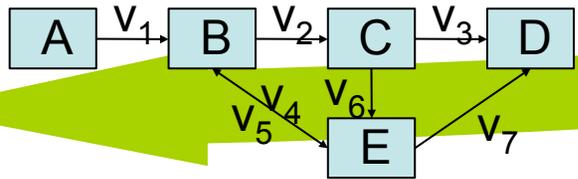
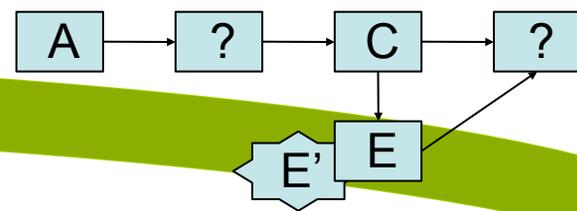
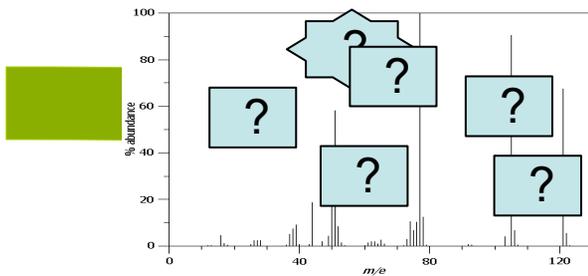
Figure 9-25b
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Omics - data provide systems-level information



Fluxomics looks at global and dynamic changes of metabolite levels over time

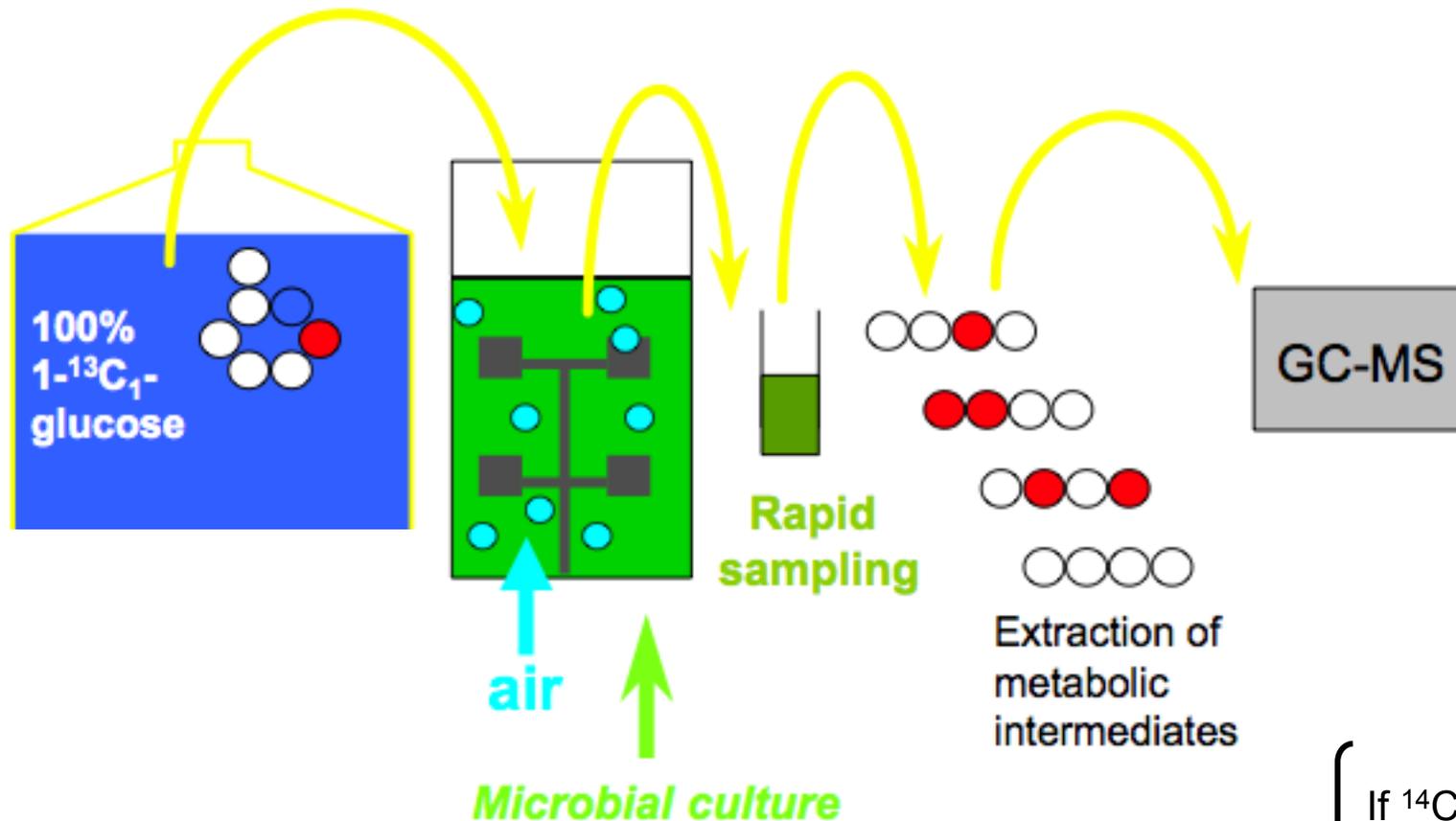
metabolite identification



metabolic flux analysis

pathway reconstruction
-> integration of omics-data
from other sources

Fluxomics looks at global and dynamic changes of metabolite levels over time



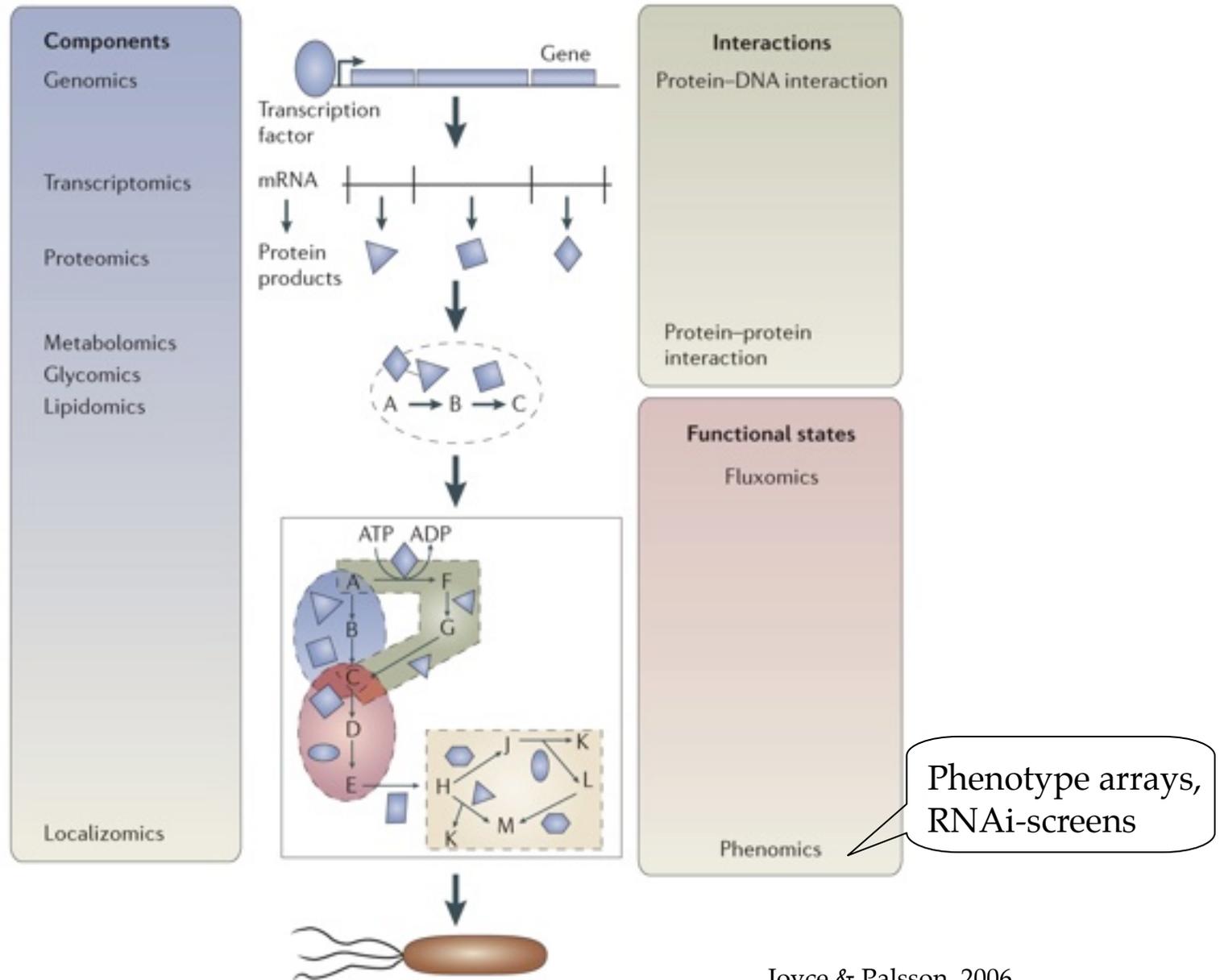
But:

Method suffers from same shortcomings as metabolomics:

- > sample prep reproducibility
- > wide variety of metabolites
- > large dynamic range

If ¹⁴C-label:
scintillation
counting

Omics - data provide systems-level information

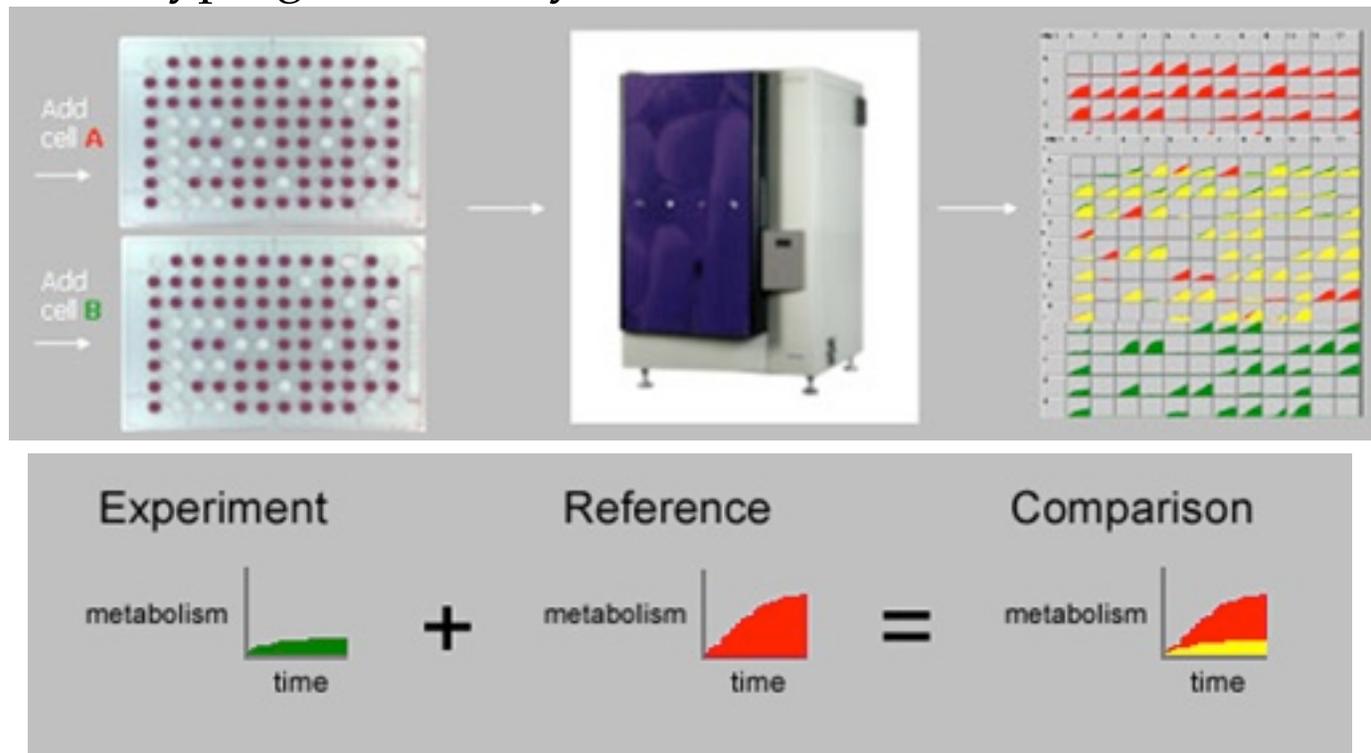


Phenomics

High-throughput approaches to determine cellular fitness or viability in response to genetic / environmental manipulation

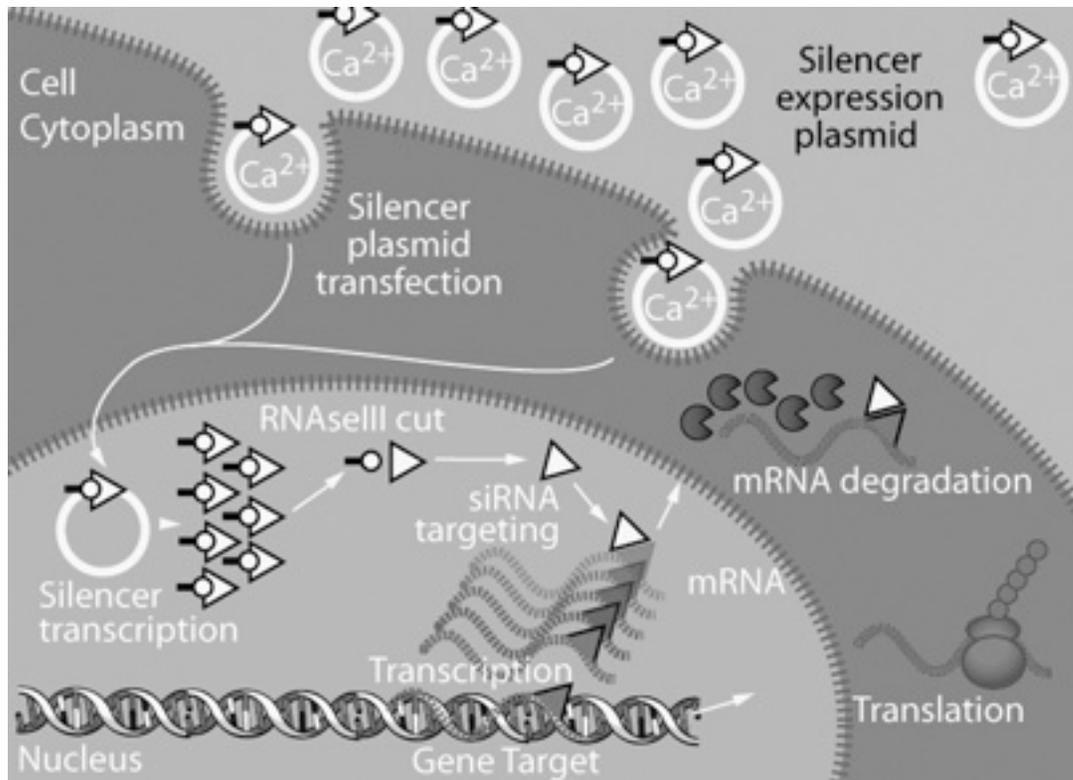
Some commonly used experimental approaches:

⇒ Phenotyping microarrays



Phenomics

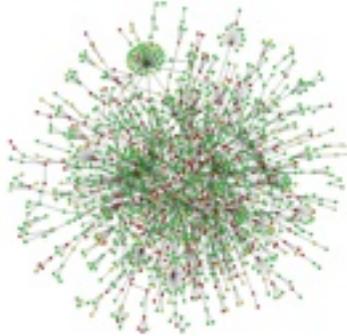
=> RNAi screens



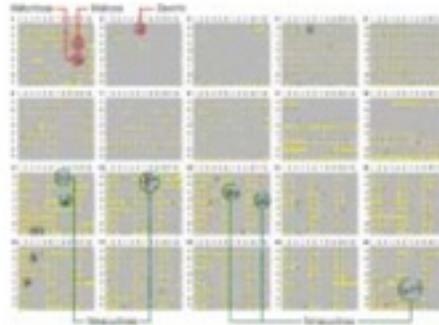
Integration of omics-data

The Challenge:
How to integrate extreme abundances of heterogeneous data from very diverse sources?

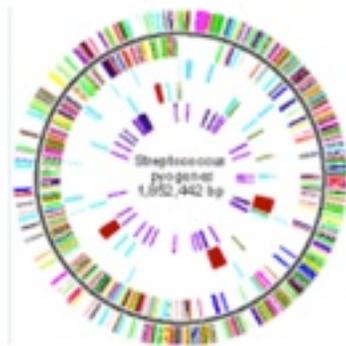
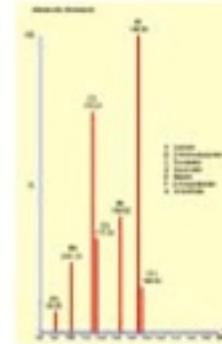
Interactomics



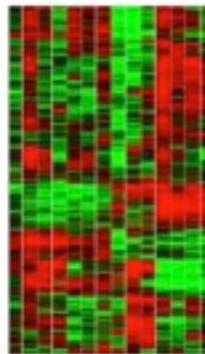
Phenomics



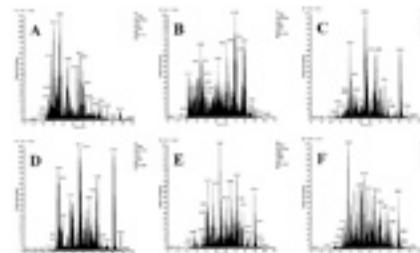
Metabolomics



Genomics

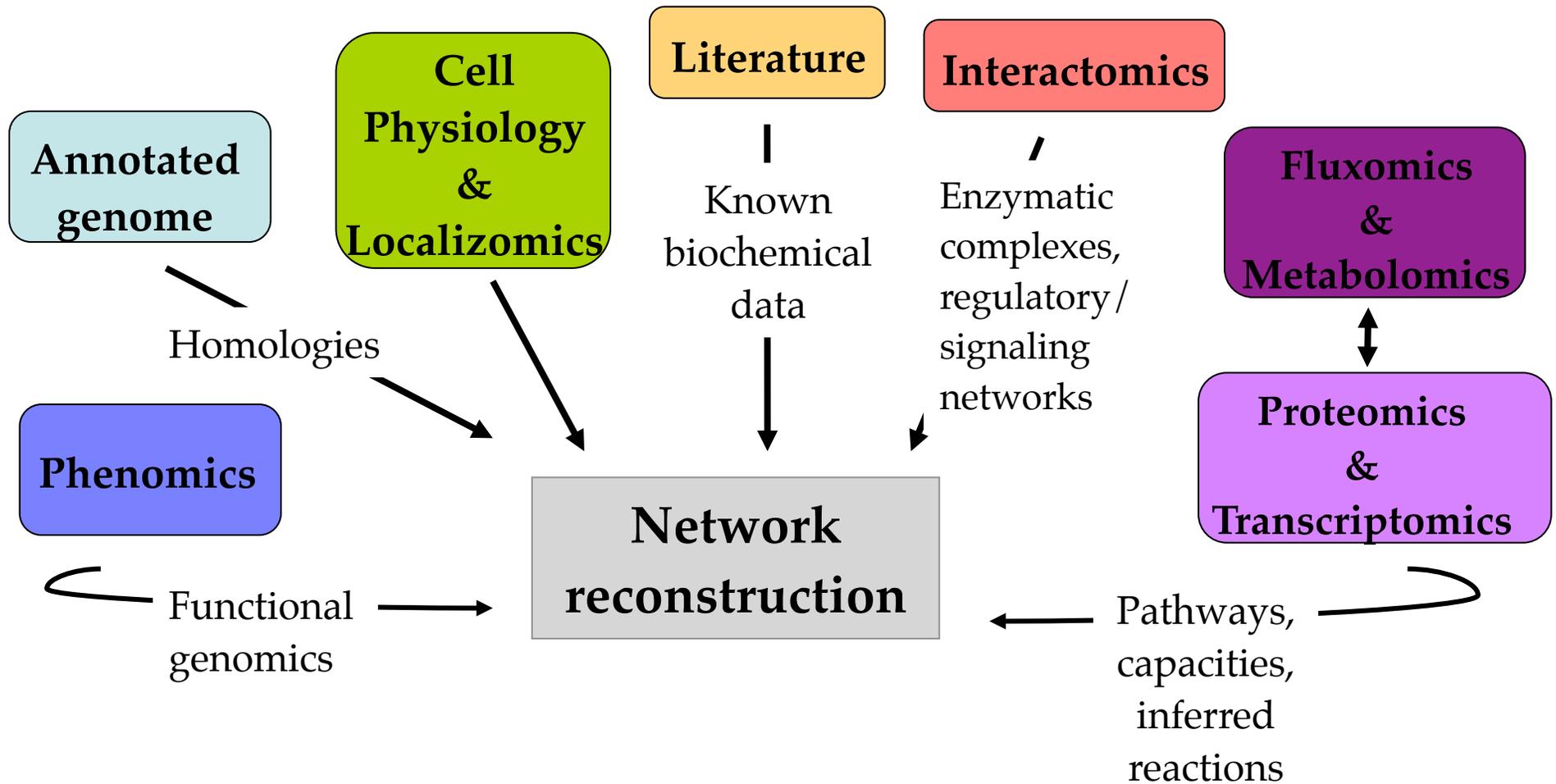


Transcriptomics

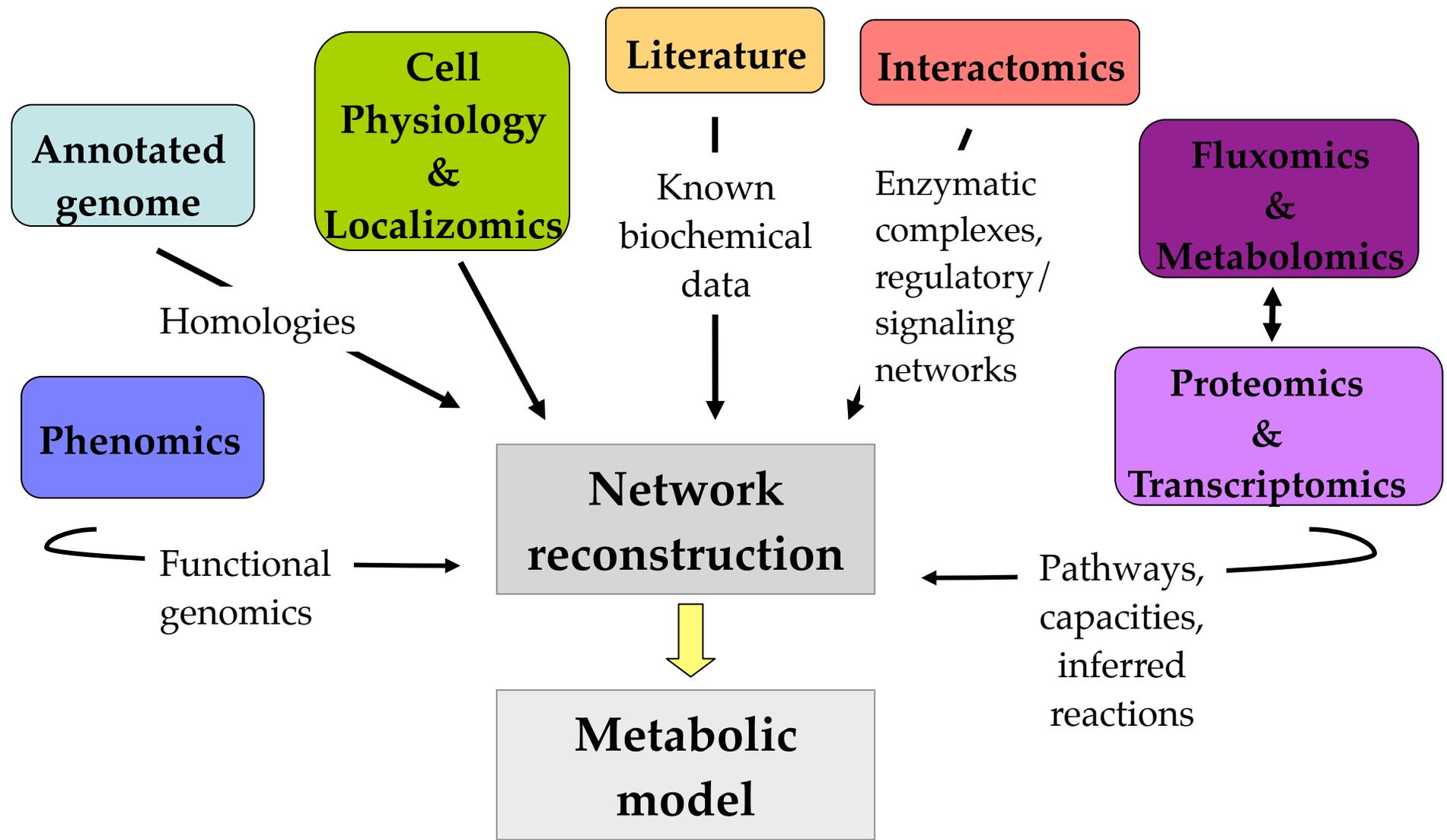


Proteomics

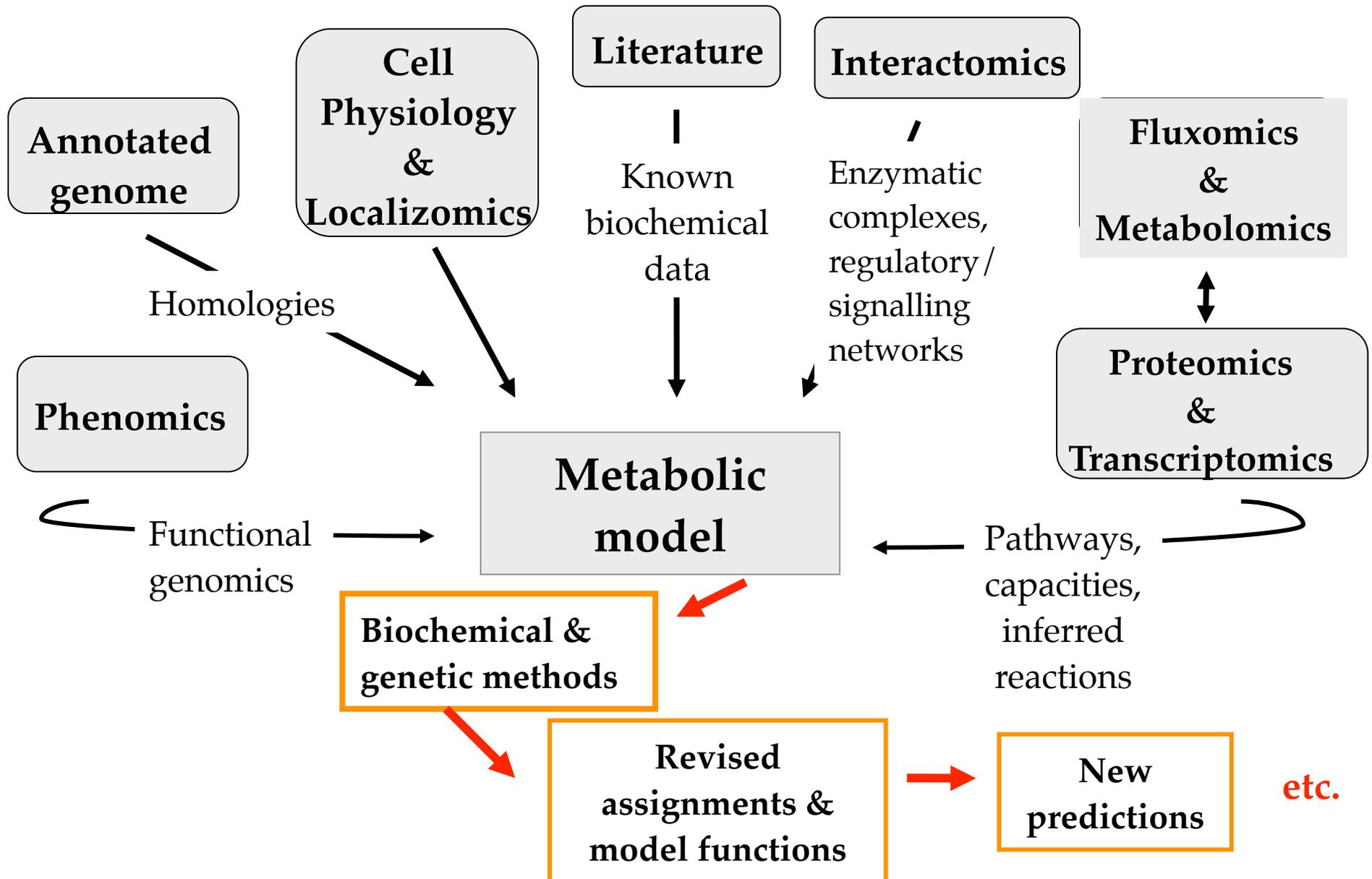
Integration of omics-data: Network reconstruction



Integration of omics-data: Network reconstruction



Integration of omics-data: Model testing and validation



The holy grail of systems biology:

Automatically updated, genome-scale, comprehensive network reconstructions for any system of interest

=> Advanced projects for some model organisms (Human, mouse, yeast, *E. coli*)

