



# Integrating clinical and molecular information in biomedical research

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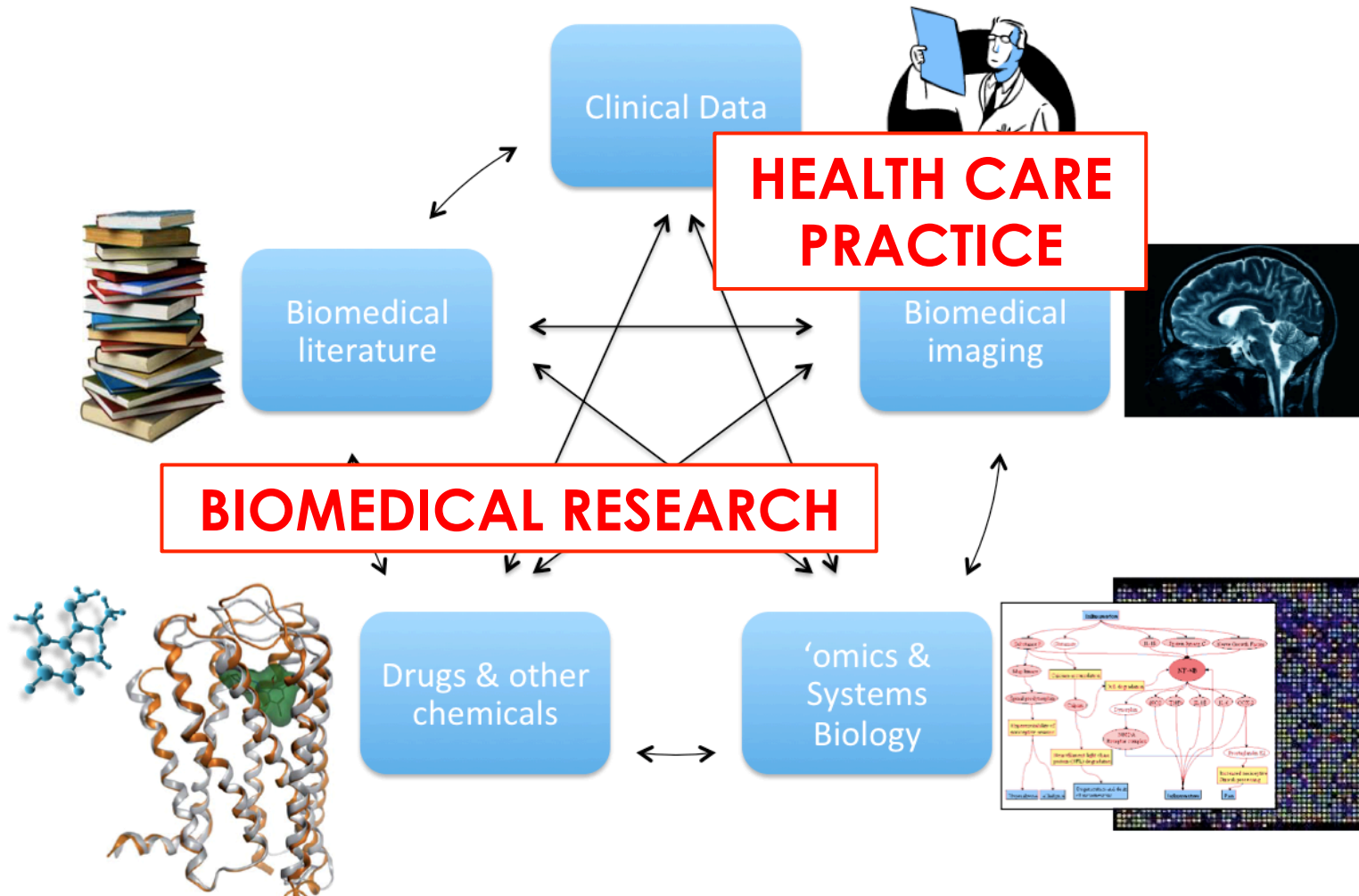
innovative  
medicines  
initiative



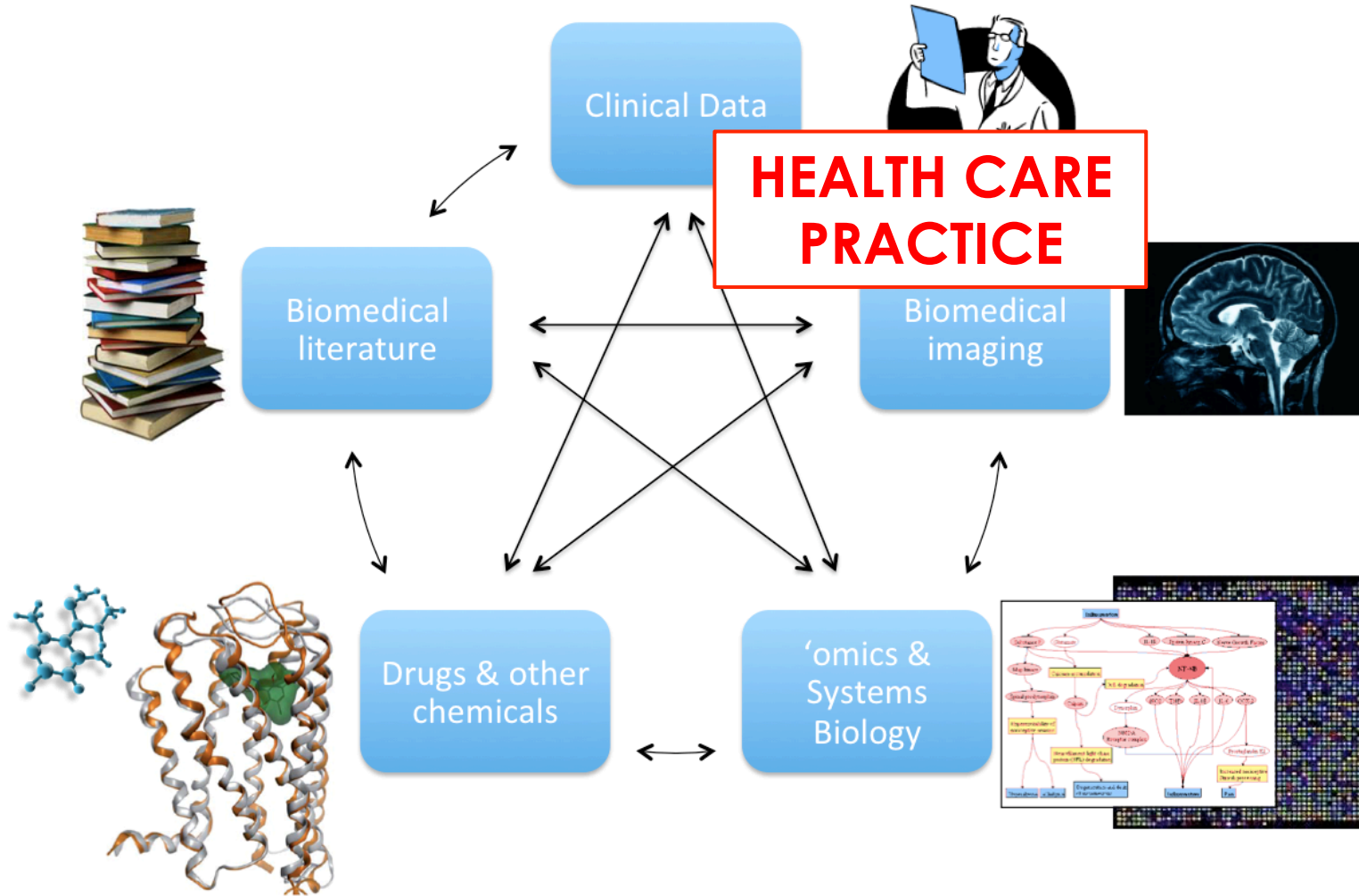
RESEARCH  
PROGRAMME  
ON BIOMEDICAL  
INFORMATICS



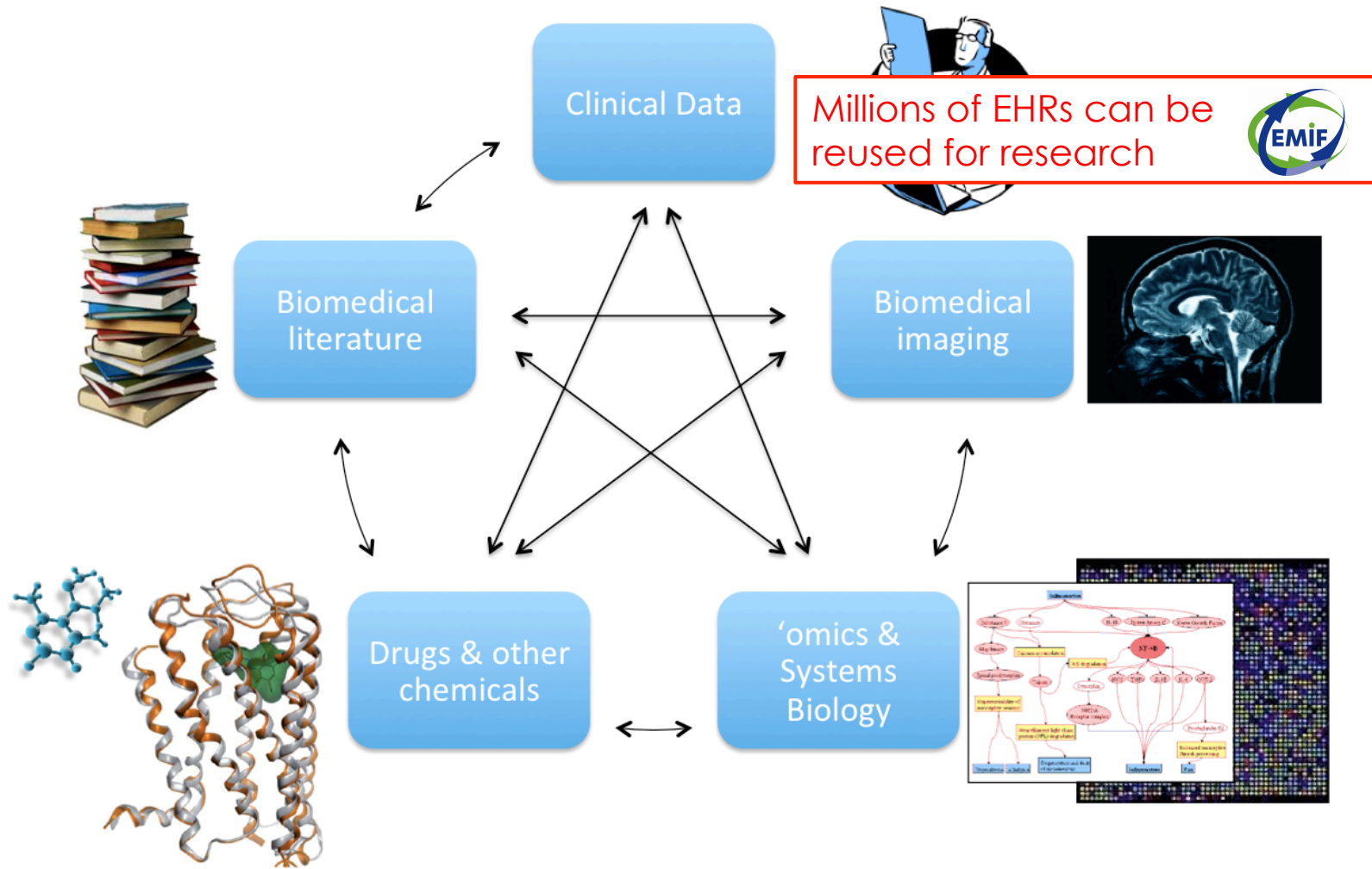
# Biomedical Big Data



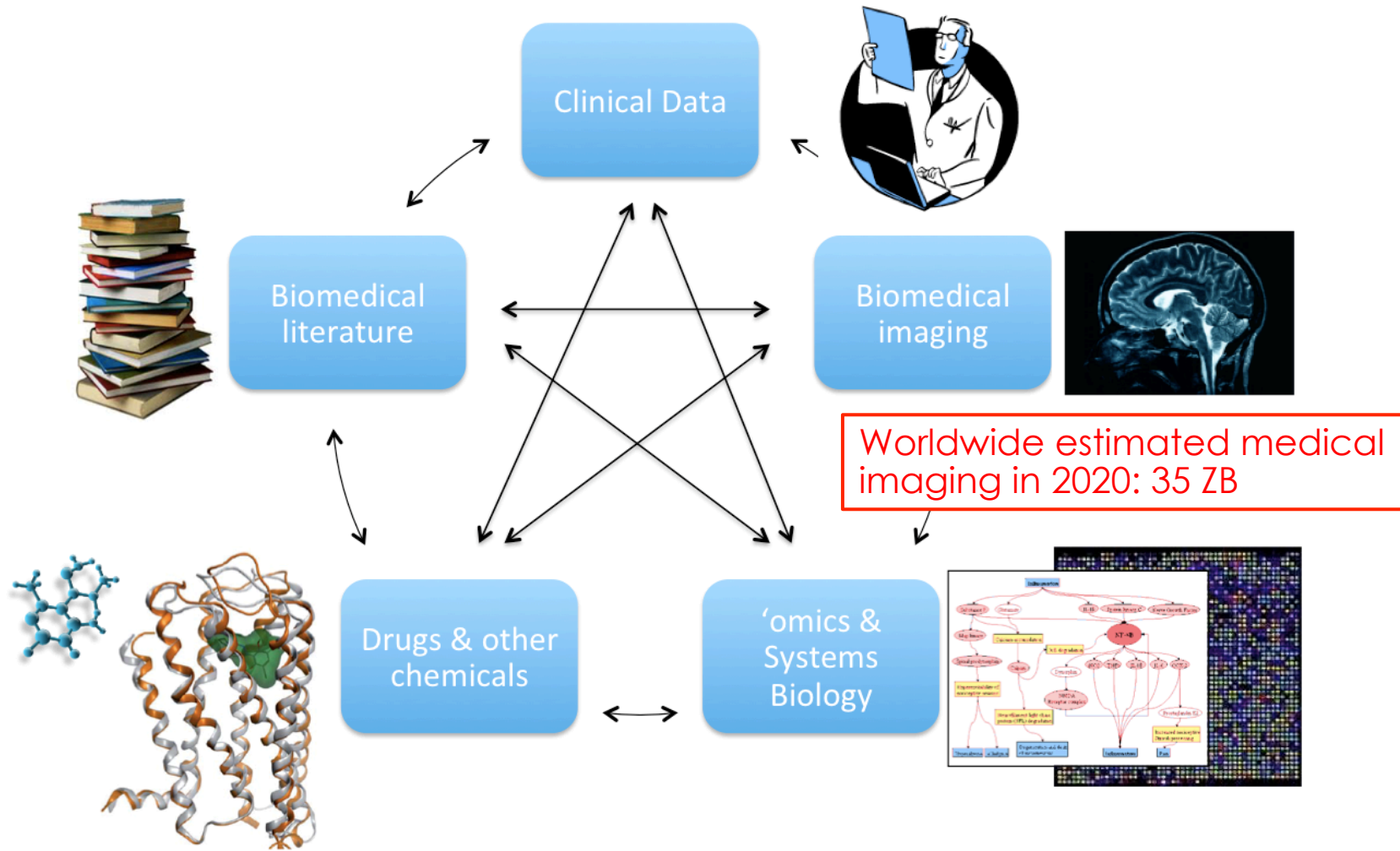
# Biomedical Big Data



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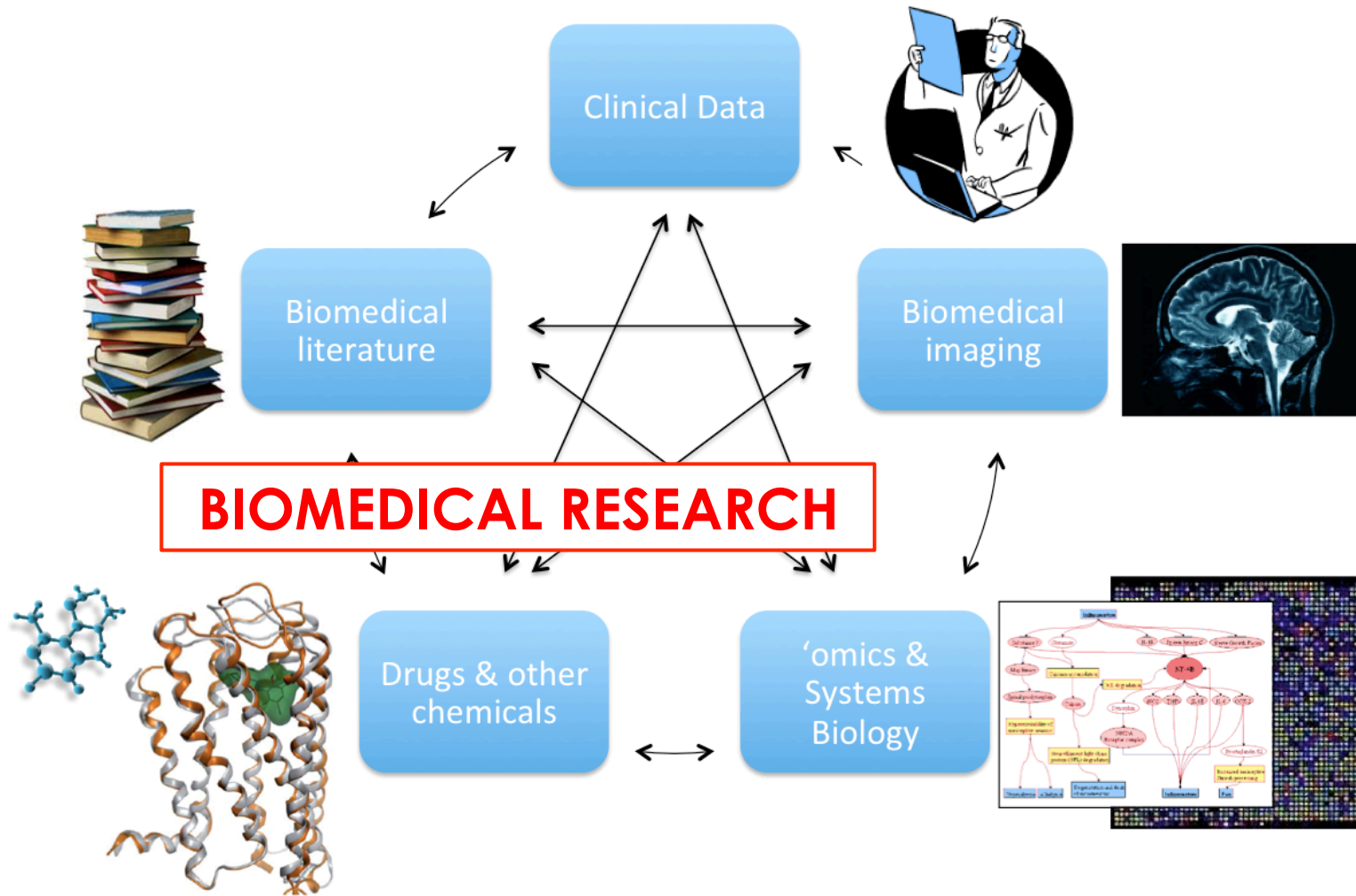


# Biomedical Big Data





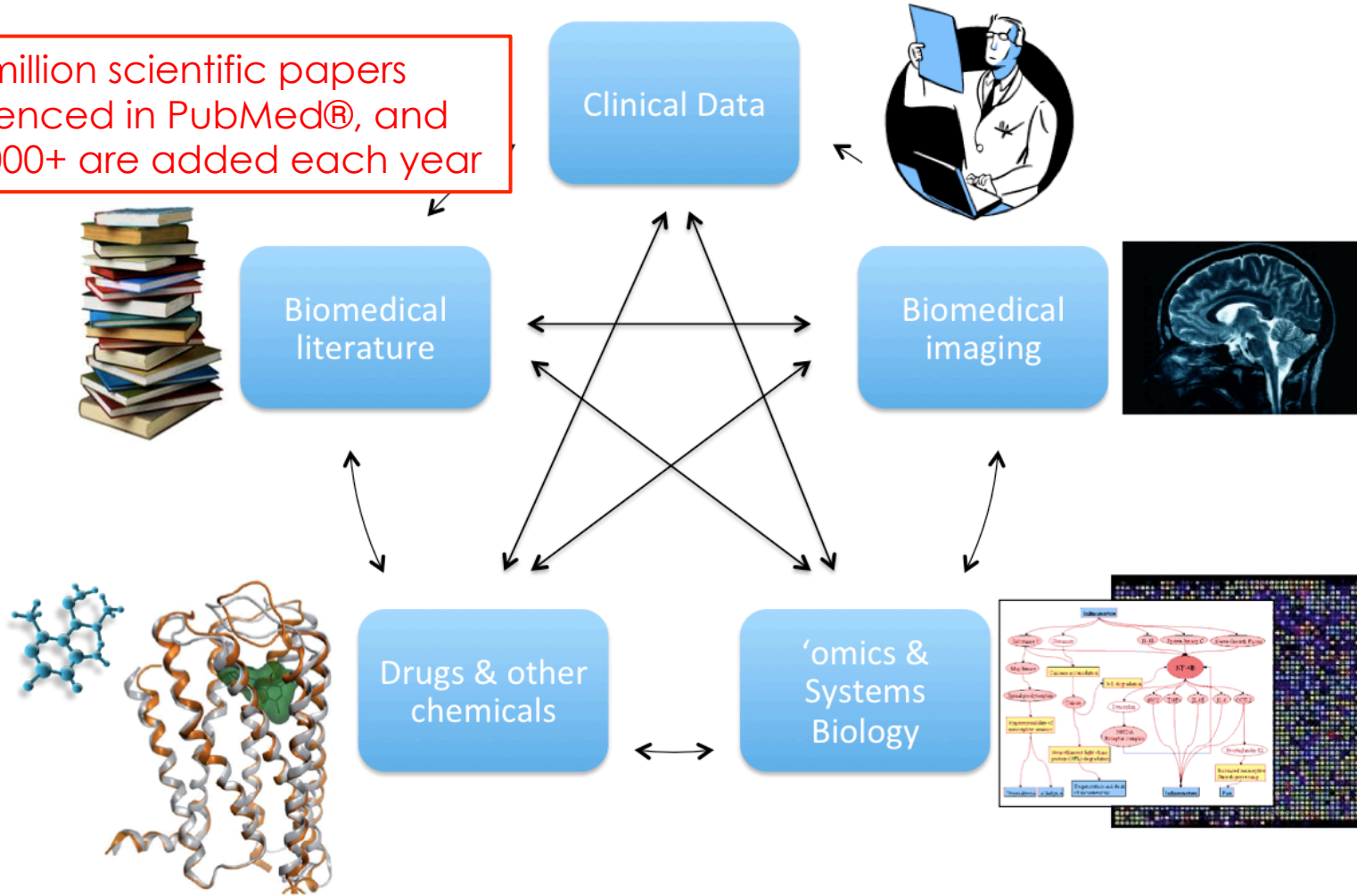
# Biomedical Big Data



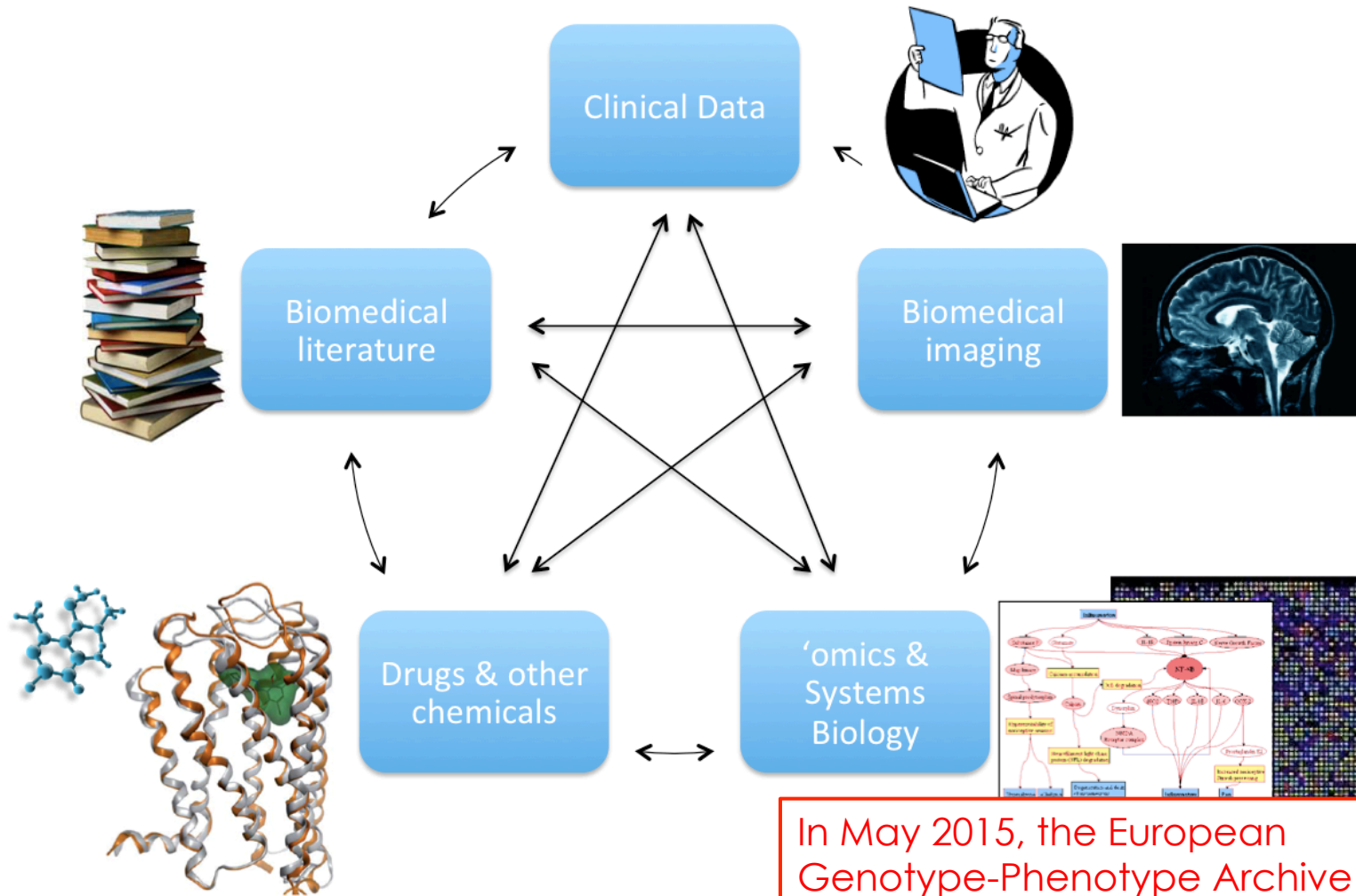
# Biomedical Big Data



20+ million scientific papers referenced in PubMed®, and 700,000+ are added each year



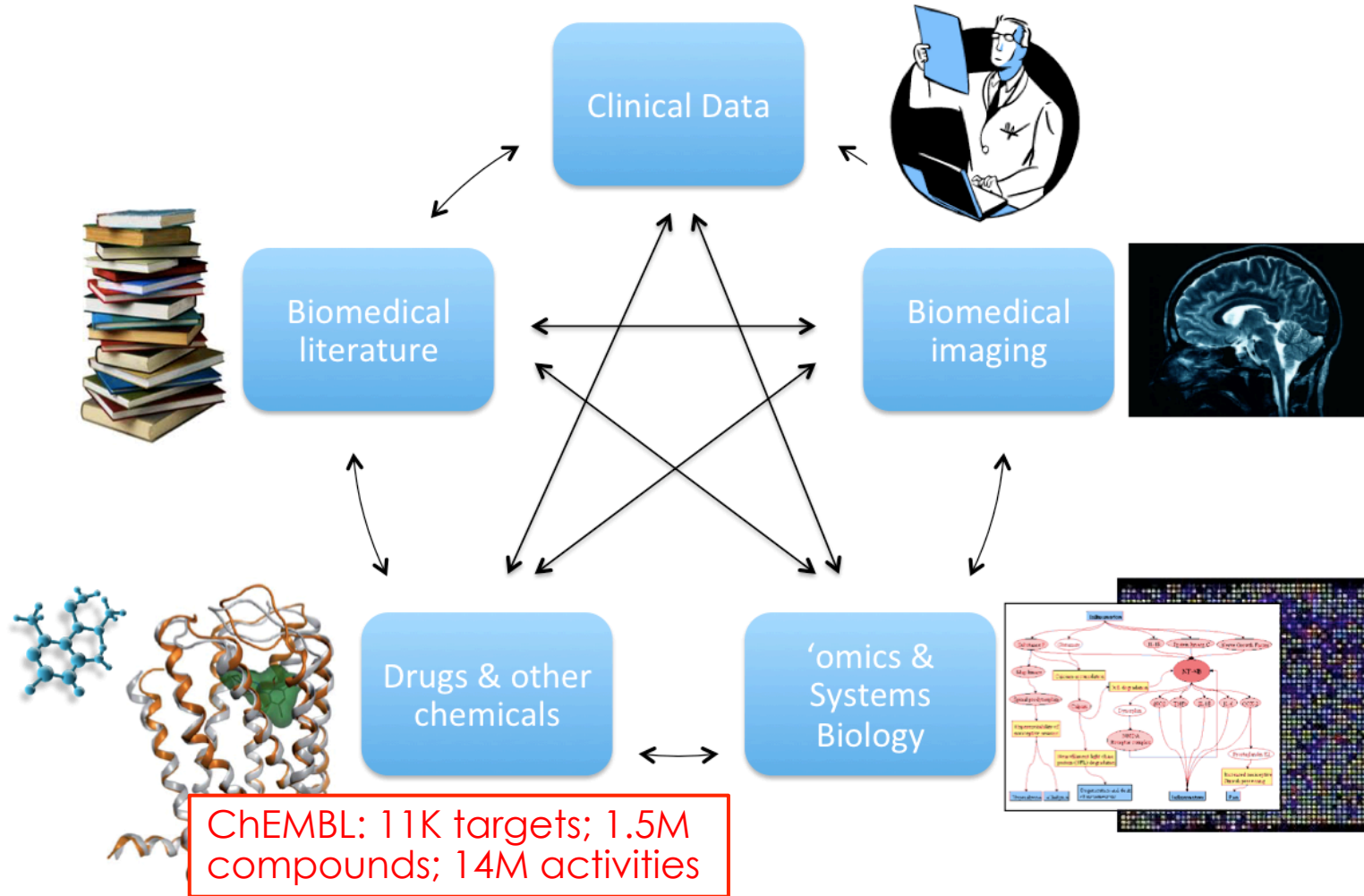
# Biomedical Big Data



In May 2015, the European Genotype-Phenotype Archive (EGA) stored 1.8 PB of human 'omics data



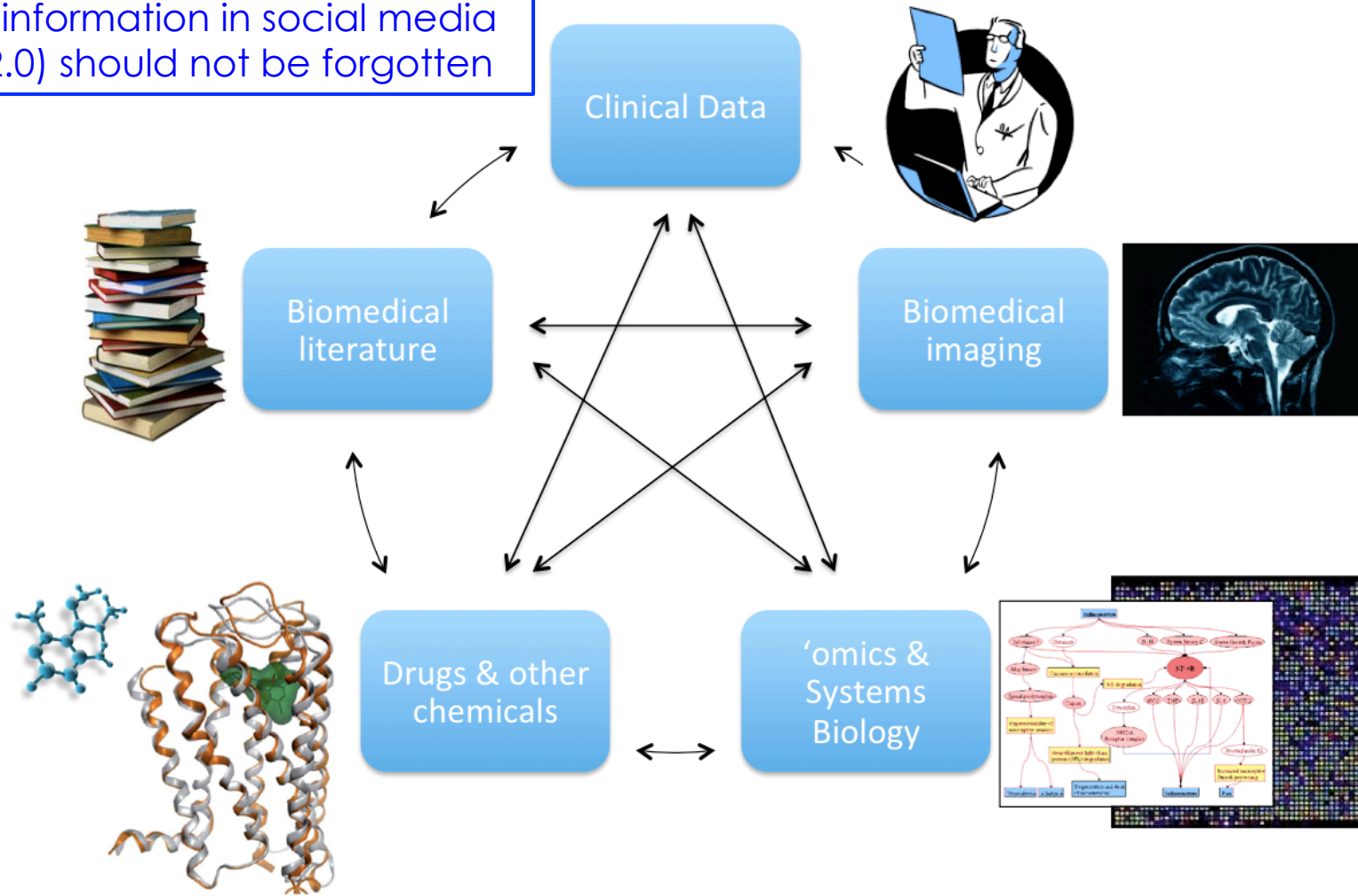
# Biomedical Big Data



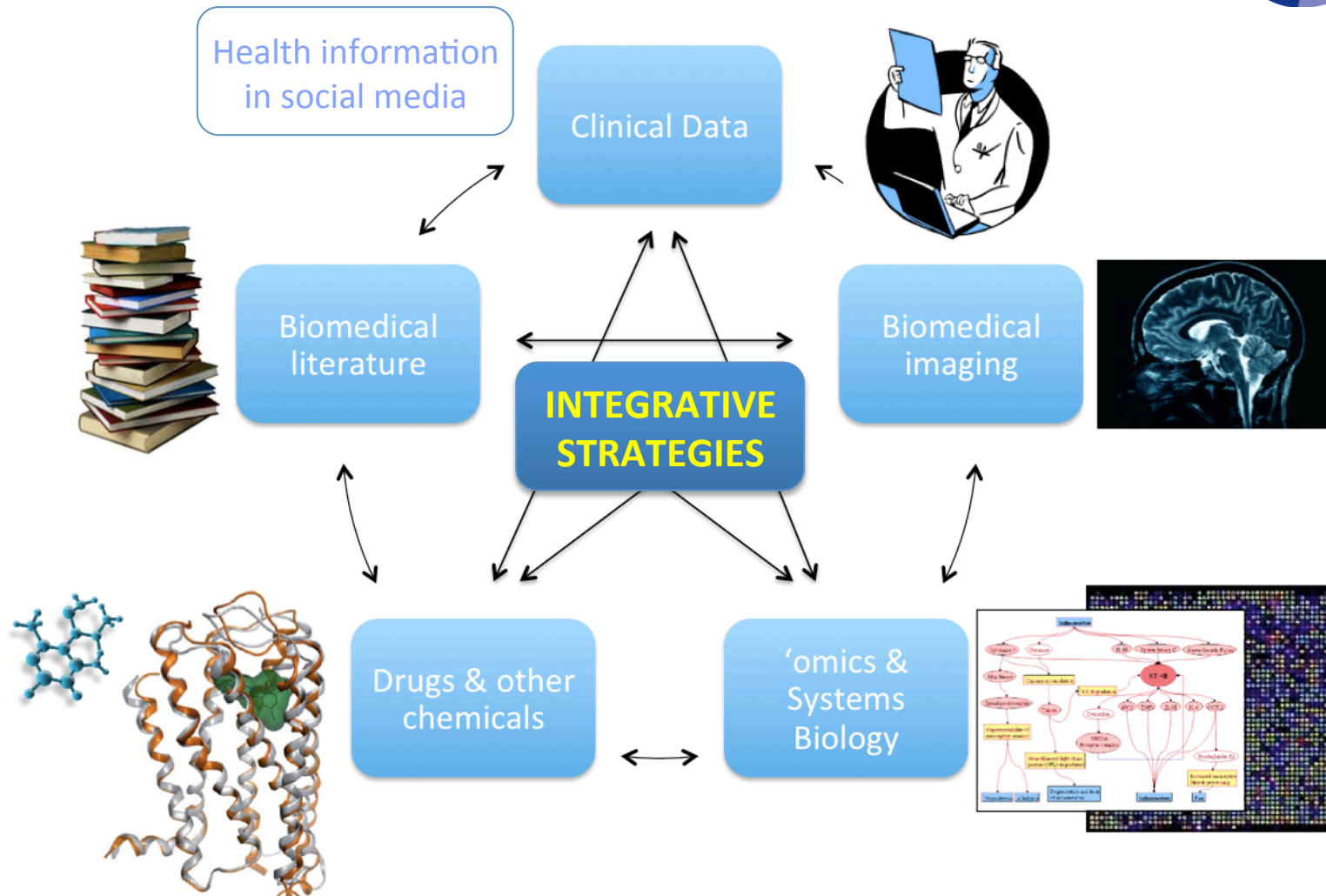
# Biomedical Big Data

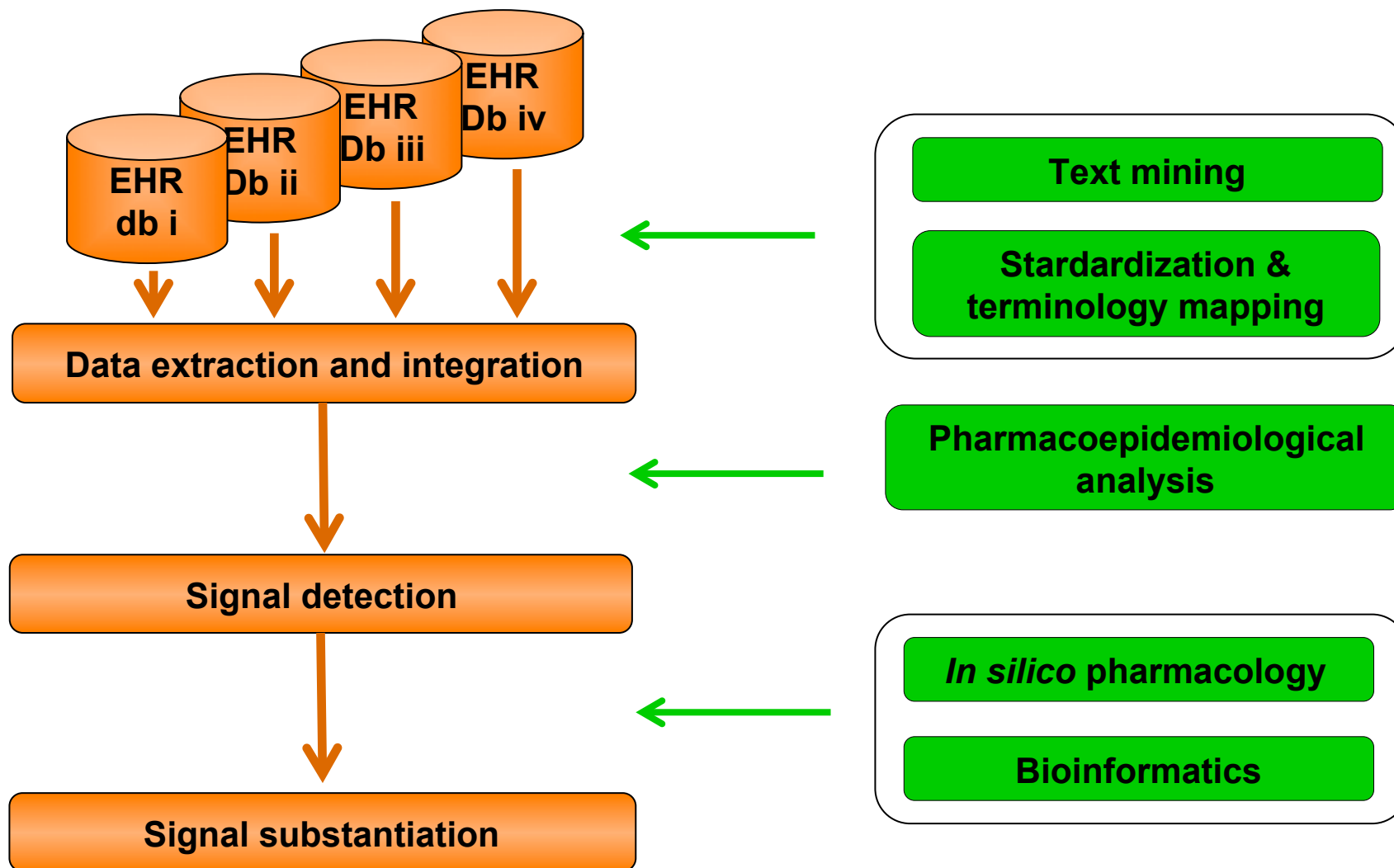


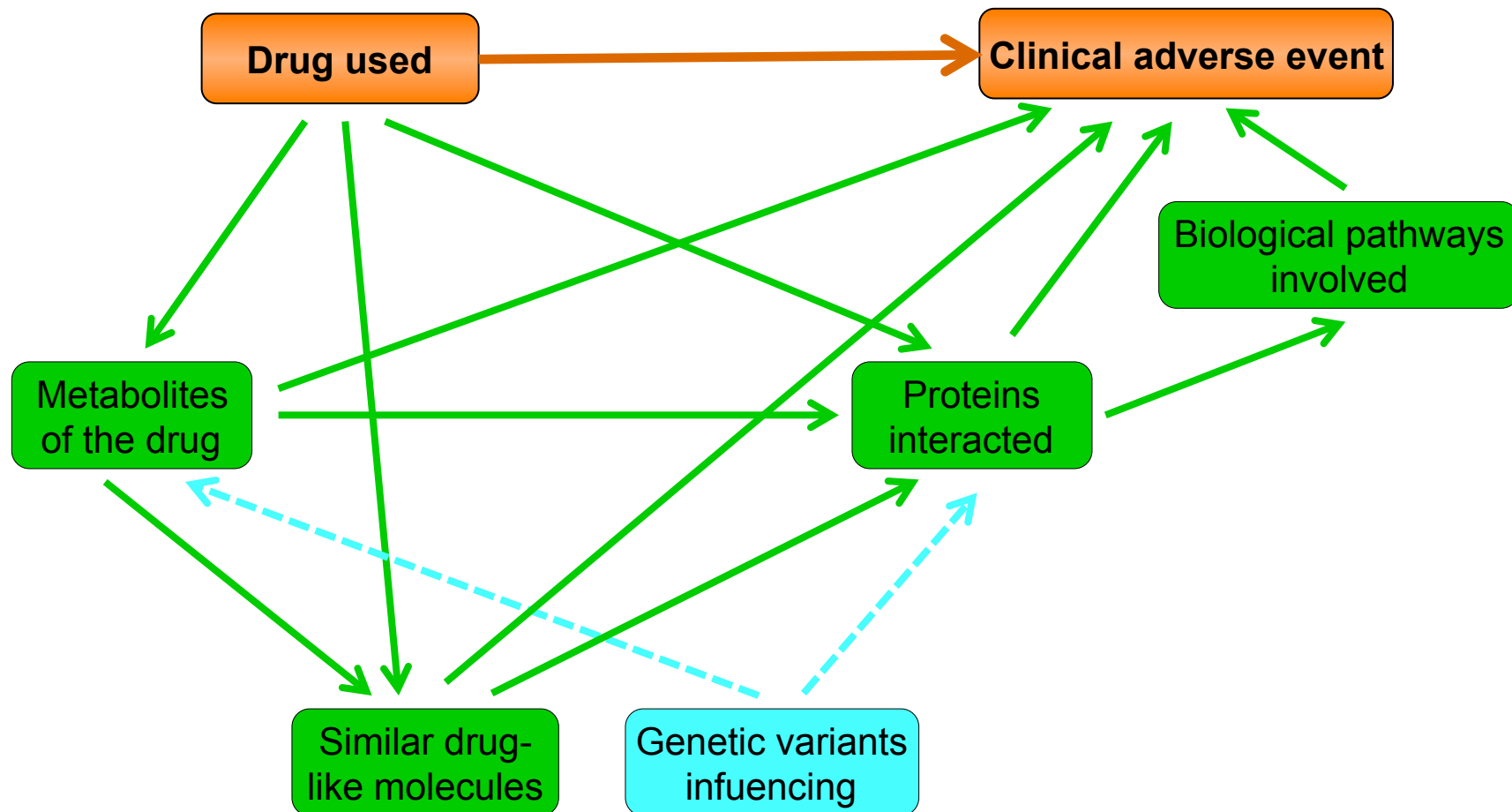
Health information in social media (Web 2.0) should not be forgotten



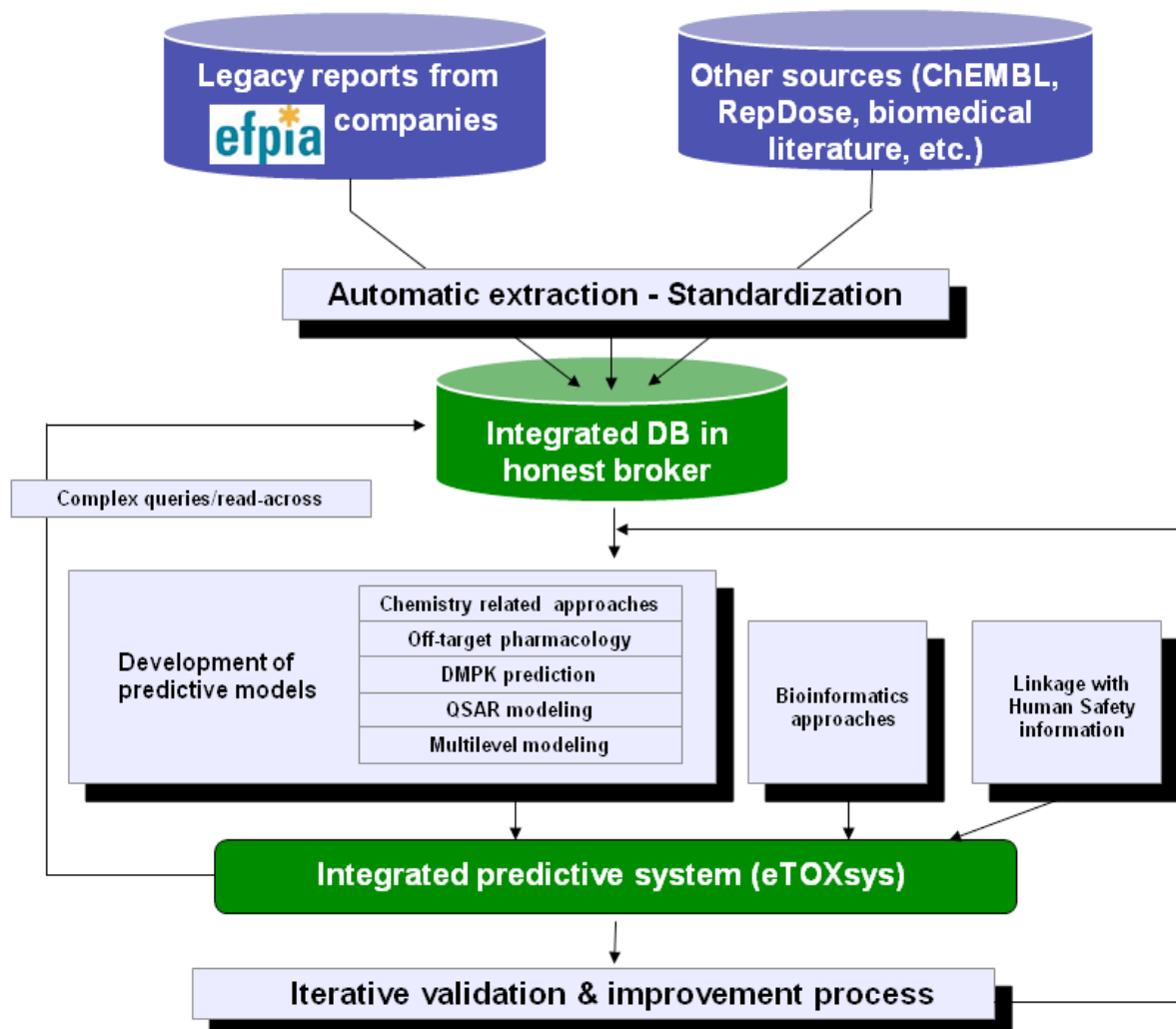
# Integration of heterogeneous biomedical information to gain a more complete and powerful view on diseases and therapeutics



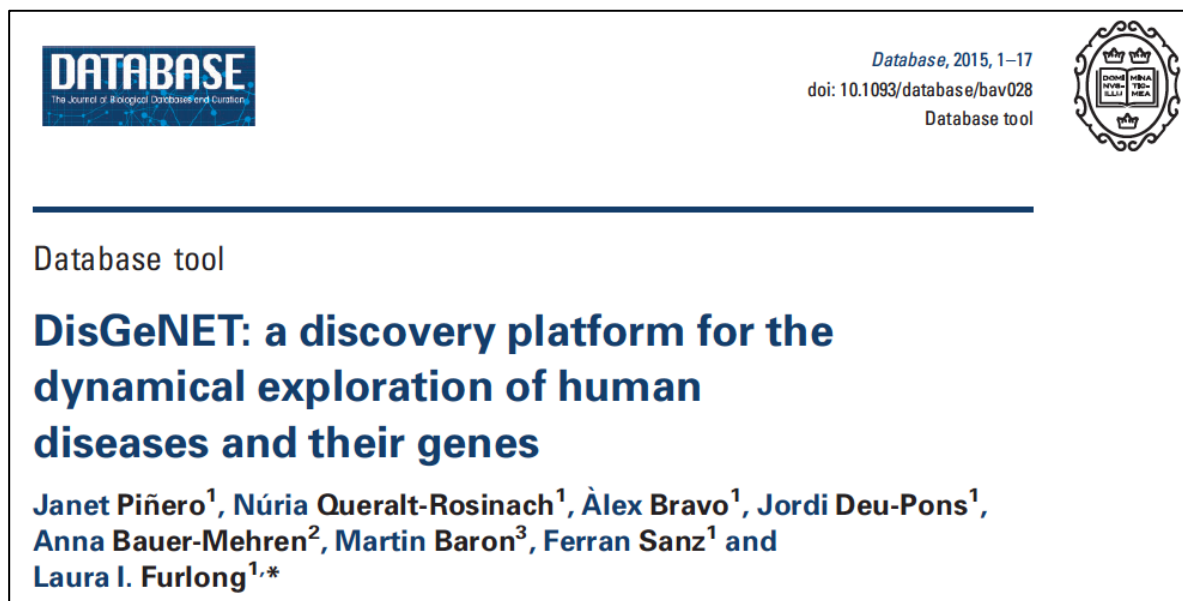









- Comprehensive resource on gene-disease associations (about 0.5M)
- Integrates information from publicly available databases and from the biomedical literature (text mining)
- Freely available at: <http://ibi.imim.es/DisGeNET>



**DATABASE**  
The Journal of Biological Databases and Curation

*Database*, 2015, 1–17  
doi: 10.1093/database/bav028  
Database tool



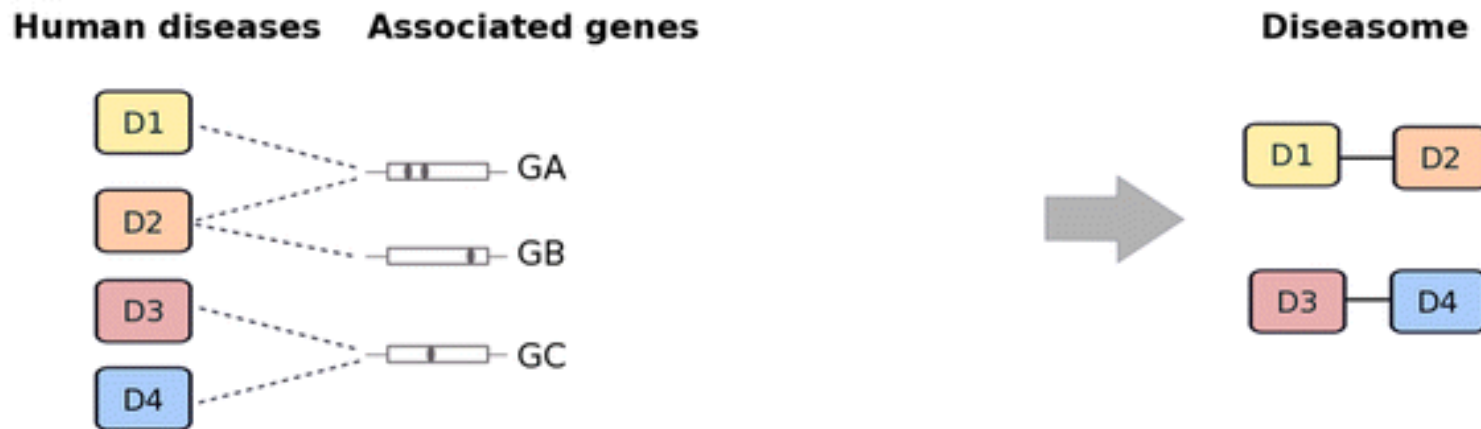
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Database tool

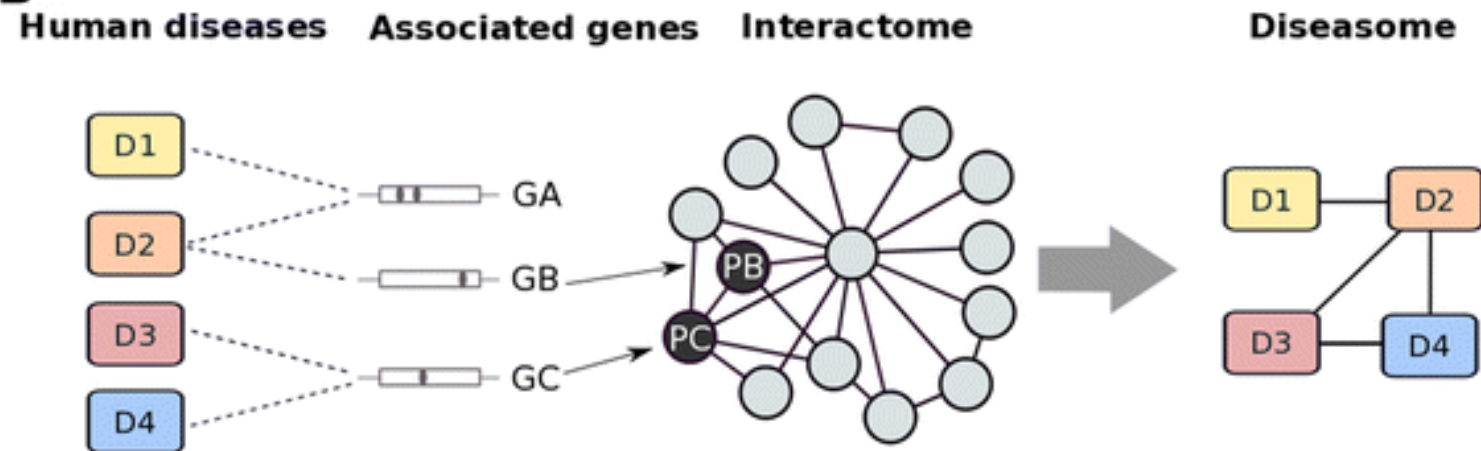
**DisGeNET: a discovery platform for the dynamical exploration of human diseases and their genes**

Janet Piñero<sup>1</sup>, Núria Queralt-Rosinach<sup>1</sup>, Àlex Bravo<sup>1</sup>, Jordi Deu-Pons<sup>1</sup>, Anna Bauer-Mehren<sup>2</sup>, Martin Baron<sup>3</sup>, Ferran Sanz<sup>1</sup> and Laura I. Furlong<sup>1,\*</sup>

**A**



**B**



Grosdidier *et al. Respiratory Research* 2014, **15**:111  
<http://respiratory-research.com/content/15/1/111>

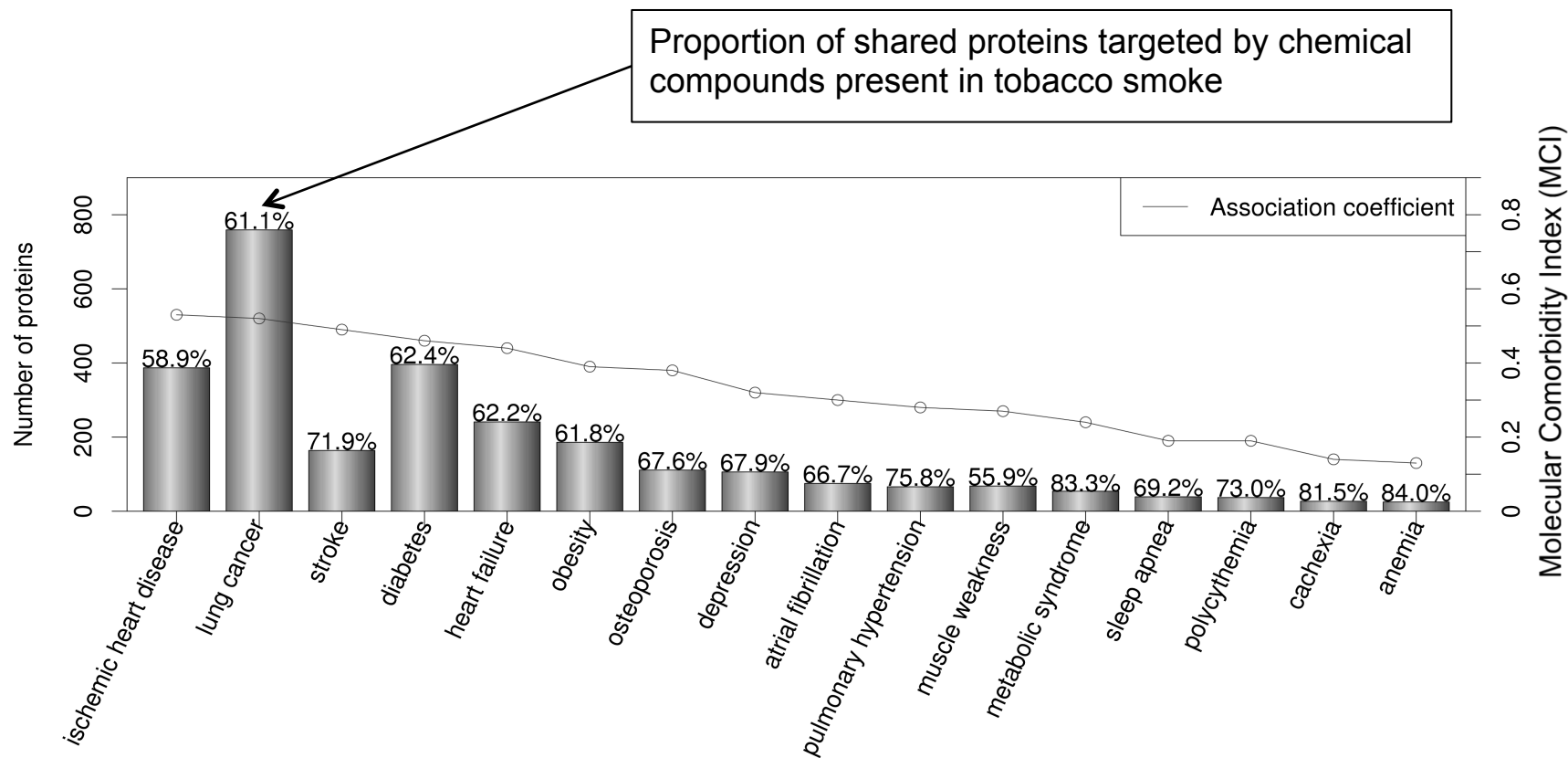


RESEARCH

Open Access

# Network medicine analysis of COPD multimorbidities

Solène Grosdidier<sup>1</sup>, Antoni Ferrer<sup>2</sup>, Rosa Faner<sup>3</sup>, Janet Piñero<sup>1</sup>, Josep Roca<sup>4</sup>, Borja Cosío<sup>5</sup>, Alvar Agustí<sup>3,4</sup>, Joaquim Gea<sup>2</sup>, Ferran Sanz<sup>1</sup> and Laura I Furlong<sup>1\*</sup>



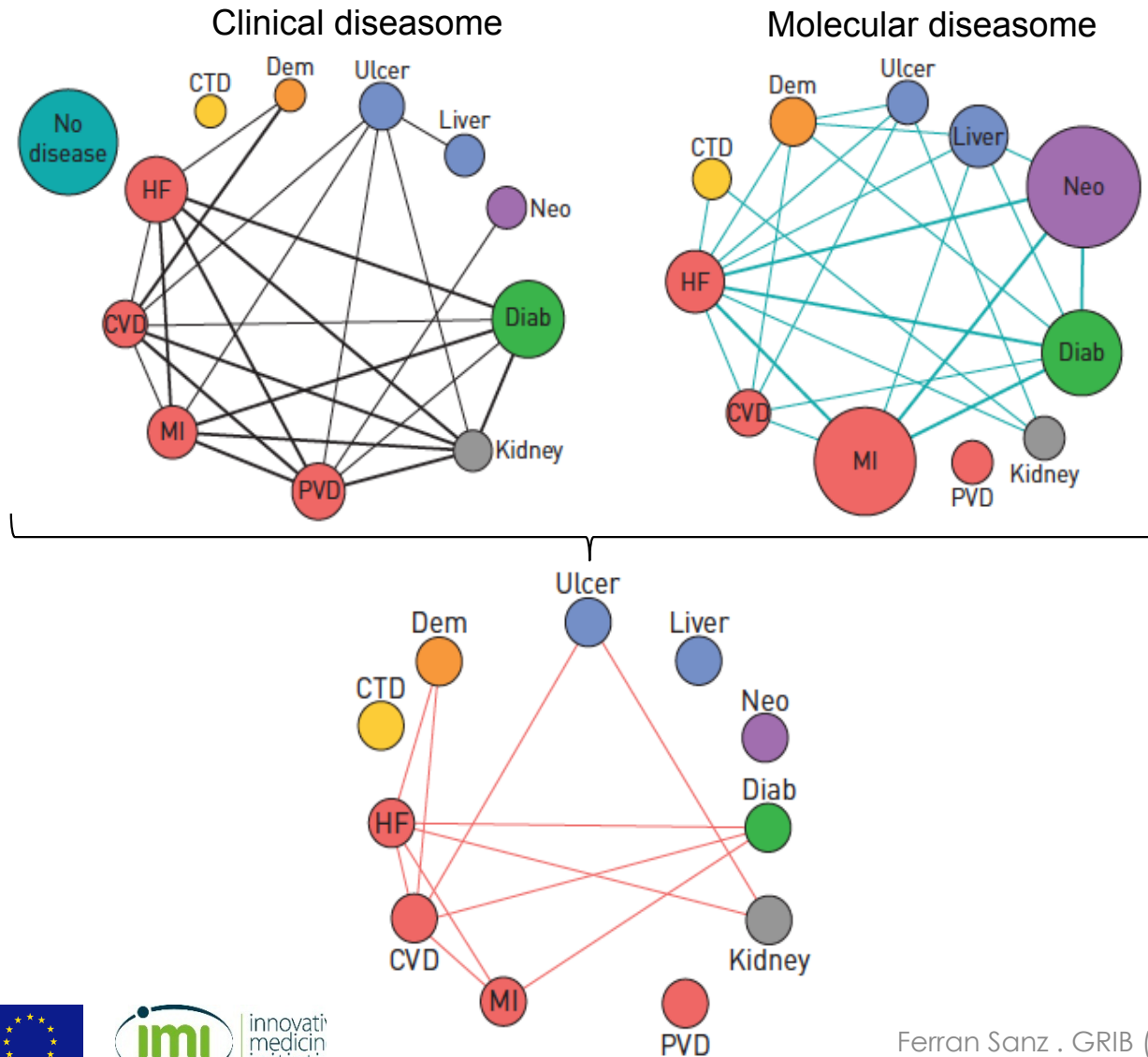
$$MCI_{dis1,dis2} = \frac{|(proteins_{dis1} \cap proteins_{dis2}) \cup proteins_{dis2 \rightarrow dis1} \cup proteins_{dis1 \rightarrow dis2}|}{|proteins_{dis1} \cup proteins_{dis2}|}$$



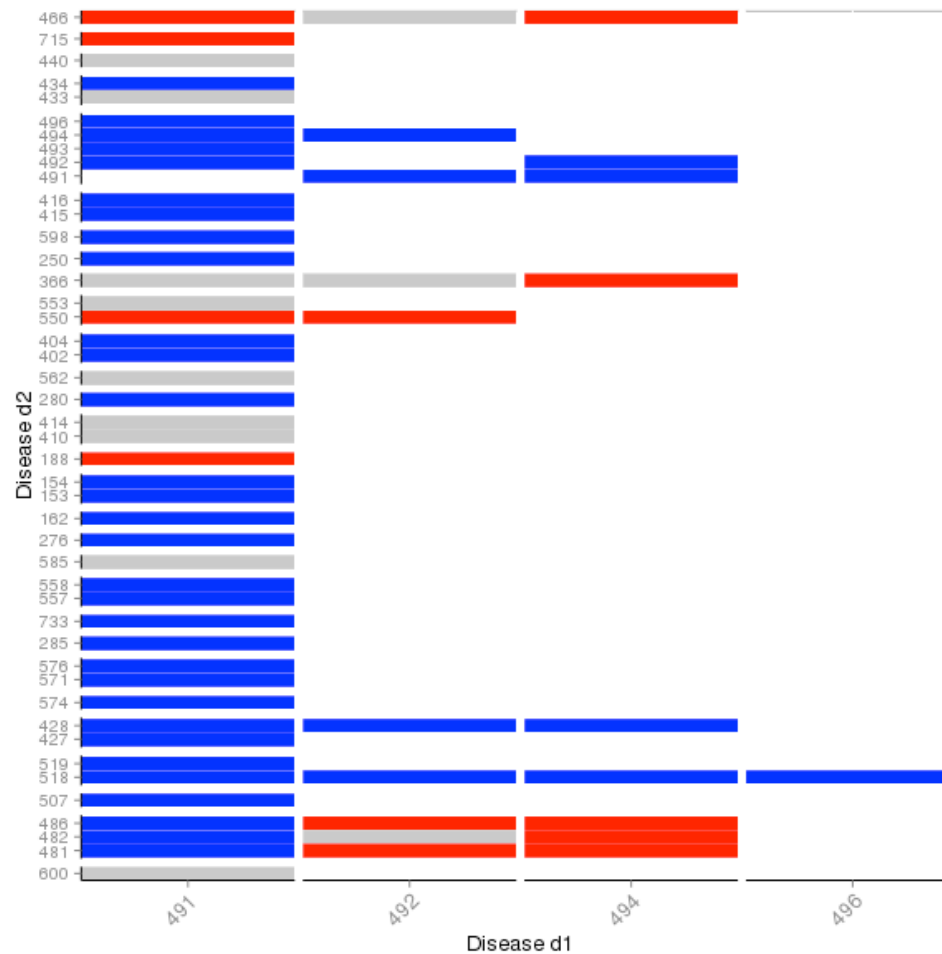
## Molecular and clinical diseaseome of comorbidities in exacerbated COPD patients

Rosa Faner<sup>1,2,8</sup>, Alba Gutiérrez-Sacristán<sup>3,8</sup>, Ady Castro-Acosta<sup>2,4</sup>,  
Solène Grosdidier<sup>3</sup>, Wenqi Gan<sup>5</sup>, Milagros Sánchez-Mayor<sup>3</sup>,  
Jose Luis Lopez-Campos<sup>2,6</sup>, Francisco Pozo-Rodriguez<sup>2,4</sup>, Ferran Sanz<sup>3</sup>,  
David Mannino<sup>5</sup>, Laura I. Furlong<sup>3</sup> and Alvar Agusti<sup>1,2,7</sup>

Eur Respir J 2015; 46: 1001–1010 | DOI: 10.1183/13993003.00763-2015



# Disease directionality analysis



- Temporal direction of the comorbidity pairs, based on a binomial test.
- Significant directionality  $d_1 \rightarrow d_2$  is indicated in blue and  $d_2 \rightarrow d_1$  in red.
- Pairs with no significant directionality are shown in gray.
- For visualization purposes, only pairs encountered in  $\geq 200$  patients are shown.



# Many thanks for your attention!

<http://grib.upf.edu>



RESEARCH  
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ON BIOMEDICAL  
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