

# Harnessing Diverse Bioinformatics Approaches to Repurpose Drugs for Alzheimer's Disease

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Peter K. Sorger, Ph.D.



**HARVARD**  
MEDICAL SCHOOL

# Acknowledgments

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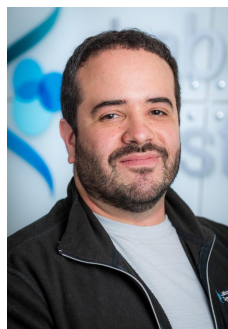
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Yi-Han Sheu



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MASSGENERAL INSTITUTE FOR  
NEURODEGENERATIVE DISEASE



Laboratory of  
Systems Pharmacology



Imperial College  
London



Massachusetts  
Institute of  
Technology

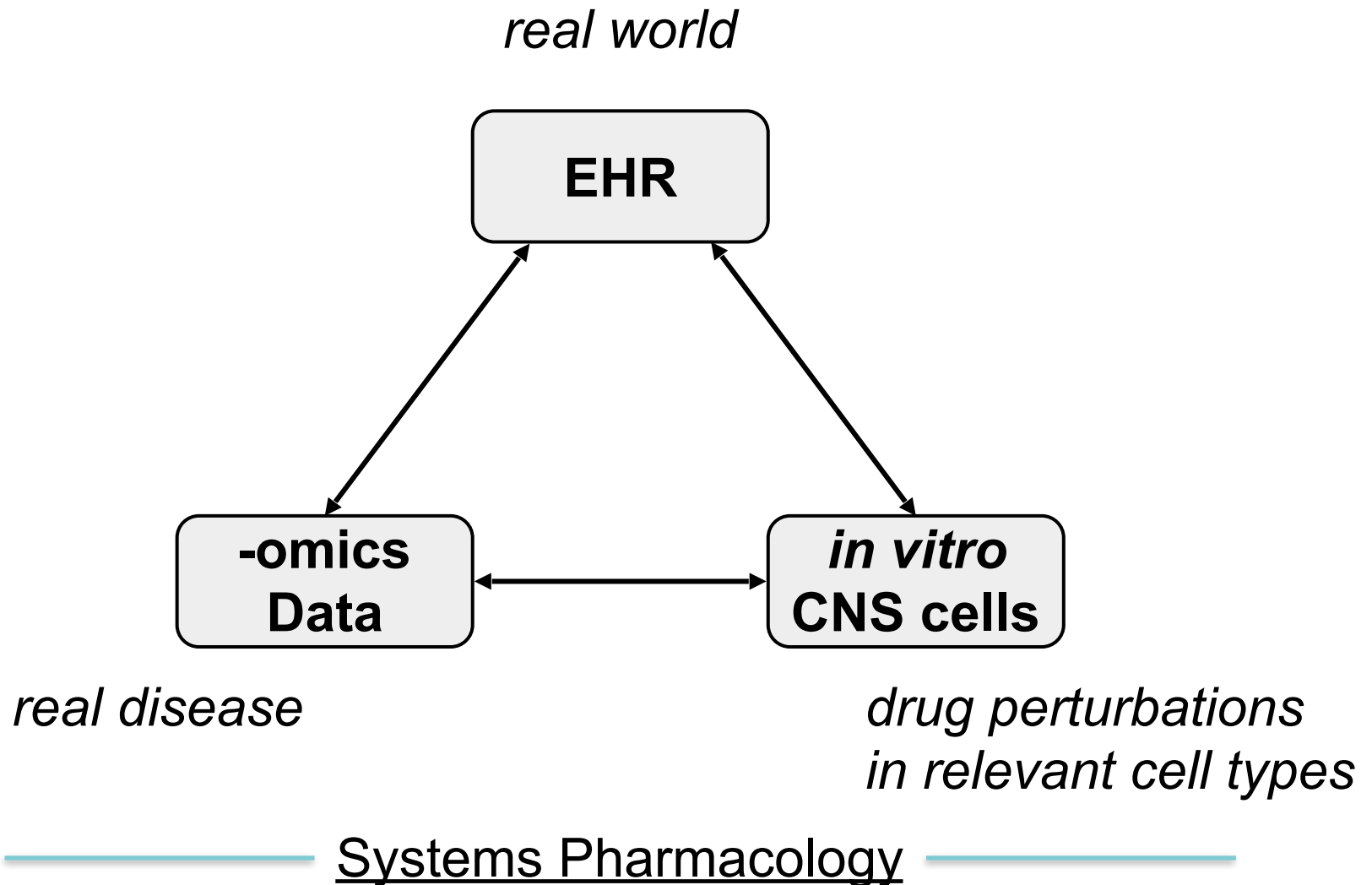


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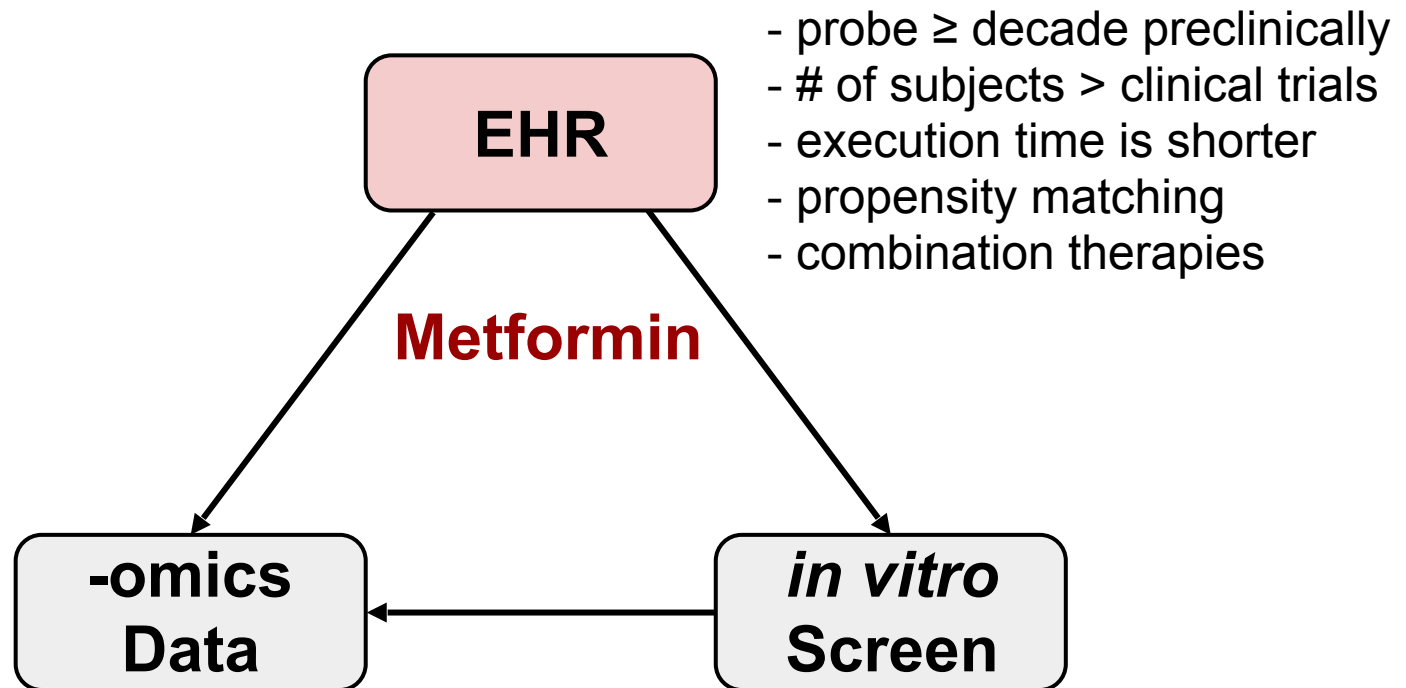
## Funding:

R56 AG058063 Partners  
P50 AG005134 Springboard

# Integrating three data sources with two informatics approaches



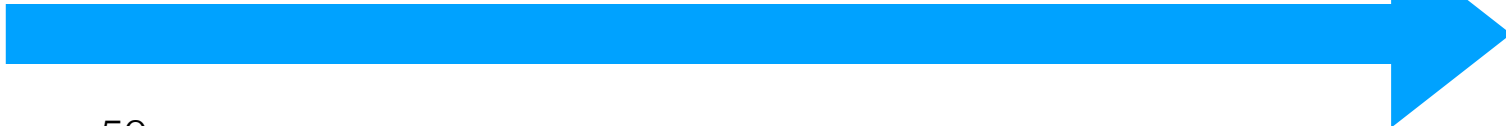
EHR analysis evaluates potential off-label use that may delay symptoms of Alzheimer's disease



# In silico drug trials - longitudinal EHR analyses

**Initiation** trial (asymptomatic to diagnosis):

age 50



age 50



Ioanna  
Tzoulaki



**Imperial College  
London**



**Massachusetts  
Institute of  
Technology**

**CPRD**

- NHS of UK
- 20 million patients
- longitudinal data from 1990's

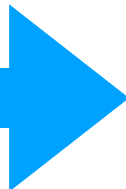
# In silico drug trials - longitudinal EHR analyses

**Initiation** trial (asymptomatic to diagnosis):

age 50



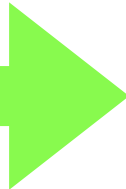
**metformin**



age 50



**sulphonylurea**



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Tzoulaki



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London**



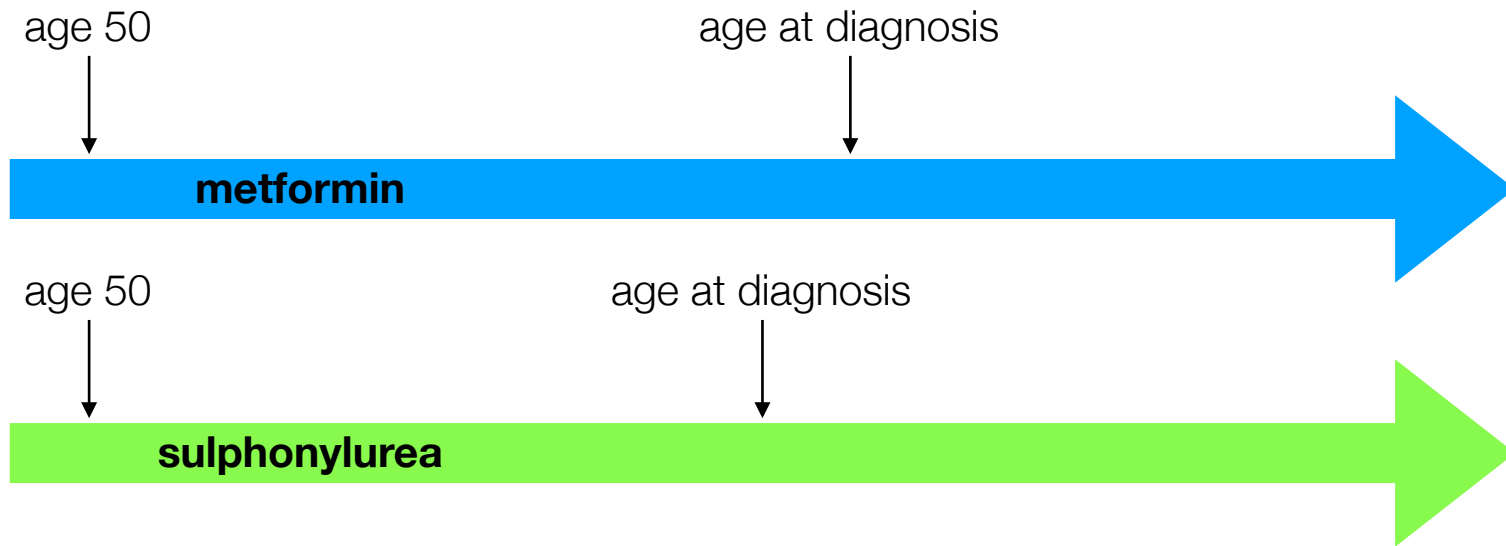
**Massachusetts  
Institute of  
Technology**

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# In silico drug trials - longitudinal EHR analyses

**Initiation** trial (asymptomatic to diagnosis):



Ioanna  
Tzoulaki



**Imperial College  
London**



**Massachusetts  
Institute of  
Technology**

**CPRD**

- NHS of UK
- 20 million patients
- longitudinal data from 1990's

# Metformin reduces progression to dementia relative to sulphonylurea in diabetics

| Strata                           | Number of obs | Hazard Ratio | P-value | [95% Conf. Interval] |       |
|----------------------------------|---------------|--------------|---------|----------------------|-------|
| <b>Follow-up for up to 10 y</b>  |               |              |         |                      |       |
| <b>Model 1: (age and gender)</b> |               |              |         |                      |       |
| <b>Metformin</b>                 | 128,727       | <b>0.615</b> | <0.001  | 0.589                | 0.643 |
| <b>Model 2: fully adjusted</b>   |               |              |         |                      |       |
| <b>Metformin</b>                 | 64,288        | <b>0.502</b> | <0.001  | 0.434                | 0.581 |

Fully adjusted includes age at prescription, gender, socioeconomic status, vascular comorbidities, smoking, BMI, and HbA1c level



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| Metformin                        | 64,288        | <b>0.502</b> | <0.001  | 0.434                | 0.581 |
| <b>Follow-up &gt;=10 years</b>   |               |              |         |                      |       |
| <b>Model 1: (age and gender)</b> |               |              |         |                      |       |
| Metformin                        | 76,065        | <b>0.825</b> | <0.001  | 0.779                | 0.874 |
| <b>Model 2: fully adjusted</b>   |               |              |         |                      |       |
| Metformin                        | 22,943        | <b>0.696</b> | <0.001  | 0.613                | 0.789 |



# AMP-AD Knowledge Portal

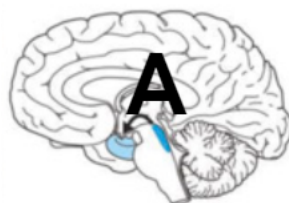


## Braak Score

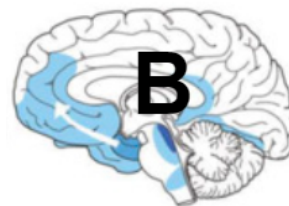
0      1      2      3      4      5      6

**ROSMAP**  
Dorsolateral prefrontal  
cortex

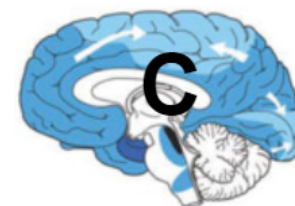
|   |    |    |     |     |     |   |
|---|----|----|-----|-----|-----|---|
| 7 | 51 | 54 | 176 | 210 | 133 | 7 |
|---|----|----|-----|-----|-----|---|



I, II



III, IV



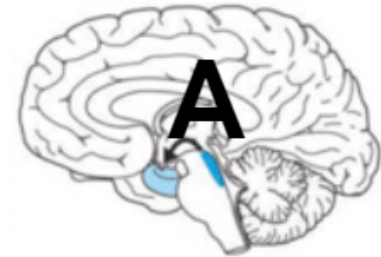
V, VI

Task definition: given an RNAseq profile,  
predict disease stage (AB, AC, BC, Ordinal)

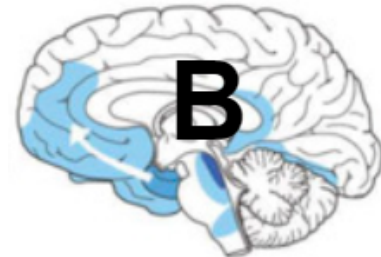
20k genes

RNAseq

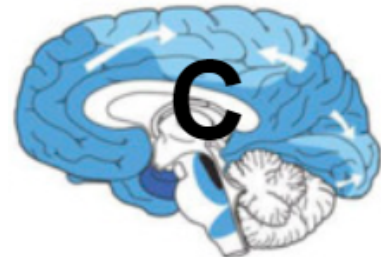
?



I, II



III, IV



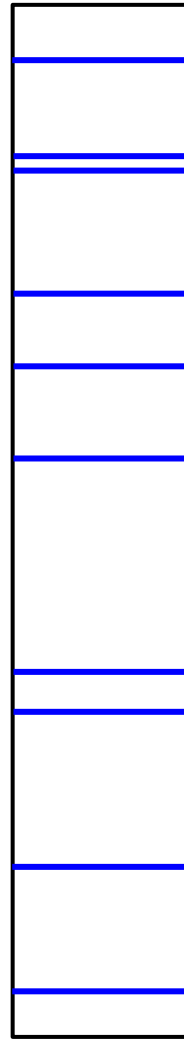
V, VI



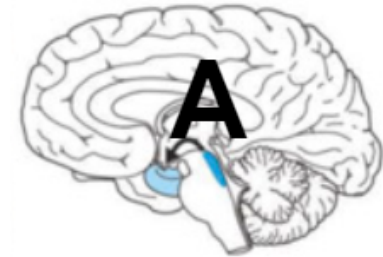
Artem  
Sokolov

Begin by asking how well does a randomly-selected subset of genes predict disease stage

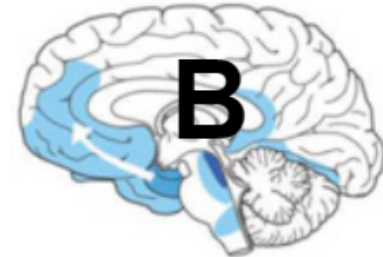
10 randomly-selected genes



?



I, II



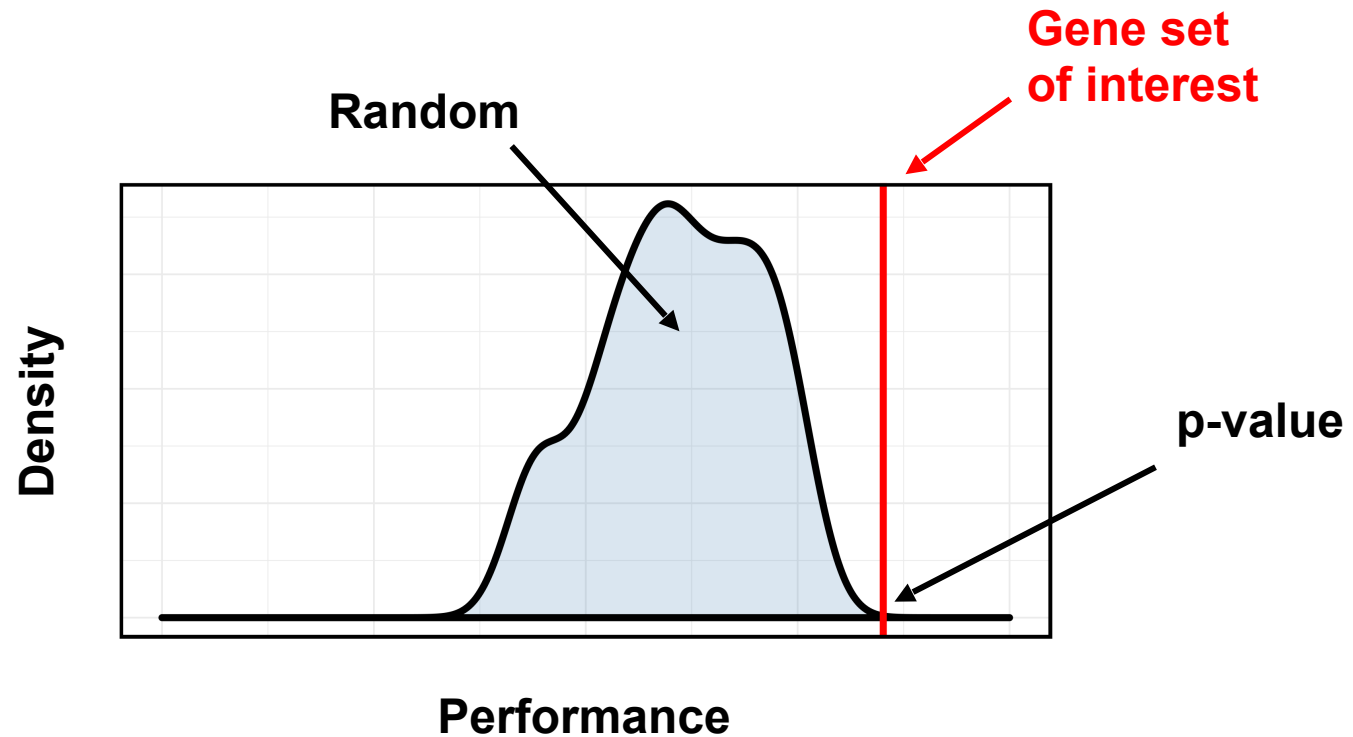
III, IV



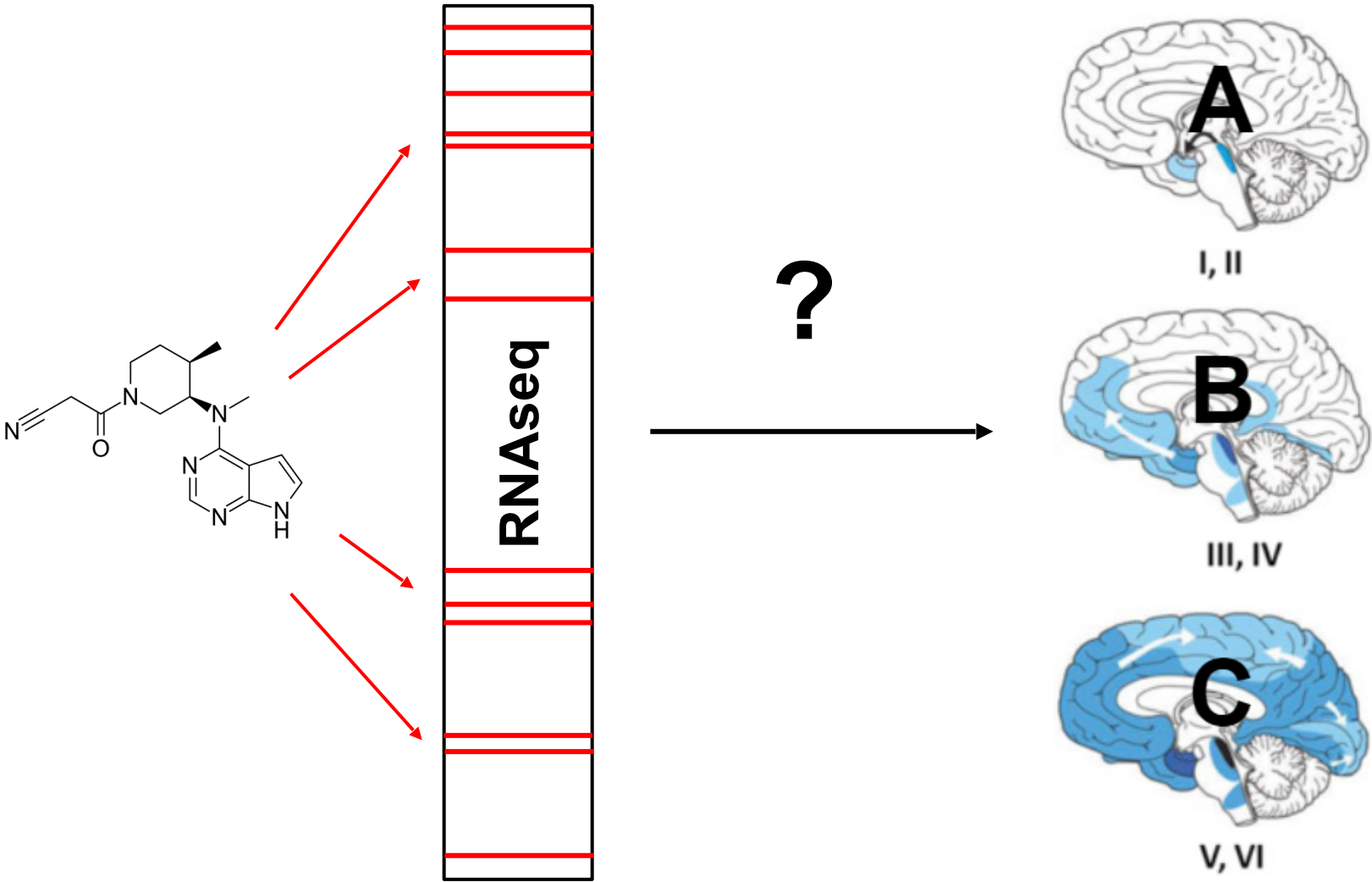
V, VI

# Gene set as a unit of prior knowledge

Intuition: if a gene set of interest is important for predicting phenotypic state, we expect to see higher prediction performance than with a randomly selected gene set of the same cardinality.

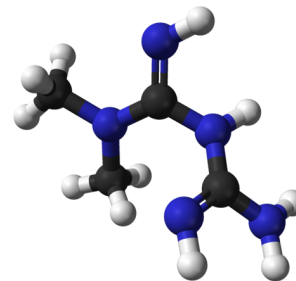
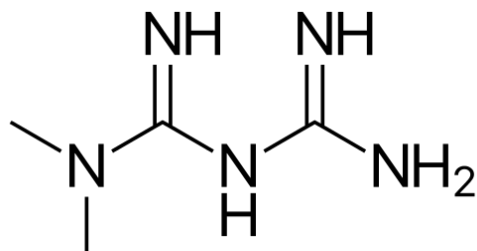


# Repurposed drug perturbations to gene expression levels as the gene set of interest



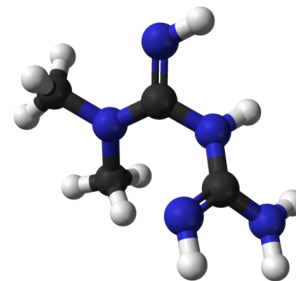
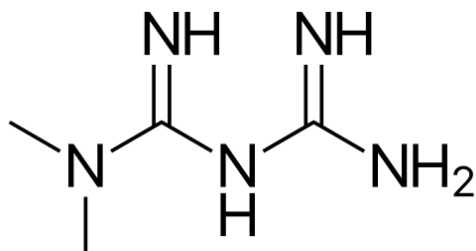
# Converting drug names to gene sets

Example:  
Metformin





# Converting drug names to gene sets

Example:  
Metformin



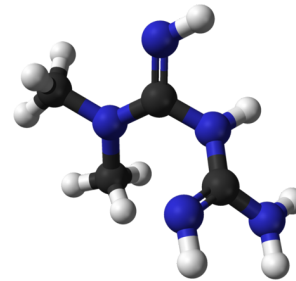
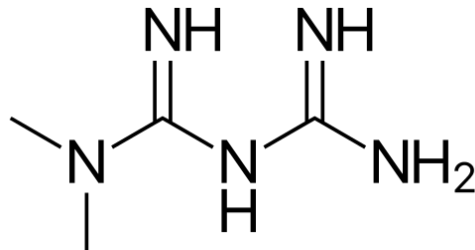
## Deciphering Signaling Pathway Networks to Understand the Molecular Mechanisms of Metformin Action

Jingchun Sun, Min Zhao, Peilin Jia, Lily Wang, Yonghui Wu, Carissa Iverson, Yubo Zhou, Erica Bowton, Dan M. Roden, Joshua C. Denny, Melinda C. Aldrich, Hua Xu , Zhongming Zhao 





# Converting drug names to gene sets

Example:  
Metformin



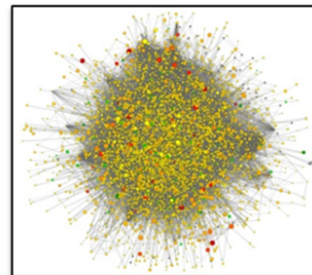
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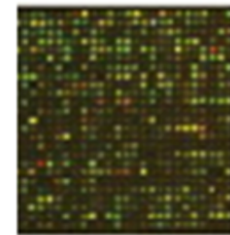
Metformin upstream  
genes

Drug targets (DrugBank)  
Pharmacogenomic genes  
Drug PD/PK pathways  
Literature mining

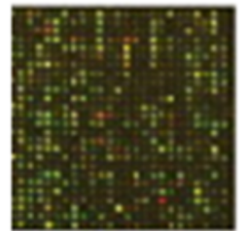
Human SPNetwork



Metformin downstream  
genes

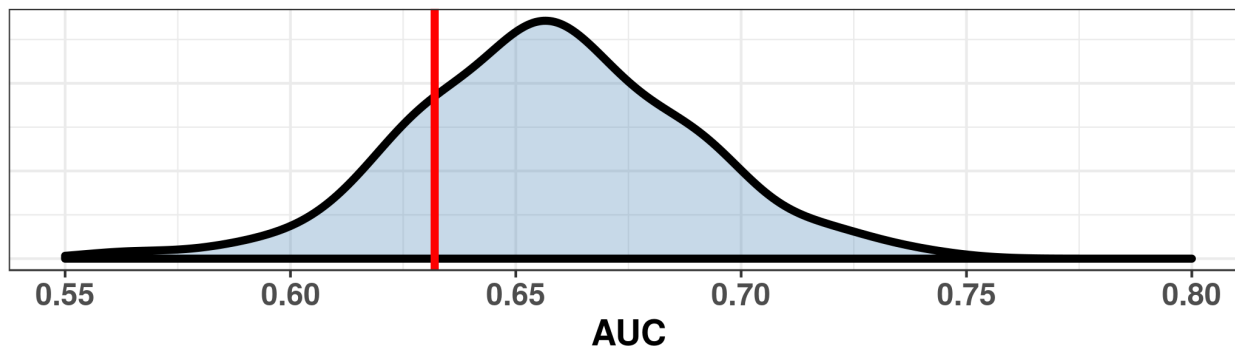


Control

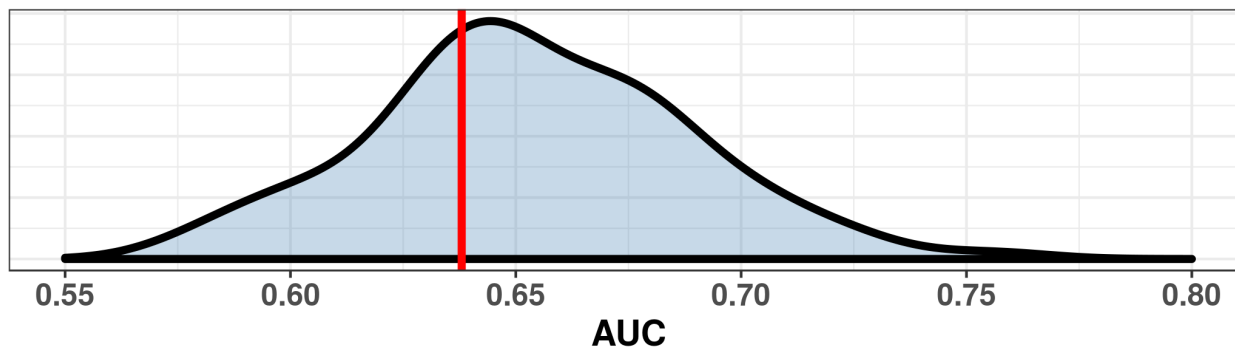


Treatment

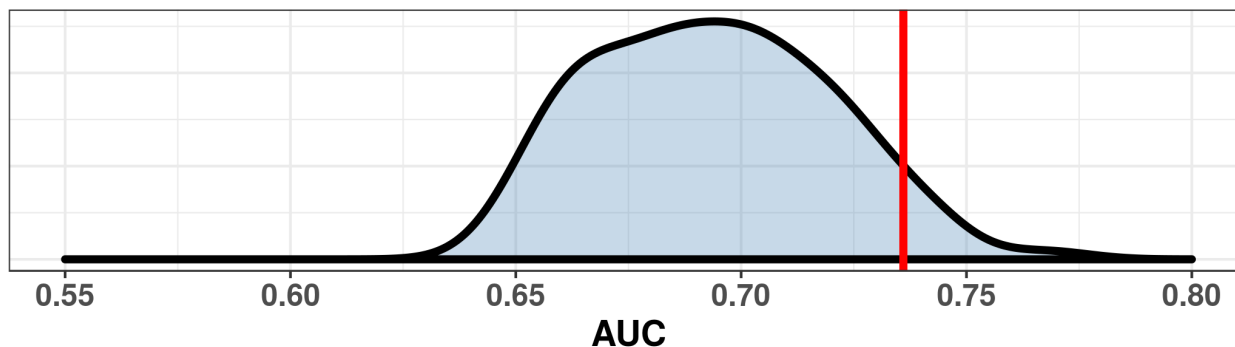
# Compare drug-related gene set against random sets for Metformin in the Break predictor



**Mined**  
**Size: 64**  
**Area UC: 0.632**  
**pval: 0.79**

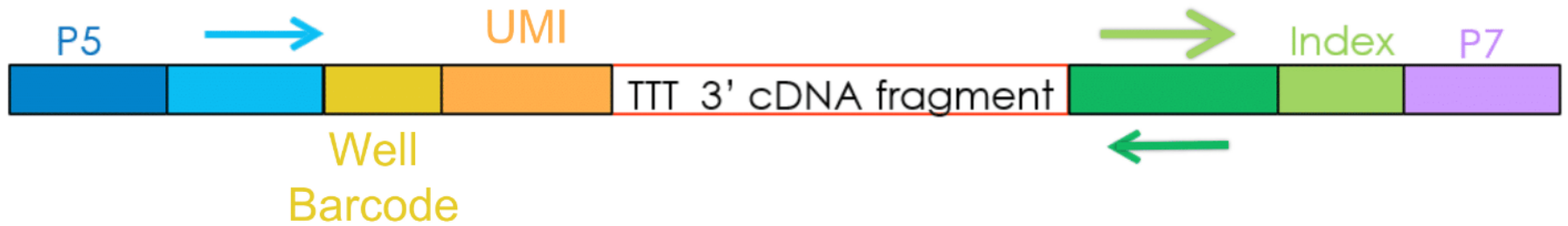


**Experimental**  
**Size: 65**  
**Area UC: 0.637**  
**pval: 0.73**



**Combined**  
**Size: 472**  
**Area UC: 0.736**  
**pval: 0.06**

# 3' Digital Gene Expression (DGE) allows for high-throughput profiling of multiple 384-well plates

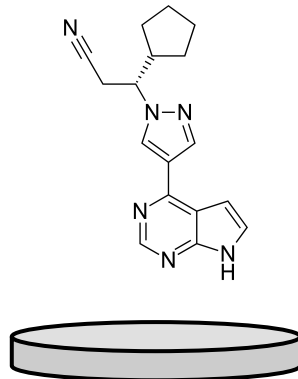


**Barcode:** Well/Cell index ( $N_6$ ) + Unique Molecular Identifier ( $N_{10}$ )  
**Index:** Plate indexing

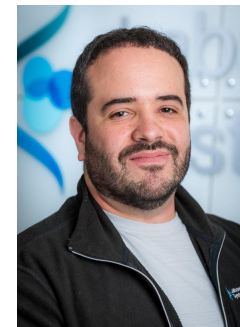
ReNcell VM  
Human



DMSO



Song.... Albers, Mitchison, Sorger, under review

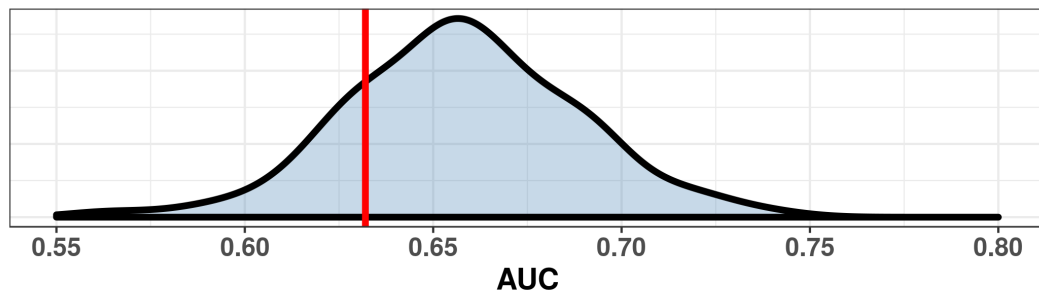


Steve  
Rodriguez

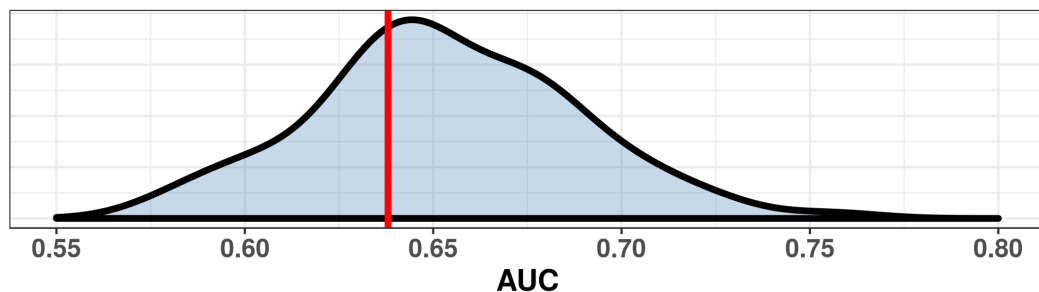


Sarah  
Boswell

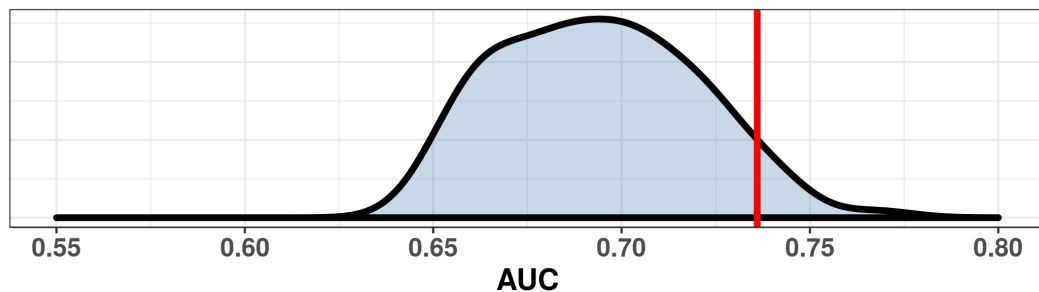
# Human neuron profiles yield improved performance for Metformin



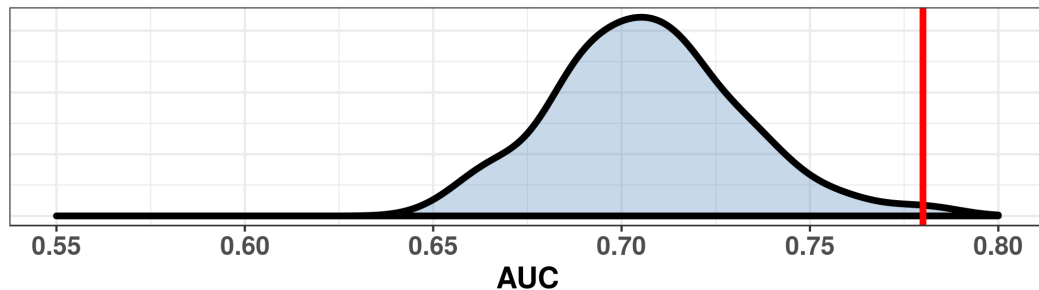
**Mined**  
**Size: 64**  
**AUC: 0.632**  
**pval: 0.79**



**Experimental**  
**Size: 65**  
**AUC: 0.637**  
**pval: 0.73**

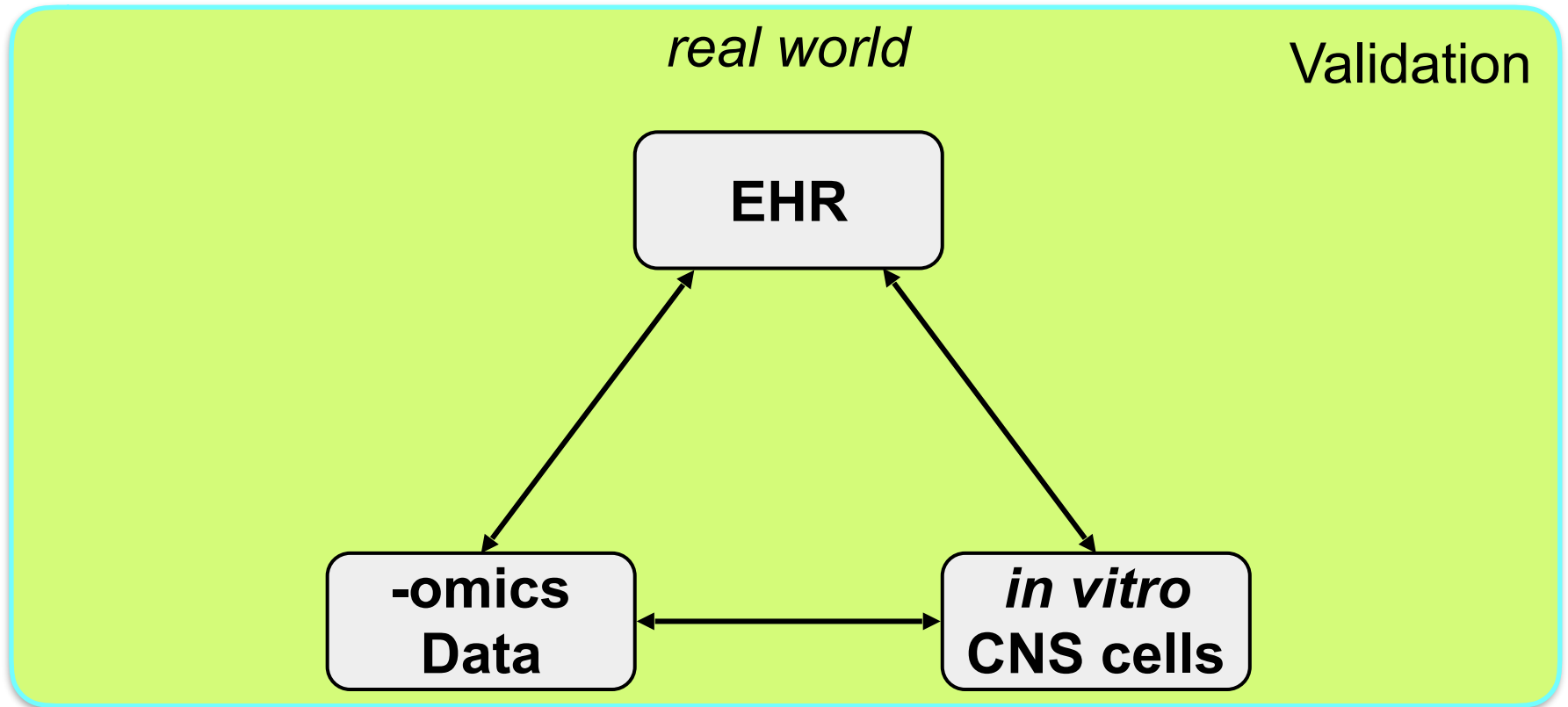


**Combined**  
**Size: 472**  
**AUC: 0.736**  
**pval: 0.06**



**DGE-derived**  
**Size: 901**  
**AUC: 0.780**  
**pval: 0.01**

# Integrating three data sources

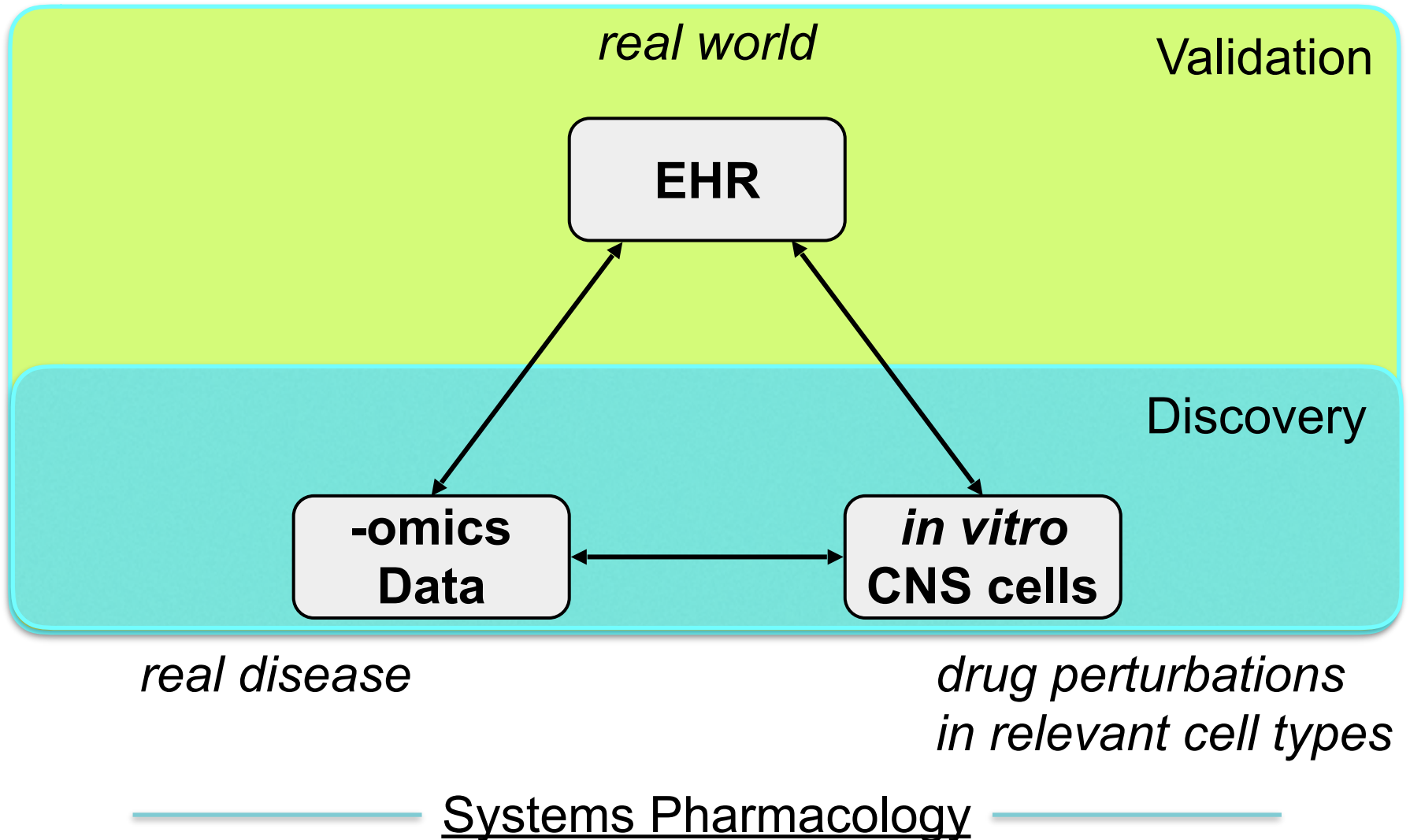


*real disease*

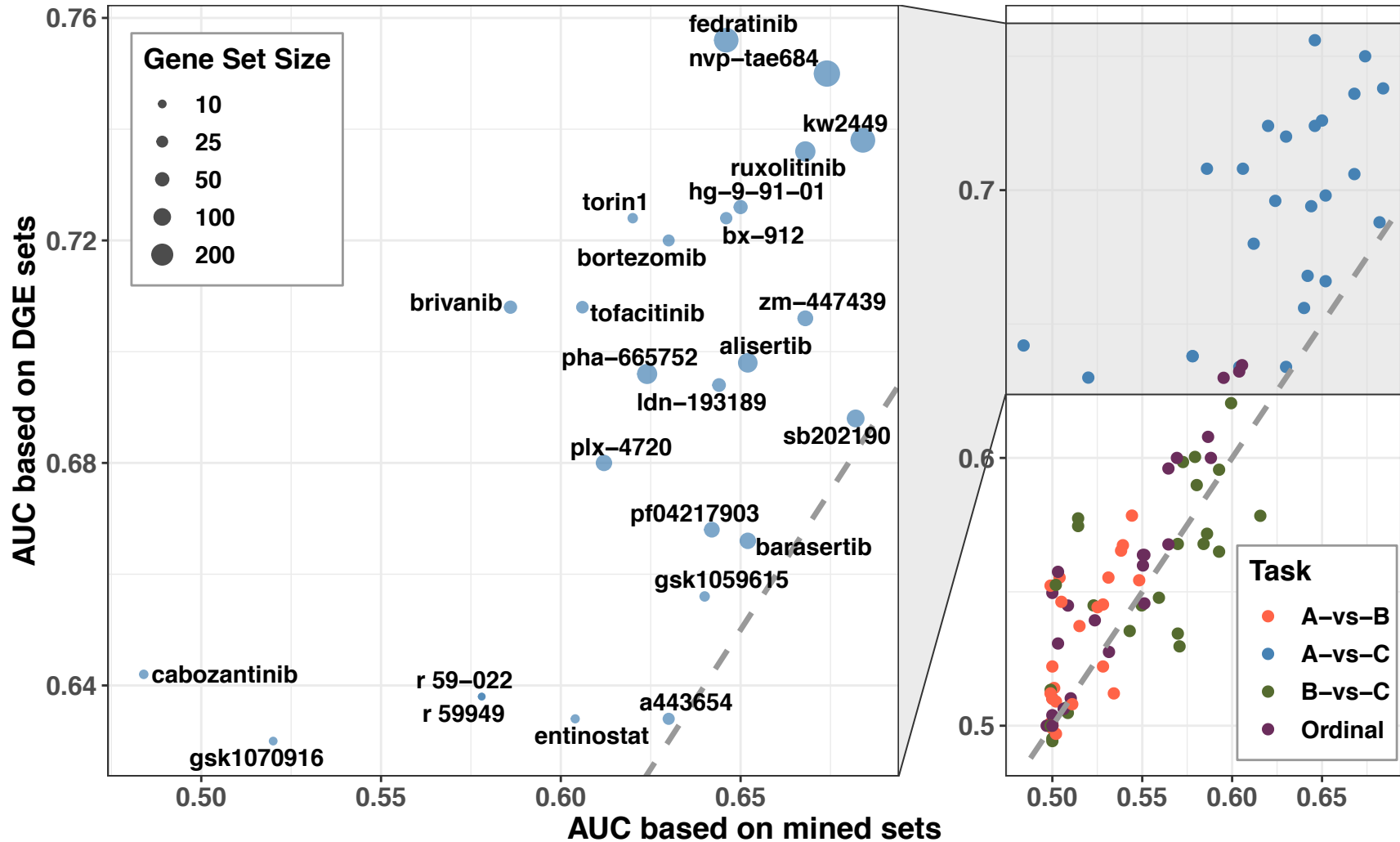
*drug perturbations  
in relevant cell types*

Systems Pharmacology

# Integrating three data sources



Discovery efforts have identified 20 more drug perturbations that associate with disease progression



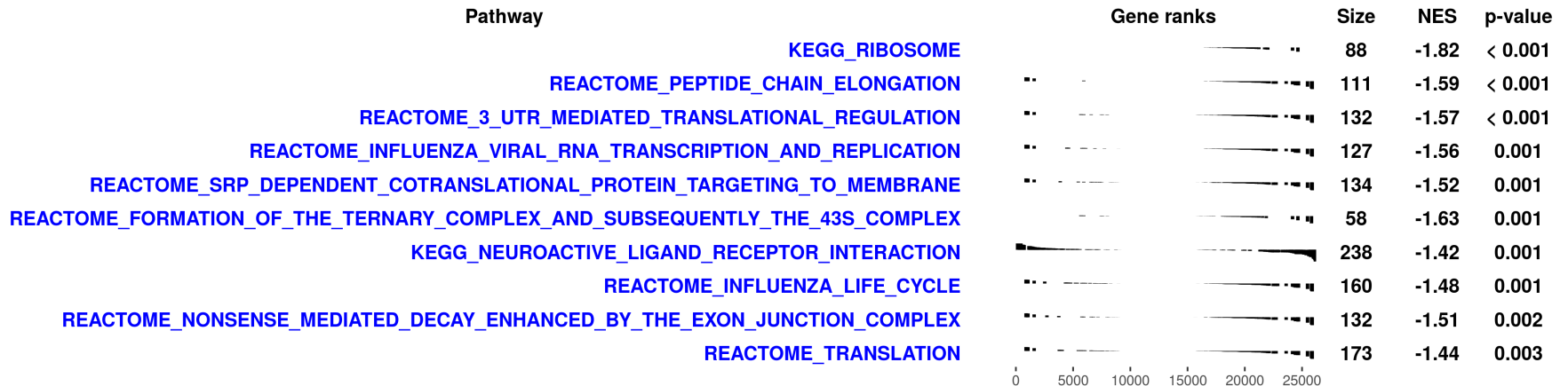
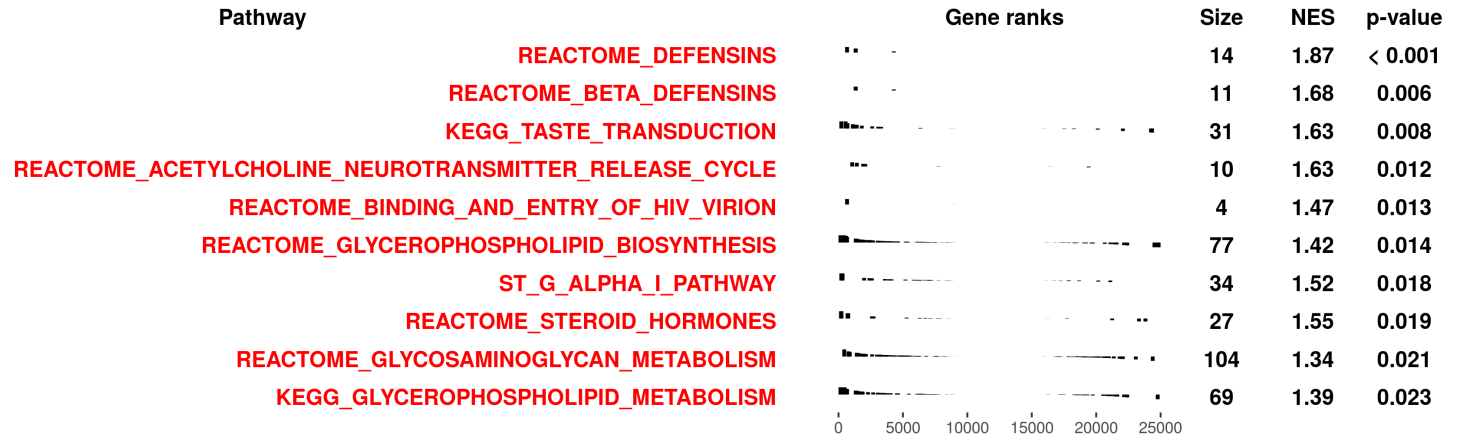
# Summary

1. In silico drug trials in EHR can evaluate a repurposed drug candidates. The hazard ratio of diabetics on metformin to develop dementia is significantly reduced relative to diabetics on sulfonylurea.
2. Genes differentially expressed by metformin in human CNS cell types predict stage of AD in human brains.
3. Cellular context matters. Drug induced patterns of differentially expressed genes in human CNS cell types predict stage of AD better than drug induced patterns derived from non-CNS cell types.



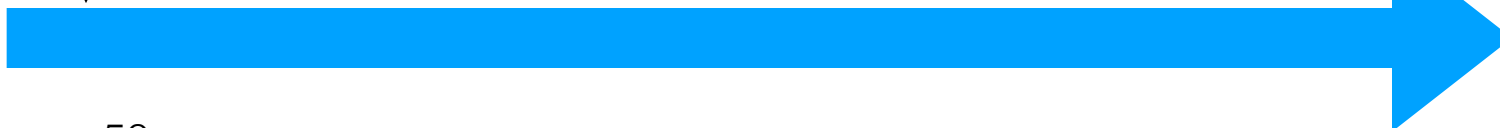


# Induction of defensins and reduced translation by Metformin in human CNS cells



**Initiation** trial (asymptomatic to diagnosis):

age 50

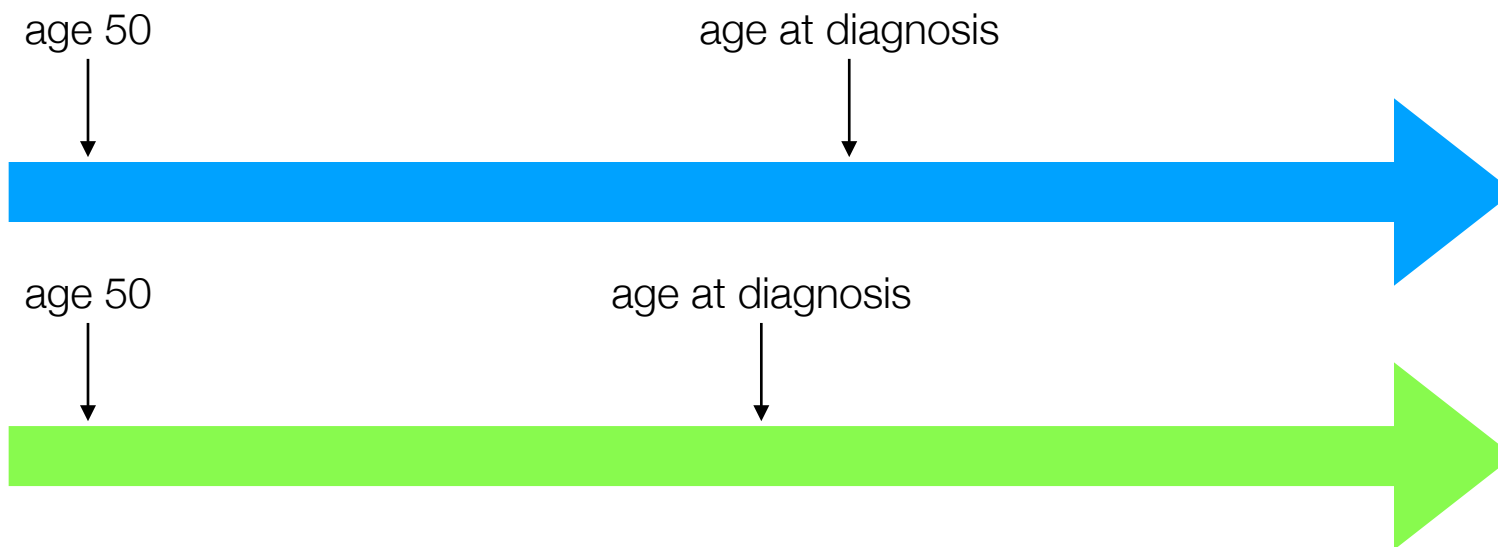


age 50



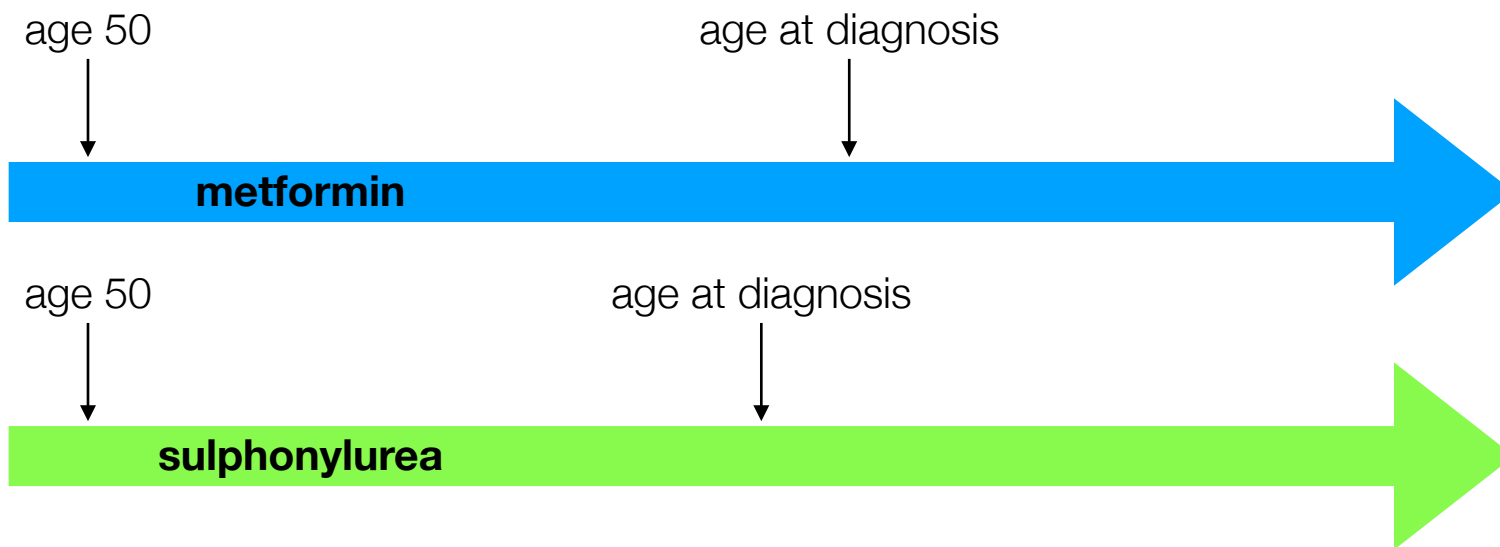
Ioanna  
Tzoulaki

**Initiation** trial (asymptomatic to diagnosis):



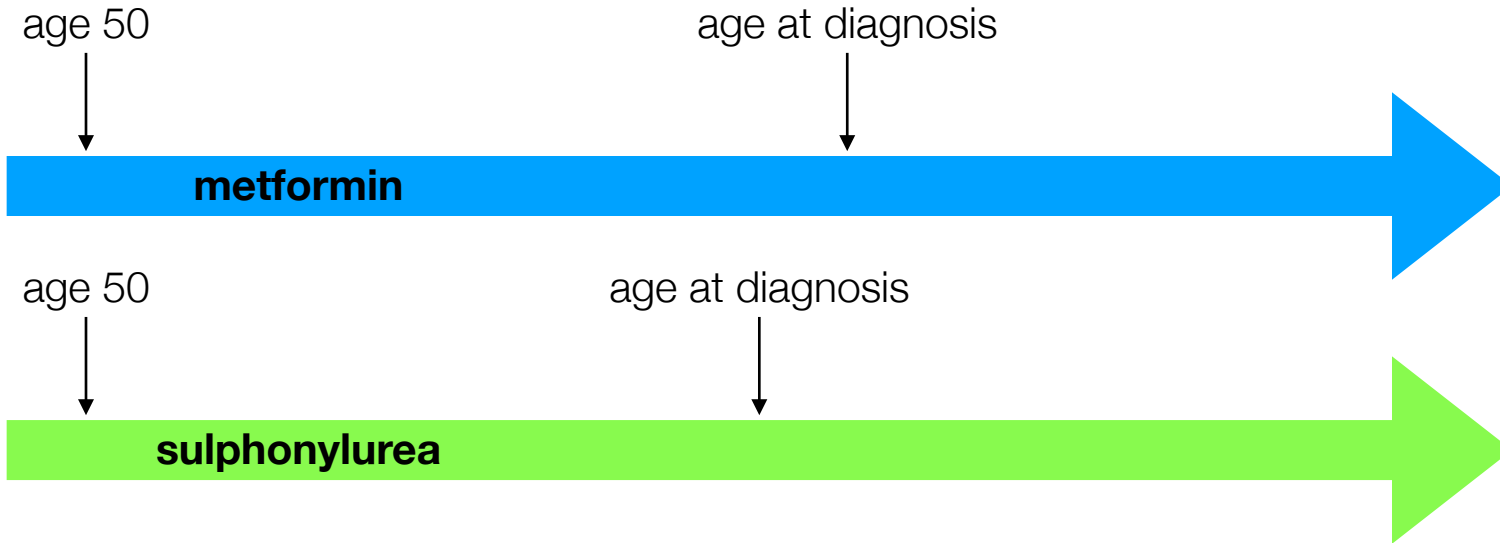
Ioanna  
Tzoulaki

**Initiation** trial (asymptomatic to diagnosis):

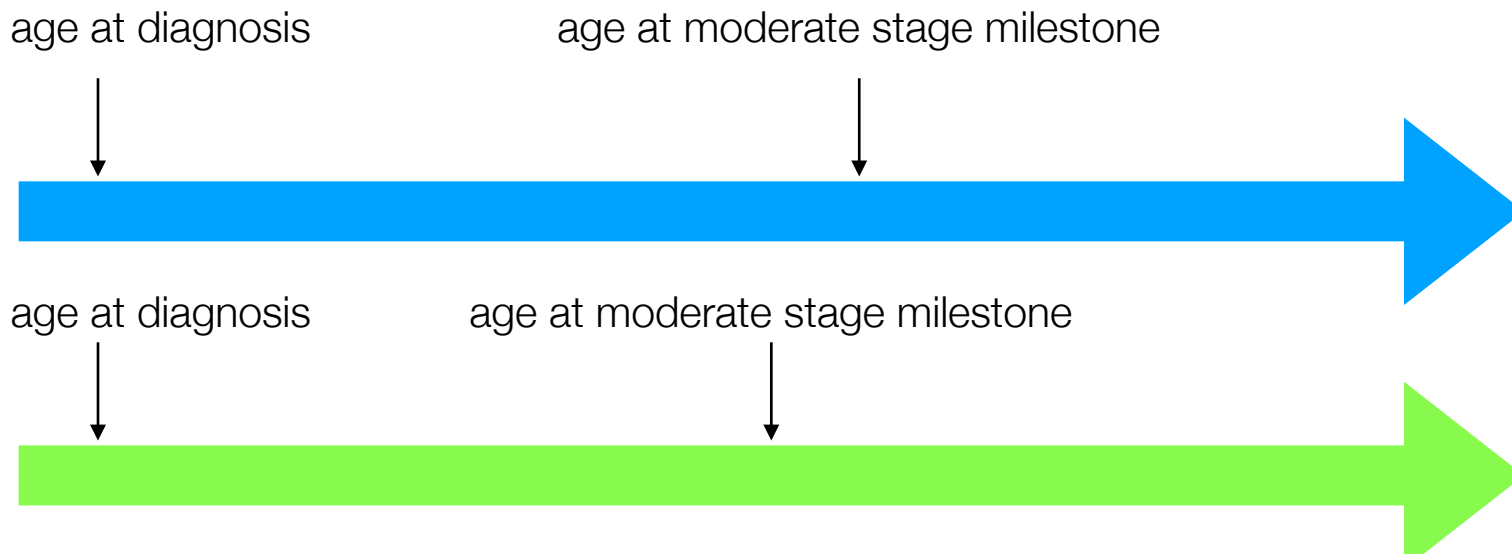


Ioanna  
Tzoulaki

**Initiation** trial (asymptomatic to diagnosis):



**Progression** trial (diagnosis to moderate stage):



Ioanna  
Tzoulaki