

# Systems biology, Systems Medicine, Big DataHow network approaches can improveIBD research and clinical outcome

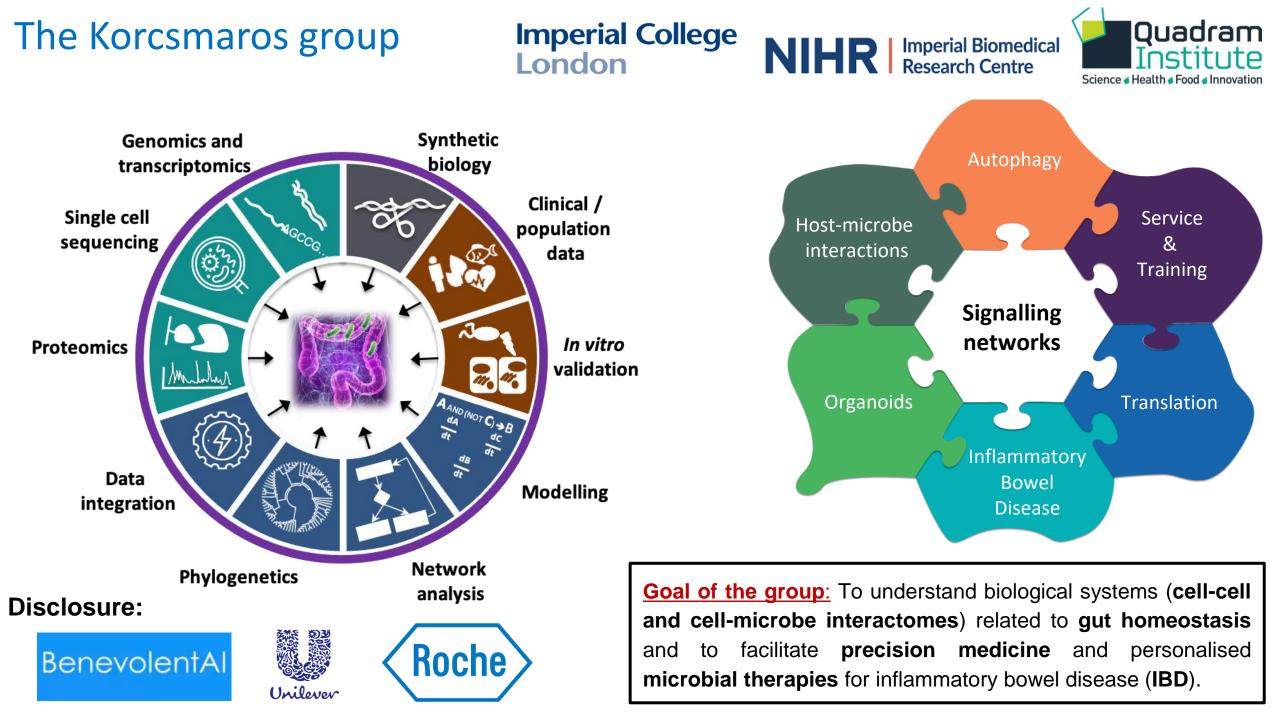
#### TAMAS KORCSMAROS

Senior Lecturer Division of Digestive Diseases



## Imperial College London





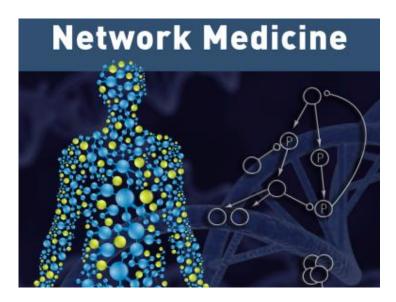
## Big data in IBD

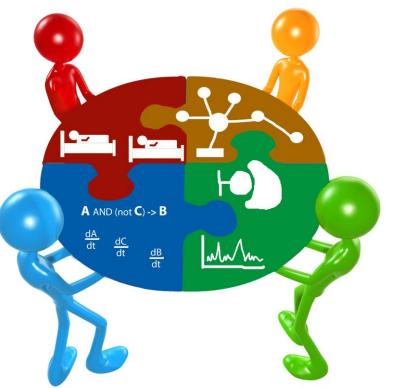


#### Seyed Tabib et al, Gut, 2020

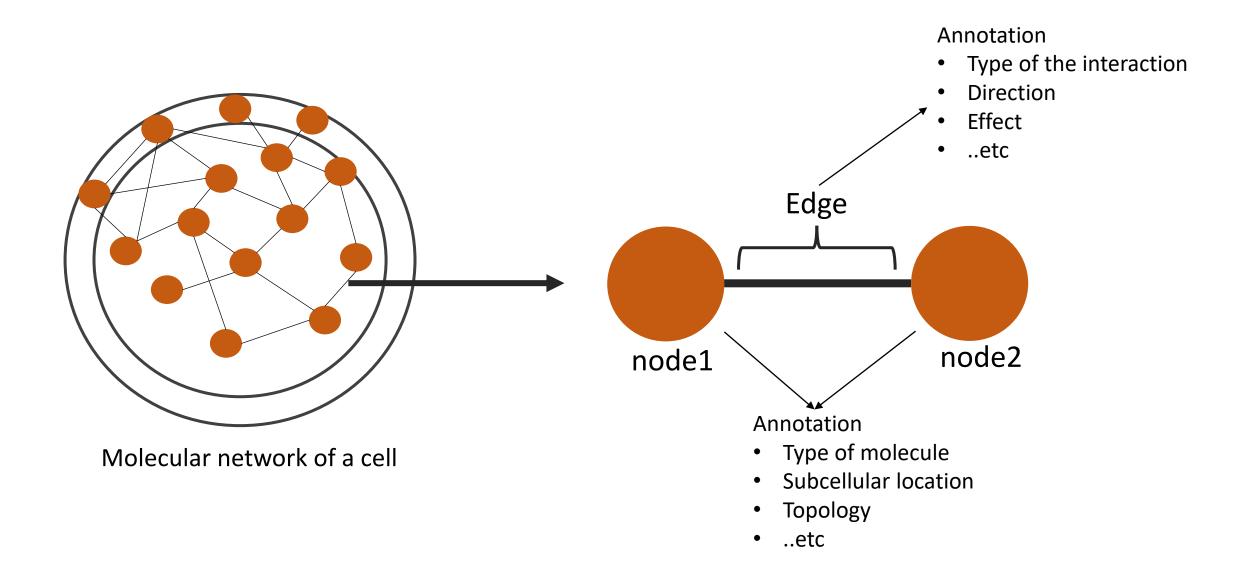
## Network medicine – a promising history

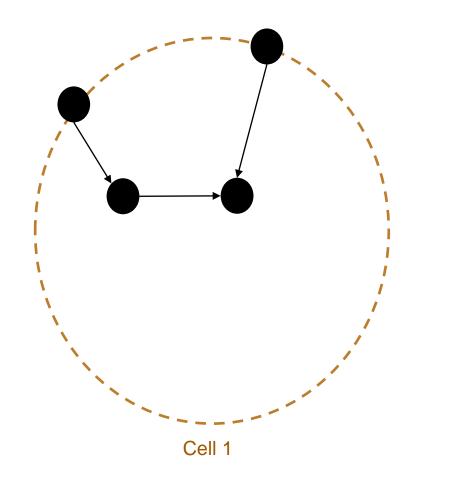
- "Network medicine" (Barabasi, 2007)
- "Systems medicine is finally coming of age" (Lemberger, 2007)
- Network as the target (Pawson and Linding, 2008)
- "Think globally, act locally" (Barabasi, Loscalzo, 2011)
- Nowadays considered as a resource for
  - biomarker discovery
  - drug target prediction
  - drug side-effect analysis
  - drug repurposing
  - suggesting
    new therapies
  - patient-stratification

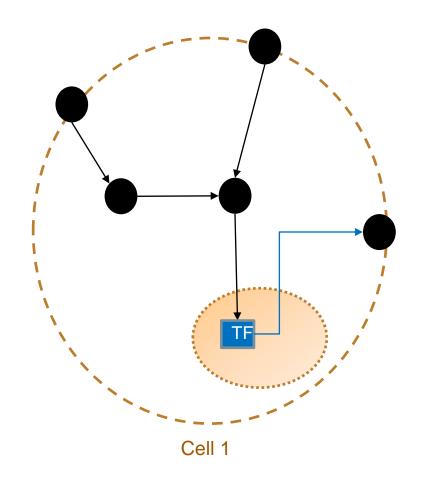




## Molecular interaction networks





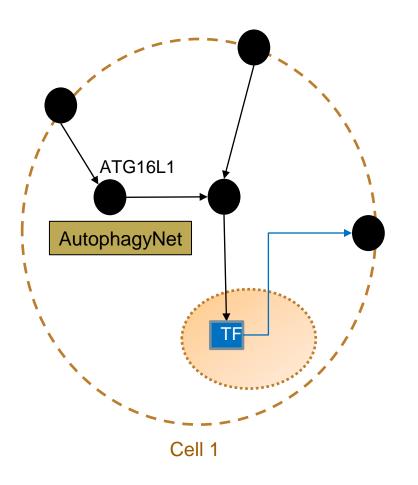


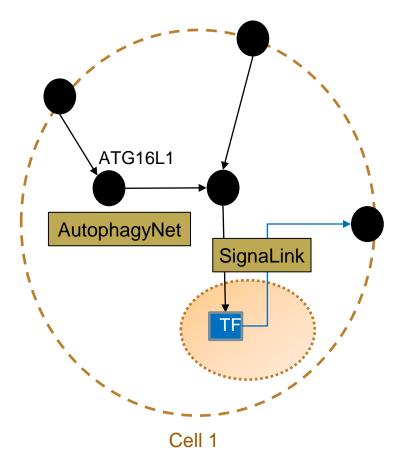


Disease Models & Mechanisms

Integrative analysis of Paneth cell proteomic and transcriptomic data from intestinal organoids reveals functional processes dependent on autophagy

Emily J. Jones<sup>1,2,3,\*</sup>, Zoe J. Matthews<sup>3,\*</sup>, Lejla Gul<sup>1,\*</sup>, Padhmanand Sudhakar<sup>1,2</sup>, Agatha Treveil<sup>1,2</sup>, Devina Divekar<sup>2,3</sup>, Jasmine Buck<sup>3</sup>, Tomasz Wrzesinski<sup>1</sup>, Matthew Jefferson<sup>3</sup>, Stuart D. Armstrong<sup>4</sup>, Lindsay J. Hall<sup>2</sup>, Alastair J. M. Watson<sup>2,3</sup>, Simon R. Carding<sup>2,3</sup>, Wilfried Haerty<sup>1</sup>, Federica Di Palma<sup>1</sup>, Ulrike Mayer<sup>5</sup>, Penny P. Powell<sup>3</sup>, Isabelle Hautefort<sup>1</sup>, Tom Wileman<sup>2,3</sup> and Tamas Korcsmaros<sup>1,2,‡</sup>





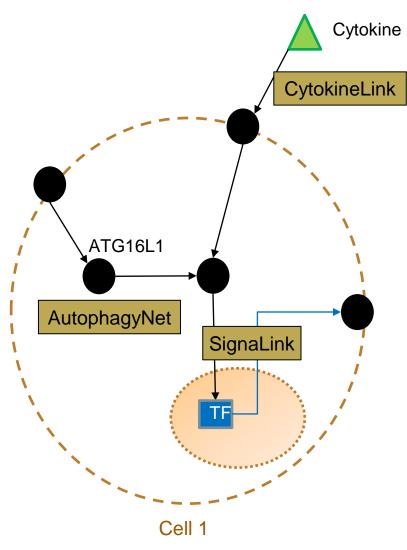
#### RESEARCH ARTICLE

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Molecular Omics		CONTRACTOR OF CHEMISTRY
RESEARCH ART	ICLE	View Article Online View Journal
Check for updates	Regulatory network analysis of Par and goblet cell enriched gut organ transcriptomics approaches†	
	A. Treveil, <sup>(0)</sup> ‡ <sup>ab</sup> P. Sudhakar,‡ <sup>ac</sup> Z. J. Matthews,‡ <sup>d</sup> T. Wrze J. Brooks, <sup>abde</sup> M. Ölbei, <sup>ab</sup> I. Hautefort, <sup>a</sup> L. J. Hall, <sup>b</sup> S. R. Ca P. P. Powell, <sup>d</sup> T. Wileman, <sup>bd</sup> F. Di Palma, <sup>a</sup> W. Haerty* <sup>a</sup> and	arding, <sup>bd</sup> U. Mayer, <sup>f</sup>



#### RESEARCH ARTICLE

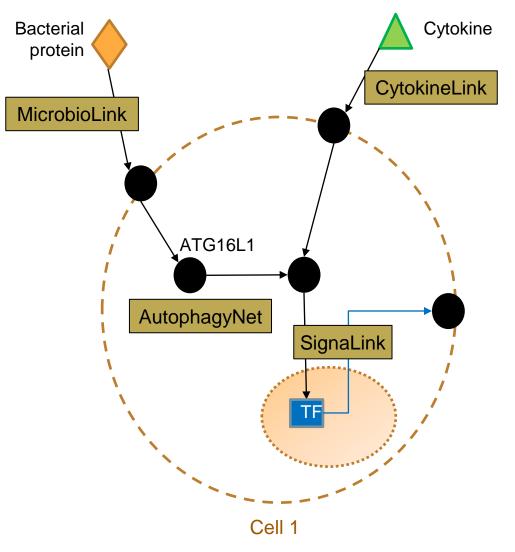


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Cytokine Responsive Networks in Human Colonic Epithelial Organoids Unveil a Novel Molecular Stratification of Inflammatory Bowel Disease



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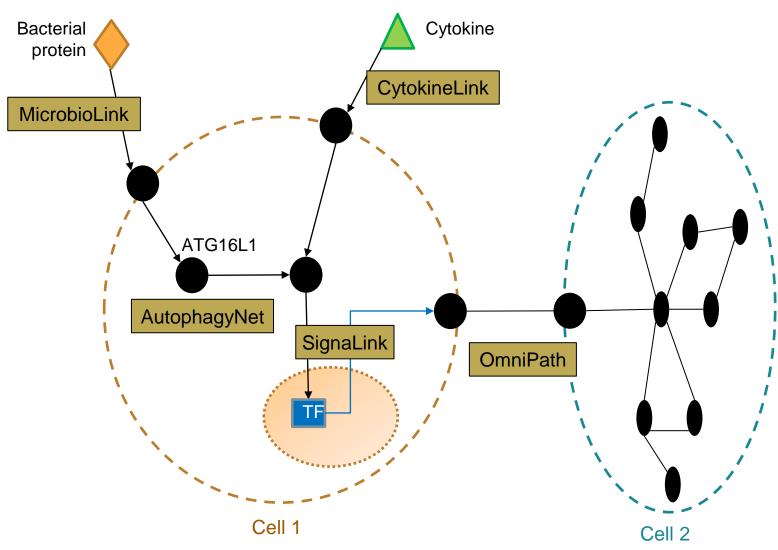
#### **iScience**

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#### Article

Integrated analysis of microbe-host interactions in Crohn's disease reveals potential mechanisms of microbial proteins on host gene expression

Padhmanand Sudhakar,<sup>1,4,\*</sup> Tahila Andrighetti,<sup>2</sup> Sare Verstockt,<sup>1</sup> Clara Caenepeel,<sup>1,3</sup> Marc Ferrante,<sup>1,3</sup> João Sabino,<sup>1,3</sup> Bram Verstockt,<sup>1,3</sup> and Severine Vermeire<sup>1,3</sup>



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#### **iScience**

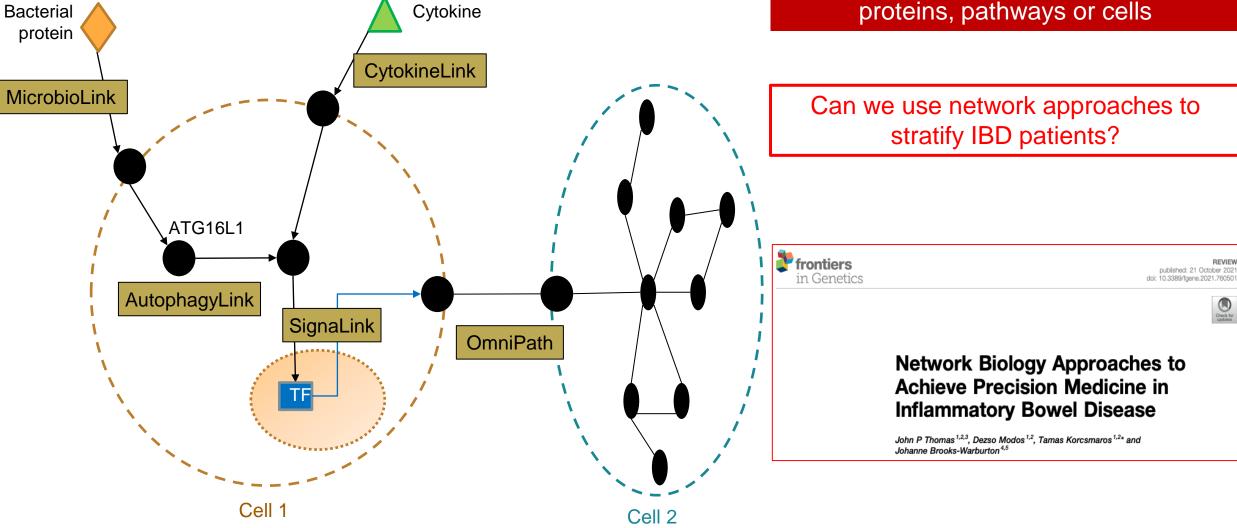
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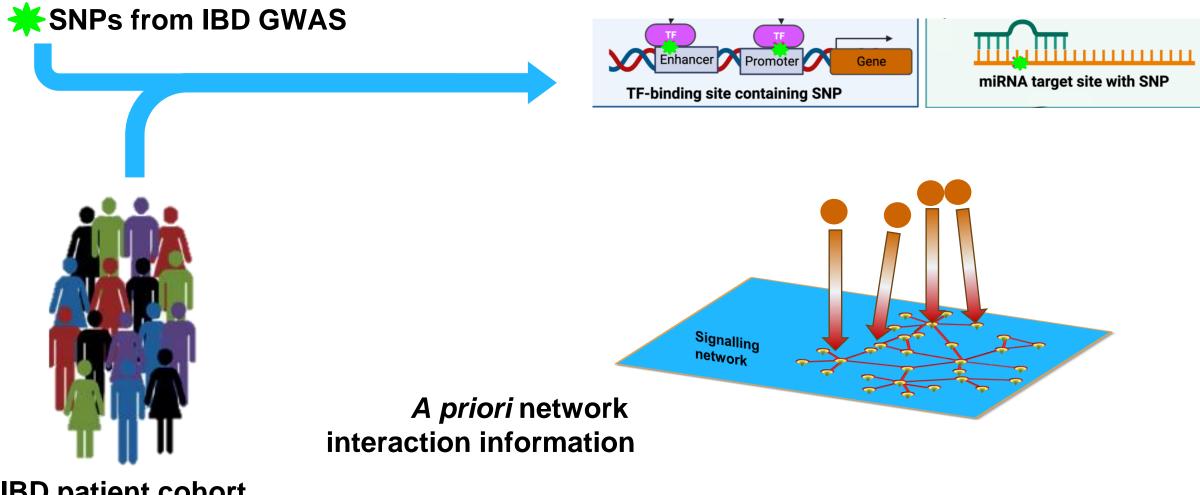
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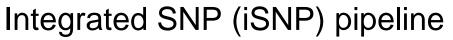
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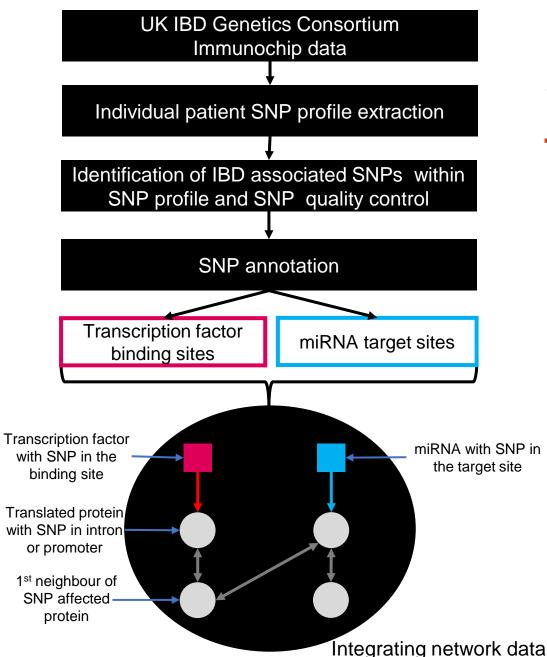
IBD patients have various sets of SNPs affecting different or overlapping sets of proteins, pathways or cells





**IBD** patient cohort





Brooks et al, *Nature Communications, 2022* Korcsmaros *et al, PCT patent application, 2019* 

#### nature communications

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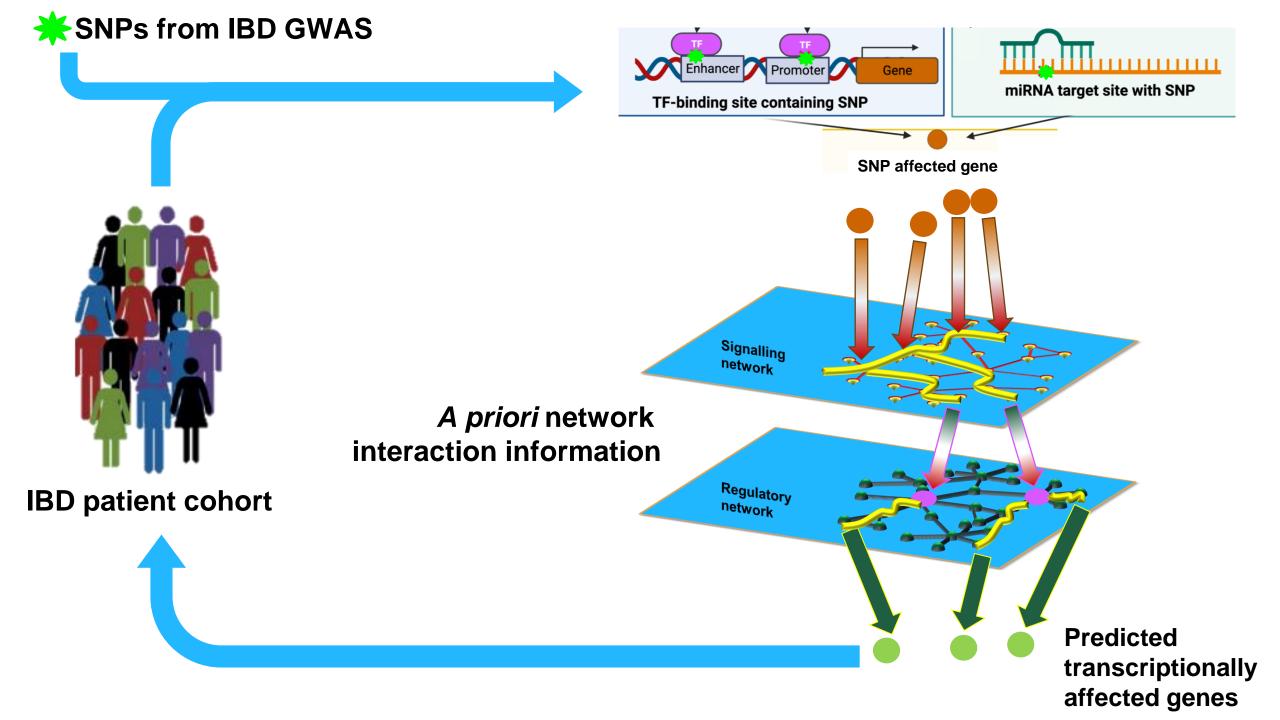
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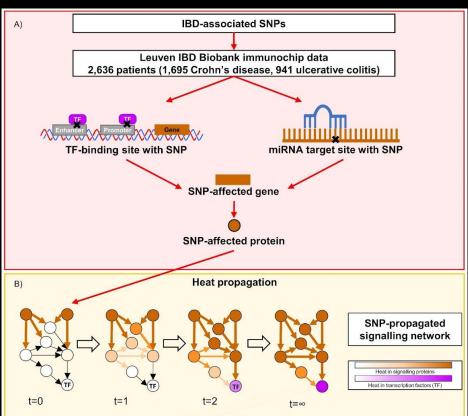
Article Open access Published: 28 April 2022

#### A systems genomics approach to uncover patientspecific pathogenic pathways and proteins in ulcerative colitis

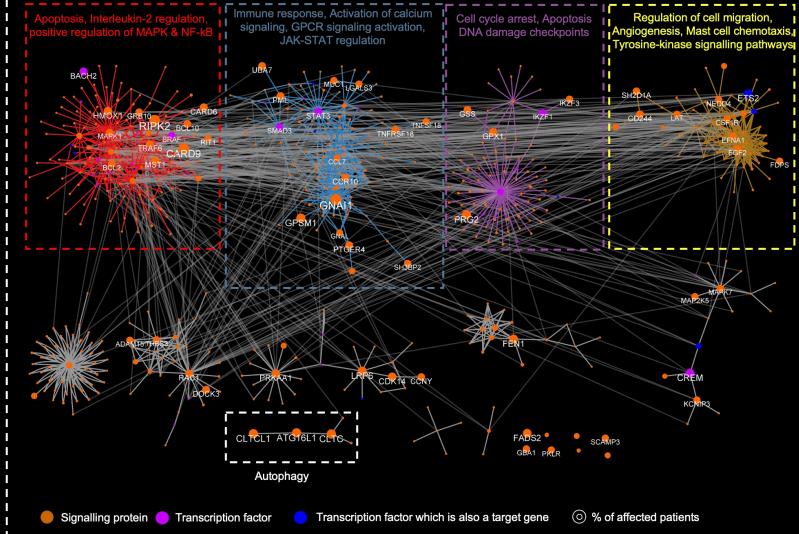
Johanne Brooks-Warburton, Dezso Modos, Padhmanand Sudhakar, Matthew Madgwick, John P. Thomas, Balazs Bohar, David Fazekas, Azedine Zoufir, Orsolya Kapuy, Mate Szalay-Beko, Bram Verstockt, Lindsay J. Hall, Alastair Watson, Mark Tremelling, Miles Parkes, Severine Vermeire, Andreas Bender, Simon R. Carding 🖾 & Tamas Korcsmaros 🖾

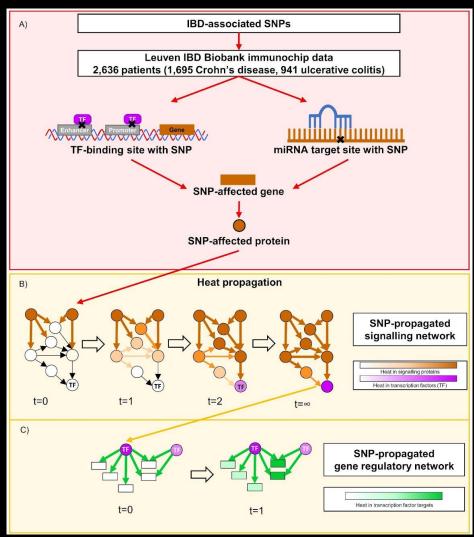
Nature Communications 13, Article number: 2299 (2022) Cite this article



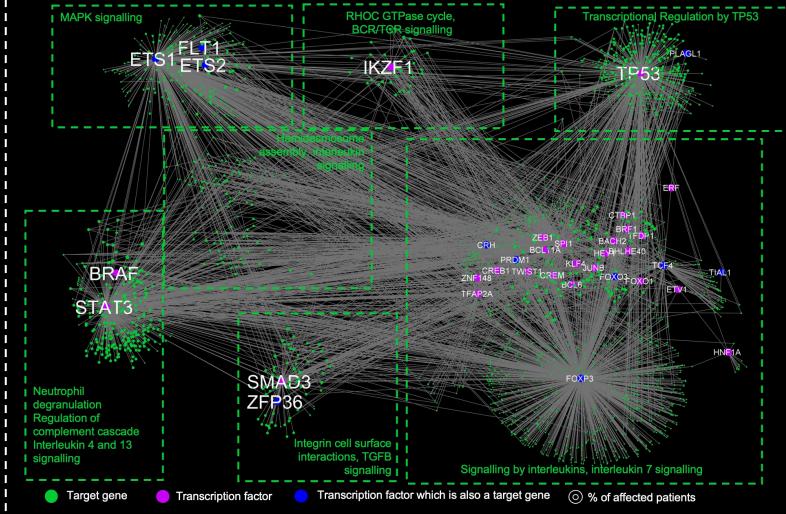


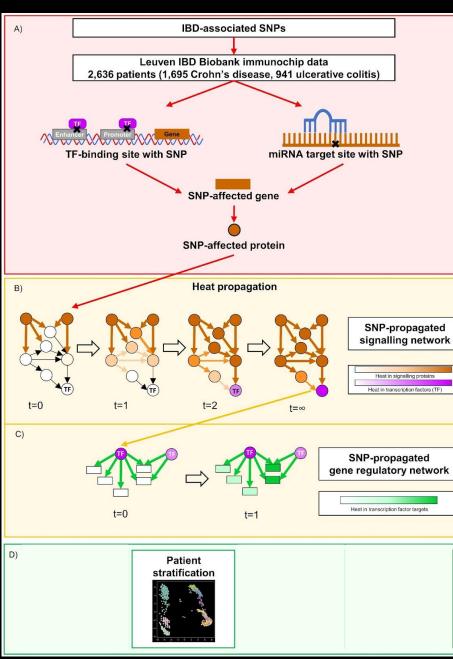
### Impact of CD non-coding SNPs on signalling Convergence on cell cycle and apoptosis





### Impact of CD non-coding SNPs on gene regulation Convergence on key transcription factors





## SNP-propagated gene regulatory networks capture disease heterogeneity in CD

Patient cluste

Number of

patients

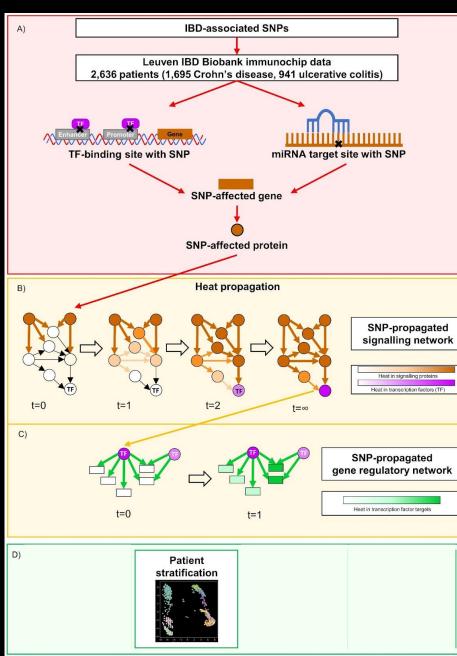
Main

transcription

factors

\_\_\_\_\_

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	119	60 376 333		9 60 376 33		9 <mark>60 376</mark> 33		333	106	4	43	142	2	124		37	11(	6	101	1	138
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					Patient cluster	1	2	3	4	5	6	7	8	9	10	11	12				
					Number of patients	119	60	376	333	106	43	142	124	37	116	101	138				
					ETS1																
	•				ETS2																
	••	•			FLT1																
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					SMAD3																
					ZFP36																



## SNP-propagated GRNs capture disease heterogeneity in CD

Pa	atient cluster	1	2	3	4	5	6	7	8	9	10	11	12		
	Number of patients	119	60	376	333	106	43	142	124	37	116	101	138		
	Main ranscription factors	ETS1, ETS2, FTL1	STAT3, ETS1, ETS2, FLT1	Various TFs, low number of targets	TP53	STAT3	STAT3, TP53	Various TFs, high number of targets	STAT3,T P53	STAT3	STAT3, IKZF1		STAT3, , SMAD3, ZFP36		
I I I ETS1/E															
1			2				3			•	4				
5			6				7				B				
9			10				11				12				
I STAT3													SMA		

### Genotype-driven patient clusters correspond to cell type-specific gene dysregulation in CD

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Patient cluster Number of patients	Main transcription factors	Tregs	Naïve T cells	CD4 FOSB T cells	IELS	B cells	Macrophages	DC1	DC2	Mast cells	Fibroblasts	Paneth cell	Enterocyte	Stem cells	Treg	Naïve CD4	CD8 T cells	CD17	CD4 FOSB	NK like	DC2	Goblet cells	Myofibroblasts	Inflammatory fibroblasts	Fibroblasts	LTC4S endothelial cells	Glial cells
1 119	ETS1, ETS2, FTL1																										
	STAT3, ETS1, ETS2, FLT1																										
3 376 lo	Various TFs, ow number of targets																										
4 333	TP53																										
5 106	STAT3																										
	STAT3, TP53																										
7 142 h	/arious TFs, igh number of targets																										
8 124 \$	STAT3,TP53																										
9 37	STAT3																										
10 116 S	STAT3, IKZF1																										
11 101	STAT3, SMAD3, ZFP36																										
12 138	STAT3, SMAD3, ZFP36																										

## Summary and next steps

- Many IBD-associated SNPs have regulatory effects
- The SNP-set (SNP co-occurrence) is more relevant marker than a single SNP
- Including downstream potentially effected processes increases the opportunity to stratify patients
- Aggregated data, randomised trials could miss key signals in complex diseases
- To assess the power of iSNP and other network approaches the combination of omics data and clinical metadata is necessary
- Patient-type specific changes in host-microbe interactions?





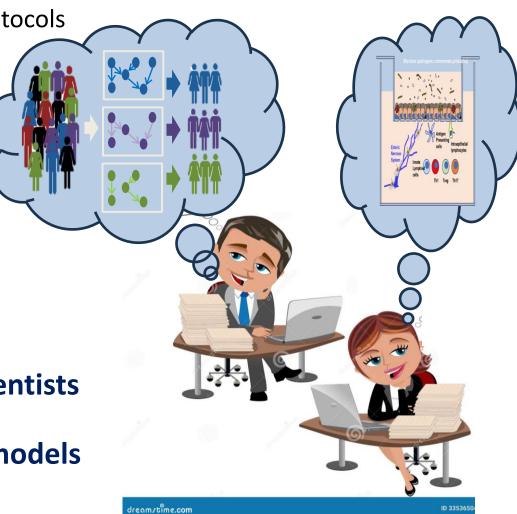




## Network Medicine in IBD – what is needed from hype to success

### • Higher complexity datasets

- Multi-omics based on IBD definition (genetics, immunology, exposome/microbiome)
- Each collected from the same patient, with standardised protocols
- With associated clinical metadata
- Higher resolution datasets
  - Single-cell data (more patients, larger sequencing depth)
  - Strain level metagenomics
  - Spatial and time-course data
  - Functional omics (proteomics, metabolomics)
- Training and community between tool developers / data analysts, academic and clinical scientists
- Human organoid based, complex IBD experimental models for hypothesis generation and validation



## Acknowledgements

#### **Korcsmaros group**

- Isabelle Hautefort
- Marton Olbei
- Leila Gul
- Balazs Bohar
- John P. Thomas
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- Luca Csabai
- Deema Alassaf
- Polina Kornilova
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- Yiran Zhang
- Cynthia Qiu
- Yik Jin Voon
- Jiyoon Choi
- Mira Mazsa

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- Martina Poletti
- Jo Brooks
- Amanda Demeter
- Agatha Treveil
- Padhmanand Sudhakar
- Emily Jones
- Denes Turei
- Tamas Kadlecsik
- David Fazekas
- Mate Szalay-Beko
- Wen-Xin Kang
- Georgina Alabone
- Tahila Andrighetti
- Zoltan Dul

## Imperial College London





Biotechnology and Biological Sciences Research Council





Medical Research Council



Decoding Living Systems

## PINITER Imperial Biomedical Research Centre

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Séverine Vermeire Marc Ferrante Bram Verstockt Kaline Arnout

UK IBD GENETICS CONSORTIUM Understanding the genetics of Crohn's & Colitis

Miles Parkes Carl Anderson



Dana Philpott Mark Silverberg Sun-Ho Lee



Gavin Bewick Chronis Pavlidis Joana Neves

## wick Pavlidis eves



Diana Papp Sandra Koigi Tamir Rashid

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**Research Centre** 

Nick Powell and the Powell lab Gary Frost David Ma



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> UNIVERSITÉ DU LUXEMBOURG Paul Wilmes

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## Thank you!

https://github.com/KorcsmarosGroup/

http://KorcsmarosLab.org

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