

# Emanuel Gonçalves

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## EDUCATION

**University of Cambridge, Cambridge, United Kingdom**

*PhD in Systems Biology, October 2012 - March 2017*

**University of Minho, Braga, Portugal**

*MSc in Bioinformatics, October 2010 - October 2012*

**University of Minho, Braga, Portugal**

*BEng in Computer Engineering, October 2006 - July 2010*

## RESEARCH & WORK EXPERIENCE

**Wellcome Sanger Institute, Cambridge, United Kingdom**

*Postdoctoral Fellow since May 2017 at Mathew Garnett Lab*

Development of computational analytical methods to unravel cancer cell dependencies from large-scale genome-wide CRISPR/Cas9 and pharmacological screens.

**University of Cambridge / EMBL-EBI, Cambridge, United Kingdom**

*Predoctoral Fellow from October 2012 to March 2017 at Saez-Rodriguez & Beltrao Labs, EMBL-EBI*

Applied and developed methods for analysing high-throughput mass-spectrometry data measuring protein and metabolite abundances across large panels of samples. Modelled the regulatory interface between signalling and metabolic processes to study cellular adaptations in cancer and yeast.

**ETH Zurich, Switzerland**

*Visitor PhD student from September 2015 to December 2015 at Sauer Lab, ETHZ*

Studied the dynamic adaptation of yeast cells to salt and pheromone *stimuli* by acquiring time-course metabolic measurements and integrating them with phosphoproteomics. Acquired basic knowledge and experience performing experimental lab work.

## **EMBL-EBI, Cambridge, United Kingdom**

*Visitor MSc student intern from January 2012 to October 2012 at Saez-Rodriguez Lab, EMBL-EBI*

Developed Java plug-ins, CySBGN and Cytocopter, for Cytoscape to visualise biological networks and to model signalling networks.

## **University of Minho, Braga, Portugal**

*Research fellow from May 2011 to November 2011 at Systems Biology Lab, University of Minho*

Implemented a computational approach, within OptFlux software, to assess the impact of over and under expression of enzymes using metabolic genome-scale models.

## **HONORS & AWARDS**

*EMBO short-term fellowship, EMBO / ETH Zurich - 2015*

*PhD Fellowship, European Molecular Biology Laboratory - 2012*

*Scholarship Award of Excellence, Master of Bioinformatics, University of Minho - 2012*

*ERASMUS placement fellowship, University of Minho / EU ERASMUS - 2011*

*Research fellowship, FCT / University of Minho - 2011*

## **REFERENCES**

*Dr. Mathew Garnett, Wellcome Sanger Institute, Cambridge, United Kingdom  
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*Prof. Dr. Julio Saez-Rodriguez, RWTH-Aachen University, Aachen, Germany  
saezrodriguez@combine.rwth-aachen.de*

*Dr. Christian Frezza, MRC Cancer Unit, Cambridge, United Kingdom  
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*Dr. Pedro Beltrão, EMBL-EBI, Cambridge, United Kingdom  
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*Dr. Miguel Rocha, University of Minho, United Kingdom  
mrocha@di.uminho.pt*

# PUBLICATIONS

## Selected publications

1. **Gonçalves E**, Fragoulis A, Garcia-Alonso L, Cramer T, Saez-Rodriguez J, Beltrao P (2017) Widespread Post-transcriptional Attenuation of Genomic Copy-Number Variation in Cancer. *Cell Syst* 5: 386–398.e4
2. **Gonçalves E\***, Sciacovelli M\*, Costa ASH, Tran MGB, Johnson TI, Machado D, Frezza C, Saez-Rodriguez J (2017) Post-translational regulation of metabolism in fumarate hydratase deficient cancer cells. *Metab Eng*
3. Sciacovelli M, **Gonçalves E**, Johnson TI, Zecchini VR, da Costa ASH, Gaude E, Drubbel AV, Theobald SJ, Abbo SR, Tran MGB, Rajeeve V, Cardaci S, Foster S, Yun H, Cutillas P, Warren A, Gnanapragasam V, Gottlieb E, Franze K, Huntly B, et al. (2016) Fumarate is an epigenetic modifier that elicits epithelial-to-mesenchymal transition. *Nature* 537: 544–547
4. **Gonçalves E**, Raguz Nakic Z, Zampieri M, Wagih O, Ochoa D, Sauer U, Beltrao P, Saez-Rodriguez J (2017) Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. *PLoS Comput Biol* 13: e1005297

## Other publications

1. Hernandez-Armenta C, Ochoa D, **Gonçalves E**, Saez-Rodriguez J, Beltrao P (2017) Benchmarking substrate-based kinase activity inference using phosphoproteomic data. *Bioinformatics* 33: 1845–1851
2. Terfve C, Sabidó E, Wu Y, **Gonçalves E**, Choi M, Vaga S, Vitek O, Saez-Rodriguez J, Aebersold R (2017) System-Wide Quantitative Proteomics of the Metabolic Syndrome in Mice: Genotypic and Dietary Effects. *J Proteome Res* 16: 831–841
3. **Gonçalves E**, Raguz Nakic Z, Zampieri M, Wagih O, Ochoa D, Sauer U, Beltrao P, Saez-Rodriguez J (2017) Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. *PLoS Comput Biol* 13: e1005297
4. Roumeliotis TI\*, Williams SP\*, **Gonçalves E**, Alsinet C, Del Castillo Velasco-Herrera M, Aben N, Ghavidel FZ, Michaut M, Schubert M, Price S, Wright JC, Yu L, Yang M, Dienstmann R, Guinney J, Beltrao P, Brazma A, Pardo M, Stegle O, Adams DJ, et al. (2017) Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. *Cell Rep* 20: 2201–2214
5. Iorio F\*, Knijnenburg TA\*, Vis DJ\*, Bignell GR\*, Menden MP\*, Schubert M, Aben N, **Gonçalves E**, Barthorpe S, Lightfoot H, Cokelaer T, Greninger P, van Dyk E, Chang H, de Silva H, Heyn H, ..., Wessels LFA, Saez-Rodriguez J, McDermott U, Garnett MJ (2016) A Landscape of Pharmacogenomic Interactions in Cancer. *Cell* 166: 740–754

6. Rohwer N, Bindel F, Grimm C, Lin SJ, Wappler J, Klinger B, Blüthgen N, Du Bois I, Schmeck B, Lehrach H, de Graauw M, **Goncalves E**, Saez-Rodriguez J, Tan P, Grabsch HI, Prigione A, Kempa S, Cramer T (2016) Annexin A1 sustains tumor metabolism and cellular proliferation upon stable loss of HIF1A. *Oncotarget* **7**: 6693–6710
7. Ryll A, Bucher J, Bonin A, Bongard S, **Gonçaves E**, Saez-Rodriguez J, Niklas J, Klamt S (2014) A model integration approach linking signalling and gene-regulatory logic with kinetic metabolic models. *Biosystems* **124**: 26–38
8. Chaouiya C, Bérenguier D, Keating SM, Naldi A, van Iersel MP, Rodriguez N, Dräger A, Büchel F, Cokelaer T, Kowal B, Wicks B, **Gonçaves E**, Dorier J, Page M, Monteiro PT, von Kamp A, Xenarios I, de Jong H, Hucka M, Klamt S, et al. (2013) SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Syst Biol* **7**: 135
9. **Gonçaves E**, Bucher J, Ryll A, Niklas J, Mauch K, Klamt S, Rocha M, Saez-Rodriguez J (2013) Bridging the layers: towards integration of signal transduction, regulation and metabolism into mathematical models. *Mol Biosyst* **9**: 1576–1583
10. **Gonçaves E**, Mirlach F, Saez-Rodriguez J (2013) Cyrface: An interface from Cytoscape to R that provides a user interface to R packages. *F1000Res* **2**: 192
11. **Gonçaves E**, van Iersel M, Saez-Rodriguez J (2013) CySBGN: a Cytoscape plug-in to integrate SBGN maps. *BMC Bioinformatics* **14**: 17
12. Pacini C, Iorio F, **Gonçaves E**, Iskar M, Klabunde T, Bork P, Saez-Rodriguez J (2013) DvD: An R/Cytoscape pipeline for drug repurposing using public repositories of gene expression data. *Bioinformatics* **29**: 132–134
13. Terfve C, Cokelaer T, Henriques D, MacNamara A, **Gonçaves E**, Morris MK, van Iersel M, Lauffenburger DA, Saez-Rodriguez J (2012) CellNOptR: a flexible toolkit to train protein signaling networks to data using multiple logic formalisms. *BMC Syst Biol* **6**: 133
14. **Gonçaves E**, Pereira R, Rocha I, Rocha M (2012) Optimization approaches for the in silico discovery of optimal targets for gene over/underexpression. *J Comput Biol* **19**: 102–114