

Emre Guney, PhD

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EDUCATION

- **Pompeu Fabra University:** PhD in Biomedicine (Bioinformatics) (2008-2012) **Barcelona, Spain**
- **Koc University:** MSc in Electrical and Computer Engineering (2005-2007) **Istanbul, Turkey**
- **Middle East Technical University:** BSc in Computer Engineering (2001-2005) **Ankara, Turkey**

EXPERIENCE

- **Research Programme in Biomedical Informatics, UPF/IMIM** **Barcelona, Spain**
 - *Senior Research Fellow (2017-present)*
 - **Translational knowledge discovery:**
In silico modeling of drug toxicity and biomarker discovery through cross-species in vitro data analysis and machine learning.
- **Scipher Medicine, DZZOM** **Boston, USA**
 - *Scientific Advisor (2016-present)*
 - **Predictive Modeling:**
Built a rheumatoid arthritis response classifier combining topological information on the disease neighborhood in the interactome and gene expression data.
- **Institute for Biomedical Research, IRB** **Barcelona, Spain**
 - *Investigator (2015-2017)*
 - **Drug Repositioning:**
Conducted research on therapeutic repurposing opportunities targeting common pathways in diseases.
- **Northeastern University & Harvard Medical School, CCNR/CCSB** **Boston, USA**
 - *Postdoctoral Research Associate (2013-2015)*
 - **Integrative Network Biology:**
Developed network pharmacology strategies to understand drug mechanism of action.
 - **Precision Medicine:**
Developed personalized diagnostic tools using transcriptomics data in Asthma, Parkinson and Huntington disease.
- **University of California, Ideker Lab, UCSD** **San Diego, USA**
 - *Visiting Researcher (2010)*
 - **Genomic Data Analysis:**
Involved in the development of a gene-expression based prediction method to identify regulators of stem cell differentiation.

SKILL HIGHLIGHTS

- **Programming/Scripting:** Python, R, C/C++, PHP, JS, Java, Matlab, SQL, Shell.
- **Specialized Libraries:** Bioconductor, caret, ggplot2, numpy, scipy, networkx, sklearn, tensorflow, pyramid (pylons), jupyter, matplotlib, jQuery, BOOST, OpenGL, OpenAL, ODE, PVM, MPI.
- **Software:** Libre Office, Microsoft Office, VIM, InkScape, Cytoscape, Galaxy, Zotero.
- **Analysis Skills:** Omics data analysis (quality control, normalization, clustering, differential expression, ANOVA), Functional enrichment analysis (pathway analysis, GSEA, interactome-based clustering), Feature engineering (renormalization, categorization, dimensionality reduction), Prediction model building and validation (regression, SVM, tree-based, ANN, ensemble approaches, cross-validation, bootstrapping).
- **Languages:** English, Spanish, Catalan, Turkish.

PROFESSIONAL DEVELOPMENT

- **Publications:** One US patent application and 20+ scientific publications in a number of prestigious peer-reviewed international journals (h-index=10, see [Google Scholar](#) for the full list).
- **Presentations:** Invited talks at various international conferences and research institutes (see [personal web page](#) for details).
- **Consortium Participations:** NIH-NHGRI funded projects P50-HG004233, U01-HG001715, U01-HG007690 for network-based analysis of effects of genetic mutations on human diseases. EU funded Innovative Medicines Initiative projects TransQST and eTRANSAFE on drug safety and H2020 REPO-TRIAL for in silico drug repurposing.
- **Organizational and Editorial Activities:** Editorial board member for *Systems Medicine* Journal. Guest editor for *Applied Network Science* Journal's Special Issue on Network Medicine (2018). Co-organizer of *ISCB RSG-Turkey SC Symposium* (2012) and *NetSci NetMed Symposium* (2015).
- **Mentorship:** Co-supervised one PhD student (Northeastern University, USA) and two Masters students (Pompeu Fabra University, Spain, Maastricht University, the Netherlands).
- **Teaching:** Algorithms and Data Structure (2005-2007, Koc University, Turkey), Introduction to Information Systems (2005-2006, Koc University, Turkey), Practice-based Learning (2011-2012, Pompeu Fabra University). Seminars on Systems Medicine at MSc on Omics Data Analysis (2018, University of Vic) and MSc on Neuroscience (2018, Autonomous University of Madrid).

FELLOWSHIPS AND AWARDS

- **Project Scholarships:** AGAUR Beatriu de Pinós Fellowship (2015-2017), FI Fellowship from the Government of Catalunya (2008-2012), Graduate Fellowship by The Scientific and Technical Research Council of Turkey (2006 - 2007), Koc University Foundation Graduate Scholarship (2005 - 2007).
- **Travel Awards for Conference Presentations:** PSB'17, ECCB'12, ISMB'11, ISMB'07.
- **Honors:** *Affiliate Fellow* at the Pharmacology & Personalised Medicine department at Maastricht University in the Netherlands, *Apte cum laude* designation for the PhD thesis, *Honor Student* in BS studies.

EXTRACURRICULAR ACTIVITIES

- **Community Involvement:** Member of *International Society of Computational Biology (ISCB)* since 2007. Co-chair of the *ISCB-SC Regional Student Group Turkey* (2012-2014) and *ISCB-SC Education and Internships committee* (2013-2017). Volunteer in PRBB Open days (2009,2011,2012) for guided visits, experiments and outreach presentation.
- **Entrepreneurship:** Participated in *Your Technology as a New Company workshop* organized by Boston Biomedical Innovation Center (May 2015), *From Science to Business workshop* organized by BIST and ESADE (May-June, 2016), CRG *BioBusiness School* (Sept 2016).
- **Reviewer:** Reviewer for *PLoS ONE*, *PLoS Computational Biology*, *Bioinformatics*, *BMC Bioinformatics*, *JAMIA*, *Pharmacological Research*, *Expert Review of Precision Medicine and Drug Development*, *Proceedings B*, *The American Journal of Psychiatry*, *Scientific Reports*, *Nature Communications*, *FWO grant applications*. Program committee member for *ISCB-SC Symposium* (2013), *CompleNet Conference* (2016, 2017) and the International Conference on Complex Networks (2018).

PUBLICATIONS

Journal Articles

- [21] * Jigisha Anupama, Margherita Francescato, et al. "The ISCB Student Council Internship Program: Expanding computational biology capacity worldwide." In: *PLoS computational biology* 14.1 (2018), e1005802–e1005802.
- [20] * Emre Guney. "Revisiting Cross-Validation of Drug Similarity Based Classifiers Using Paired Data." In: *Genomics and Computational Biology* (2018), e100047–e100047.

- [19] Friederike Langhauser, Ana I Casas, et al. “A diseasome cluster-based drug repurposing of soluble guanylate cyclase activators from smooth muscle relaxation to direct neuroprotection.” In: *npj Systems Biology and Applications* 4.1 (2018), p. 8.
- [18] Javier Garcia-Garcia, Victòria Valls-Comamala, et al. “iFraG: A protein–protein interface prediction server based on sequence fragments.” In: *Journal of molecular biology* 429.3 (2017), pp. 382–389.
- [17] Jörg Menche⁺, Emre Guney⁺, et al. “Integrating personalized gene expression profiles into predictive disease-associated gene pools.” In: *Npj Systems Biology and Applications* 3 (2017), p. 1.
- [16] Carlota Rubio-Perez⁺, Emre Guney⁺, et al. “Genetic and functional characterization of disease associations explains comorbidity.” In: *Scientific Reports* 7.1 (2017), p. 6207.
- [15] Emre Guney, Jörg Menche, Marc Vidal, and Albert-László Barabási. “Network-based in silico drug efficacy screening.” In: *Nature communications* 7 (2016), p. 10331.
- [14] Maksim Kitsak, Amitabh Sharma, et al. “Tissue specificity of human disease module.” In: *Scientific reports* 6 (2016).
- [13] Solveig K Sieberts, Fan Zhu, et al. “Crowdsourced assessment of common genetic contribution to predicting anti-TNF^α treatment response in rheumatoid arthritis.” In: *Nature communications* 7 (2016), p. 12460.
- [12] Sonja Hänzelmann, Jinling Wang, et al. “Thrombin stimulates insulin secretion via protease-activated receptor-3.” In: *Islets* 7.4 (2015), e1118195.
- [11] Antonio Martínez-Aranda, Vanessa Hernández, et al. “FN14 and GRP94 expression are prognostic/predictive biomarkers of brain metastasis outcome that open up new therapeutic strategies.” In: *Oncotarget* 6.42 (2015), p. 44254.
- [10] Emre Guney, Javier Garcia-Garcia, and Baldo Oliva. “GUILDify: a web server for phenotypic characterization of genes through biological data integration and network-based prioritization algorithms.” In: *Bioinformatics* 30.12 (2014), pp. 1789–1790.
- [9] Emre Guney and Baldo Oliva. “Analysis of the robustness of network-based disease-gene prioritization methods reveals redundancy in the human interactome and functional diversity of disease-genes.” In: *PLoS one* 9.4 (2014), e94686.
- [8] H Billur Engin, Emre Guney, Ozlem Keskin, Baldo Oliva, and Attila Gursoy. “Integrating structure to protein-protein interaction networks that drive metastasis to brain and lung in breast cancer.” In: *PLoS one* 8.11 (2013), e81035.
- [7] Naiara Santana-Codina, Rafael Carretero, et al. “A transcriptome-proteome integrated network identifies endoplasmic reticulum thiol oxidoreductase (ERp57) as a hub that mediates bone metastasis.” In: *Molecular & Cellular Proteomics* 12.8 (2013), pp. 2111–2125.
- [6] Javier Garcia-Garcia, Jaume Bonet, et al. “Networks of Protein-Protein Interactions: From Uncertainty to Molecular Details.” In: *Molecular informatics* 31.5 (2012), pp. 342–362.
- [5] Emre Guney and Baldo Oliva. “Exploiting protein-protein interaction networks for genome-wide disease-gene prioritization.” In: *PLoS one* 7.9 (2012), e43557.
- [4] Joan Planas-Iglesias, Emre Guney, et al. “Extending Signaling Pathways with Protein–Interaction Networks. Application to Apoptosis.” In: *Omics: a journal of integrative biology* 16.5 (2012), pp. 245–256.

- [3] Javier Garcia-Garcia, Emre Guney, Ramon Aragues, Joan Planas-Iglesias, and Baldo Oliva. “Biana: a software framework for compiling biological interactions and analyzing networks.” In: *BMC bioinformatics* 11.1 (2010), p. 56.
- [2] Nurcan Tuncbag, Attila Gursoy, Emre Guney, Ruth Nussinov, and Ozlem Keskin. “Architectures and functional coverage of protein–protein interfaces.” In: *Journal of molecular biology* 381.3 (2008), pp. 785–802.
- [1] Emre Guney, Nurcan Tuncbag, Ozlem Keskin, and Attila Gursoy. “HotSprint: database of computational hot spots in protein interfaces.” In: *Nucleic acids research* 36.suppl.1 (2007), pp. D662–D666.

Book Chapters

- [2] * Emre Guney. “Investigating side effect modules in the interactome and their use in drug adverse effect discovery.” In: *Complex Networks VIII. CompleNet 2017. Springer Proceedings in Complexity*. Springer, Cham, 2017, pp. 239–250.
- [1] Emre Guney, Rebeca Sanz-Pamplona, Angels Sierra, and Baldo Oliva. “Understanding Cancer Progression Using Protein Interaction Networks.” In: *Systems Biology in Cancer Research and Drug Discovery*. Springer, Dordrecht, 2012, pp. 167–195.

Proceedings

- [3] * Emre Guney. “Reproducible Drug Repurposing: When Similarity Does Not Suffice.” In: *Proceedings of the Pacific Symposium on Biocomputing*. World Scientific, 2017, pp. 132–143.
- [2] Ana I Casas, Friederike Langhauser, et al. “A systems biology approach to cGMP suggests a prominent role for sGC in stroke: Validation by mechanism-based activation of apo-sGC in non-steal dosing conveys neuroprotection and increased survival.” In: *BMC Pharmacology and Toxicology*. Vol. 16. S1. BioMed Central. 2015, A39.
- [1] Emre Guney and Baldo Oliva. “Toward PWAS: discovering pathways associated with human disorders.” In: *BMC bioinformatics*. Vol. 12. S11. BioMed Central, 2011, A12.

Patent

- [1] Emre Guney, Albert-László Barabási, and Jörg Menche. “Methods and systems for quantifying closeness of two sets of nodes in a network.” US Patent App. 15/461,834. 2017.

Manuscripts under review

- [2] * Joaquim Aguirre-Plans, Janet Piñero, et al. “GUILDify v2.0: From phenotype to druggable targets in the era of network pharmacology.”
- [1] * Antonio Cuadrado, Gina Manda, et al. “Transcription factor NRF2 as a therapeutic target for degenerative diseases: a systems medicine approach.”

(*) Corresponding / senior author publications