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, UO1-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 in MSc on Omics Data Analysis at University of Vic and MSc on Neuroscience at 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 Francescatto, 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 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 coveys 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] * Juaquim 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