Cagri Ozcaglar

Applied Researcher LinkedIn Sunnyvale, CA

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Education • Ph.D., Computer Science

2008-2012

Rensselaer Polytechnic Institute, Troy, NY

Thesis: Algorithmic Data Fusion Methods for Tuberculosis

• M.S., Computer Science

2006-2008

Rensselaer Polytechnic Institute, Troy, NY

Thesis: Classification of Email Messages into Topics Using Latent Dirichlet Allocation

• B.S., Computer Science

2002-2006

Bilkent University, Ankara, Turkey

Skills

- Languages: Java, C++, Python, Scala, R, MATLAB, Shell Scripting, Groovy, Perl, PHP, HTML.
- Modeling Software: Python (scikit-learn), R, MATLAB, Amazon Machine Learning, Photon-ML, Tensorflow, Keras.
- Big Data Processing: Hadoop, Spark, Apache Pig, Amazon Web Services.
- Database Management: SQL, PostgreSQL, MySQL, Oracle 10g/11g.
- Tools and Applications: Latex, Eclipse, IntelliJ, Visual Studio .NET, Git, SVN.

Research Interests

Machine Learning, Data Mining, Data Fusion, User Intent Analysis, Social Network Analysis, Multiway Analysis, Bioinformatics, Population Biology.

Experience • LinkedIn

Sunnyvale, CA

Applied Researcher

October 2016 - Present

Team: Talent Relevance

• Relevance in Recruiter product, including Recruiter Search, Contextual Search.

Amazon

Seattle, WA

Research Scientist

September 2013 - October 2016

Team: Consumer Marketing Analytics

- o Designed, built, and productionized product category purchase propensity models within Amazon in 11 marketplaces using weighted logistic regression, including General Ledger Purchase (GLP) and Browse Node Purchase (BNP) propensity models.
- o Designed, built, and productionized channel response propensity models using weighted logistic regression, including Email Risk and Response models (ERR), Mobile click and conversion propensity models.
- Designed, built, and productionized uplift / incremental models to calculate the differential propensity of a customer to take an action after targeting. Various applications include direct mail targeting for streaming Prime Instant Video (PIV), making a purchase from Fashion product categories, signing up for Amazon Business program. Live test results for PIV streaming show that incremental models return a lift of 32% and 121% on the percentage of streamers respectively, compared to overall response models and random targeting.

- Designed and built uplift models with importance weighting, in order to measure the
 differential propensity of a customer to take an action after targeting in case of treatment set selection bias. In live experiments, bias-corrected uplift models returned
 higher incremental response rate compared to treatment model and biased uplift model.
- Mobile channel acquisition and engagement models: Designed, built, and productionized Amazon Mobile shopping app download propensity models for mobile acquisition. Designed, built, and productionized mobile channel adjusted product category purchase propensity models for engagement with mobile channel. In live tests, compared to Mobile App First Sign-in (FSI) rate of 0.3% for universal control set, targeting Mobile shopping app download propensity model based segments with BAU offer and 5\$ incentive offer returned 413% and 1476% incremental lift on FSI rate, respectively.
- Designed, built, and productionized Prime Free-Trial program sign-up propensity models using thresholded model ensembles. Using two different ranking methods in live experiments, customer segments selected based on Prime Free-Trial sign-up propensity models returned 94% and 74% higher Prime Free-Trial program sign-up rates compared to the baseline sign-up rate of 7%.
- Designed and ran live experiments for targeting Amazon customers on Facebook, using browse node purchase propensity models (BNP), and deal seeker propensity models.
 In live tests, campaigns targeting browse node purchase propensity segments drove \$431K at 23.4% E%O, and campaigns targeting deal seeker segments along with BNP segments drove \$15MM at 14.67%.
- Designed, built, and productionized various channel usage propensity models and customer life-cycle propensity models, including Kindle Cross-Platform reader download propensity models (KCP), Google channel reliance models, Amazon Attrition propensity models.
- Helped internal customers onboard to Predix, an automated predictive modeling platform, by helping them with model target generation, model building, and model evaluation.
- Organized and held Machine Learning Talk Series for Consumer Marketing organization as a monthly recurring event.
- Filed a patent on Uplift Modeling with Importance Weighting, which is a method to measure the increase in the likelihood of a customer to take an action after treatment in case of selection bias.
- Published articles, presented posters, gave talks in Amazon internal machine learning conferences.
- Conducted 50+ interviews for hiring research scientists to various teams.

• Bank of America Merrill Lynch

New York, NY

Software Developer

August 2012 - August 2013

Team: Equity Linked Technology

- $\circ\,$ Designed and implemented software for processing TESS real time feeds within trading systems.
- Designed and implemented a connector between Access Request Management (ARM) and RAM database.

• Rensselaer Polytechnic Institute

Troy, NY 2006 - 2012

Research Assistant

TB-Insight: http://tbinsight.cs.rpi.edu
 Supervisor: Prof. Bulent Yener (PI: Prof. Kristin Bennett)

- UBF: Developed the Unified Biclustering Framework (UBF) to find host-pathogen associations among *M. tuberculosis* complex strains and TB patients.

- Developed an algorithm to find the mutation history in the DR region of M. tuberculosis complex and found topological attributes of the resulting phylogenetic tree. Built two new models for mutation length frequency: Starting Point Model (SPM) and Longest Block Model (LBM).
- TCF: Developed the Tensor Clustering Framework (TCF) to cluster *M. tubercu-losis* complex strains into coherent groups using multiple-biomarker tensors.
- TB-Vis: Designed and implemented a visualization program for pathogen and host analysis of tuberculosis. The visualizations include: 1) Spoligoforests which display spoligotype evolution using various distance measures of genomic data of *M. tuberculosis* complex, 2) Host-pathogen maps which display patient characteristics classified by the genotype of *M. tuberculosis* complex which infects the patients. Spoligoforests are used in TB-Lineage tool at http://tbinsight.cs.rpi.edu/about_tb_lineage.html . Both spoligoforests and host-pathogen maps are used in the design of interactive version of TB-Vis at http://tbinsight.cs.rpi.edu/about_tb_vis.html .

• Enron Email Classification Into Topics

Supervisor: Prof. Sibel Adali, Prof. Boleslaw Szymanski

Classified email messages of Enron into topics using the Latent Dirichlet Allocation.
 Described new metrics for classification assessment of email distribution into topics.

o MetPetDB: http://metpetdb.rpi.edu

Supervisor: Prof. Sibel Adali, Prof. Boleslaw Szymanski

 Contributed to the design and implementation of the client-server architecture of a database for Metamorphic Petrology.

• TUBITAK (Scientific and Technological Research Council) Software Engineer Intern

Ankara, Turkey Summer 2005

• Designed and implemented a program which calculates the salaries of the employees using their entrance and exit time to/from the building.

• TRT (Turkish Radio and Television)

Software Engineer Intern

Ankara, Turkey Summer 2004

Contributed to the implementation of user interface of Eurovision Song Contest website
of Turkey.

Teaching

• Teaching Assistant

Rensselaer Polytechnic Institute

• Introduction to Algorithms

Fall 2010

o Computer Science II: Data Structures

Spring 2008

o Computer Organization

Spring 2007

o Artificial Intelligence

Fall 2006

• Undergraduate Teaching Assistant

Bilkent University

 \circ Discrete Mathematics

Spring 2006

Journal Papers

- S. Salem, C. Ozcaglar. Hybrid coexpression link similarity graph clustering for mining biological modules from multiple gene expression datasets. *BioData Mining*, 2014.
- K. P. Bennett, <u>C. Ozcaglar</u>, J. Ranganathan, S. Raghavan, J. Katz, D. Croft, B. Yener, A. Shabbeer. **TB-vis: Visualizing TB patient-pathogen relationships**. *Tuberculosis*, 2013.

- C. Ozcaglar, A. Shabbeer, N. Kurepina, N. Rastogi, B. Yener, K. P. Bennett. Inferred spoligoforest topology unravels spatially bimodal distribution of mutations in the DR region. IEEE Transactions on NanoBioscience, 2012.
- C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. Epidemiological models of Mycobacterium tuberculosis complex infections. Mathematical Biosciences, 2012. (Featured as the most downloaded paper of Mathematical Biosciences journal in March-May 2012).
- A. Shabbeer, L. Cowan, C. Ozcaglar, N. Rastogi, S. L. Vandenberg, B. Yener, K. P. Bennett. TB-Lineage: an online tool for classification and analysis of strains of Mycobacterium tuberculosis complex. Infection, Genetics and Evolution, 2012.
- A. Shabbeer, C. Ozcaglar, B. Yener, K. P. Bennett. Web tools for molecular epidemiology of tuberculosis. Infection, Genetics and Evolution, 2012. (Featured as the most downloaded paper of Infection, Genetics and Evolution journal as of December 2011).
- C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. Sublineage structure analysis of Mycobacterium tuberculosis complex strains with multiple-biomarker tensors. BMC Genomics, 2011.

Workshop **Papers**

- Conference / S. Salem, C. Ozcaglar. MFMS: Maximal frequent module set mining from multiple human gene expression datasets. ACM SIGKDD International Workshop on Data Mining in Bioinformatics (BIOKDD), Chicago, August 2013.
 - C. Ozcaglar, A. Shabbeer, N. Kurepina, B. Yener, K. P. Bennett. Data-driven insights into deletions of Mycobacterium tuberculosis complex chromosomal DR region using spoligoforests. IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Atlanta, November 2011.
 - K. P. Bennett, C. Ozcaglar, J. Ranganathan, S. Raghavan, J. Katz, D. Croft, B. Yener, A. Shabbeer. Visualization of tuberculosis patient and Mycobacterium tuberculosis complex genotype data via host-pathogen maps. IEEE BIBM Workshop on Computational Advances in Molecular Epidemiology, Atlanta, November 2011.
 - M. Aminian, A. Shabbeer, K. Hadley, C. Ozcaglar, S. Vandenberg, K. P. Bennett. Knowledgebased Bayesian network for the classification of Mycobacterium tuberculosis complex sublineages ACM Conference on Bioinformatics, Computational Biology and Biomedicine (BCB), Chicago, August 2011.
 - C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. Examining the sublineage structure of Mycobacterium tuberculosis complex strains with multiplebiomarker tensors. IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Hong Kong, December 2010.
 - A. Shabbeer, C. Ozcaglar, M. Gonzalez, K. P. Bennett. Optimal Embedding of Heterogeneous Graph Data with Edge Crossing Constraints. NIPS Workshop on Challenges of Data Visualization, Whistler, BC, Canada, December 2010.
 - J. M. Pyle, F. S. Spear, S. Adali, B. K. Szymanski, S. Pearce, A. Waters, Z. Linder, C. Ozcaglar. MetPetDB: The Unique Aspects of Metamorphic Geochemical Data and Their Influence on Data Model, User Interface and Collaborations. Geological Society of America Abstracts with Programs, Vol. 39, No. 6, 2007.

Technical Reports

- A. Shabbeer, C. Ozcaglar, K. P. Bennett. Crossing minimization within graph embeddings. arXiv, 2012.
- C. Ozcaglar, B. Yener, K. P. Bennett. Host-pathogen association analysis of tuberculosis patients via Unified Biclustering Framework. Rensselaer Polytechnic Institute. TR-12-05, 2012.
- C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. A clustering framework for Mycobacterium tuberculosis complex strains using multiple-biomarker tensors. Rensselaer Polytechnic Institute. TR-10-08, 2010.

• F. S. Spear, J. M. Pyle, S. Adali, B. K. Szymanski, A. Waters, Z. Linder, C. Ozcaglar, S. O. Pearce. MetPetDB: A database for metamorphic geochemistry. Rensselaer Polytechnic Institute. TR-08-14, 2008.

Theses

- Algorithmic Data Fusion Methods for Tuberculosis, Ph.D. thesis, Rensselaer Polytechnic Institute, 2012.
- Classification of Email Messages into Topics Using Latent Dirichlet Allocation, M.S. thesis, Rensselaer Polytechnic Institute, 2008.

Poster

- C. Ozcaglar, B. Yener, K. P. Bennett. **UBF: Unified Biclustering Framework**. New Presentations York Academy of Sciences (NYAS) 7th Annual Machine Learning Symposium, NYC, October 2012.
 - C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. A clustering framework for Mycobacterium tuberculosis complex strains using multiple-biomarker tensors. RPI-NSF Workshop on Multiscale Modeling of Complex Data, Troy, NY, September 2011.
 - C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. Insights into Camin-Sokal Parsimony and evolution of spoligotypes via spoligoforests. New York Academy of Science (NYAS) Symposium on Imaging, Visualization and Simulation: New Tools for Technology and Healthcare, NYC, June 2011.
 - C. Ozcaglar, A. Shabbeer, S. Vandenberg, B. Yener, K. P. Bennett. Multiple-biomarker tensor analysis for tuberculosis lineage identification. NIPS Workshop on Tensors, Kernels and Machine Learning, Whistler, BC, Canada, December 2010.
 - C. Ozcaglar, B. Yener, A. Shabbeer, M. Aminian, K. P. Bennett. A clustering framework for Mycobacterium tuberculosis complex strains using multiple-biomarker tensors. New York Academy of Science (NYAS) 5th Annual Machine Learning Symposium, NYC, October 2010.
 - C. Ozcaglar, B. Yener, A. Shabbeer, M. Aminian, K. P. Bennett. Examining sublineage structure of Mycobacterium tuberculosis complex strains with multiway modeling. Eigenvector University, Seattle Washington, May 2010. (Best poster award)

Talks

- MFMS: Maximal frequent module set mining from multiple human gene expression datasets. ACM SIGKDD International Workshop on Data Mining in Bioinformatics (BIOKDD), Chicago, August 2013.
- TCF: Tensor clustering framework on multiple-biomarker tensors. Bogazici University, Middle East Technical University, Bilkent University, January 2012.
- Data-driven insights into deletions of Mycobacterium tuberculosis complex chromosomal DR region using spoligoforests. IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Atlanta, November 2011.
- Examining the sublineage structure of Mycobacterium tuberculosis complex strains with multiple-biomarker tensors. IEEE International Conference on Bioinformatics and Biomedicine (BIBM), Hong Kong, December 2010.
- Extracting Associations from Activities. NSF Cyber-Enabled Discovery and Innovation Symposium, Troy, NY, September 2007.

Awards

- Transaction Risk Management Systems Modeling Hackathon at Amazon, first place, 2015.
- Student Travel Award to attend IEEE BIBM 2010.
- Full scholarship awarded by Rensselaer Polytechnic Institute for graduate study, 2006 2012.
- Full scholarship awarded by Bilkent University for undergraduate education, 2002 2006.
- Top 0.01% in nationwide University Entrance Exam among 1.5 million candidates, 2002.

- Ranked 1st in the Mediterranean Region in 8th and 9th Turkish Mathematics Olympiad, 2000, 2001.
- Bronze medal in 3rd and 4th Turkish Secondary School Mathematics Olympiad, 1998, 1999.

Activities

- Reviewer for Journals: ACM Transactions on Algorithms (2013), Machine Learning (2017), IEEE Transactions on Knowledge and Data Engineering (2013, 2017), Computational Intelligence (2012, 2013), Network Modeling Analysis in Health Informatics and Bioinformatics (2011), Computational and Mathematical Methods in Medicine (2013).
- Member: IEEE, ACM.

- Affiliations Treasurer of Turkish Student Association at RPI, 2011-2012.
 - Member of Building Planning Committee, Computer Science, RPI, 2011-2012.
 - RPI School of Science Graduate Council, Computer Science Representative, 2010-2011.
 - Member of Graduate Recruiting Committee, Computer Science, RPI, 2007-2008.