

florian leitner

machine learning engineer

contact

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leitner@
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languages

German: native

English: master

Spanish: proficient

computing

artificial intelligence and
deep learning

natural language
processing

distributed and
cloud computing

data warehousing
and engineering

statistical and
numerical analyses

software development
and operations on
(GNU) POSIX systems

C++/Python,
Java/Scala
(R, SQL, C/CUDA)

experience

- 2015–now **Data Catalytics, S.L.** Madrid, Spain (Remote)
Operations consultant
Scaling natural language processing technology to operate on large (B+) document “lakes” and infinite real-time message streams. Engineering an inter-data center, low-latency, reactive data processing architecture (similar to Akka Cluster). Architecting an analytics engine to track the progression of multi-state, parallel financial transactions in fixed income trading chat-rooms. Relevance prediction, semantic labeling, and entity linking on the Twitter fire hose, financial research documents, multilingual business news, and job resumes. Remotely managing globally distributed software engineering and financial analyst teams. Designing data curation processes for machine teaching. Teaching & hiring.
- 2014–2015 **Technical University of Madrid (UPM)** Madrid, Spain
NeuroNLP researcher (Juan de la Cierva research fellow)
Training neurobiology-specific NER taggers (Wapiti, Factorie, word2vec). Mining the graph of molecular interactions between neuro-entities using deep parsing (GENIA parser), extracting semantic triplets from (2M+) full-text documents (Spark MLlib). Working on a graph-based entity linking system (OrientDB). Statistical analyses of citation data (R, Postgres). Teaching.
- 2013–2014 **National Cancer Research Centre (CNIO)** Madrid, Spain
BioNLP researcher
Extracting the mammalian transcriptome from all (22M+) abstracts in medicine & biology. Detecting abstracts containing mammalian gene regulation information (SciKit Learn, SPECIES, GENIA tagger). Linking mentions of genes and transcription factors to their sequences by developing a rule-based gene symbol mapper. Shallow parsing (Wapiti, CRFSuite) sentences containing genes and factors for transcription event detection (LibSVM). Leading a team of scientists to conduct the curation of mammalian transcriptome data. Teaching.
- 2006–2013 **National Cancer Research Centre (CNIO)** Madrid, Spain
Bioinformatician
Steering BioCreative (BC) community challenges: task design, orchestrating data curation, deep systems analyses, conference organization, and systematic evaluations (in R) of participating systems. Lead architect of the BioCreative Meta-Server, a geographically distributed, streaming NLP and text mining platform (TwistedPython, Postgres), in coop. with a dozen intl. research teams. Designing an application to maintain up-to-date, local mirrors of PubMed, UniProt, and GenBank (Postgres). Mining abstracts for protein-protein interaction information using the Meta-Server. Developing the challenges’ web interface and team management framework (Django, Postgres).
- 2003–2006 **Institute for Molecular Pathology (IMP)** Vienna, Austria
Data architect
Implementing a molecular sequence repository (Postgres) to analyze post-translational modifications. Creating interfaces for sequence meta-data via a DSL to bootstrap a web framework (LISP, Struts). Distributed indexing of the repository and designing an information retrieval interface (Lucene, Struts).

profile

Engineering artificial intelligence solutions that reduce marginal cost. Developing natural language processing technology to mimic the workflow of domain experts. Designing distributed, reactive stream processing architectures. Remotely managing engineering and analyst teams. Domain expertise: Biotech/pharma and finance/trading.

education

- 2012-now **Continuous professional education** MOOCs
Deep learning, distributed data processing, scalable machine learning, IT Sec certifications, etc.
- 2012 **PhD Bioinformatics, with distinction** Autonomous University of Madrid (UAM), Spain
Online assessment of protein interaction information extraction systems.
- 2006 **MSc Molecular Biology, with distinction** Vienna University, Austria
Integration of biological databases and mining for post-translational modifications.

accomplishments

- 2018 **Faculty Member** IE University
teaching in Spain's top-rated business school/MBA
- 2015 **Company Founder** Data Catalytics, S.L.
of my own consultancy, with U.S. market coverage
- 2013 **Special Award - Premio Extraordinario** Autonomous University of Madrid (UAM)
for my PhD thesis work
- 2009 **Main Conference Organizer** BioCreative, CNIO, Madrid
three-day conference with nearly 100 participants
- 2009 **Services Cup** IEEE Services-I World Conference
3rd place behind competitors from SAP and IBM

communication skills

- 2015 **Invited Talk** Jornada de Tecnología y Salud, Real Academia de Ingeniería, Madrid, Spain
The BioCreative challenges: Critical assessments of biomedical information extraction.
- 2014 **Invited Talk** Institute for Computational Linguistics (UZH), Zurich, Switzerland
From the BioCreative challenges to transcription regulation network extraction.
- 2014 **Progress Report** National Cancer Research Centre (CNIO), Madrid, Spain
Retracing transcription regulation networks.
- 2013 **Presentation** BioLINK @ Intelligent Systems for Molecular Biology (ISMB), Berlin, Germany
Mining cis-regulatory transcription networks from literature.
- 2013 **Panel Host** BioLINK @ Intelligent Systems for Molecular Biology (ISMB), Vienna, Austria
Integration across genomics and medicine.
- 2011 **Invited Talk** FEBS Journal Board Meeting, Cambridge, UK
Annotating scientific manuscripts and the role of text-mining.
- 2010 **Presentation** Intelligent Systems for Molecular Biology (ISMB), Stockholm, Sweden
Comparative community assessments for applied biomedical text mining.
- 2009 **Presentation** Semantic Mining in Biomedicine (SMBM), Turku, Finland
The BioCreative Meta-Server platform.
- 2008–2013 **Presentations** BioCreative, Madrid, Spain and Bethesda, MD, USA
Various presentations throughout the BC II-IV workshops (see conference proceedings).

publications

journal articles

Data publications correlate with citation impact

Leitner, F, C Bielza, SL Hill, and P Larrañaga

Frontiers in Neuroscience 10.419 (2016). 2016

CHEMDNER: The drugs and chemical names extraction challenge

Krallinger, M, F Leitner, O Rabal, M Vazquez, J Oyarzabal, and A Valencia

Journal of Cheminformatics 7.Suppl 1 (2015) S1. 2015

The CHEMDNER corpus of chemicals and drugs and its annotation principles

Krallinger, M, O Rabal, F Leitner, M Vazquez, D Salgado, ..., J Oyarzabal, and A Valencia

Journal of Cheminformatics 7.Suppl 1 (2015) S2. 2015

BioC: a minimalist approach to interoperability for biomedical text processing

Comeau, DC, R Islamaj Dogan, P Ciccarese, KB Cohen, M Krallinger, F Leitner, ..., and WJ Wilbur

Database 2013 (Sept. 2013) bat064–bat064. 2013

How to link ontologies and protein-protein interactions to literature: text-mining approaches and the BioCreative experience.

Krallinger, M, F Leitner, M Vazquez, D Salgado, C Marcelle, M Tyers, A Valencia, and A Chatr-Aryamontri

Database 2012 (2012) bas017. 2012

MyMiner: a web application for computer-assisted biocuration and text annotation

Salgado, D, M Krallinger, M Depaule, E Drula, A Tendulkar, F Leitner, A Valencia, and C Marcelle

Bioinformatics (2012) bts435. 2012

The Protein-Protein Interaction tasks of BioCreative III: ranking of articles and linking bio-ontology concepts to full text

Krallinger, Martin, Miguel Vazquez, Florian Leitner, ..., and Alfonso Valencia

BMC Bioinformatics 12.Suppl 8 (2011) S3. 2011

Text Mining for Drugs and Chemical Compounds: Methods, Tools and Applications

Vazquez, M., M Krallinger, F Leitner, and A Valencia

Molecular Informatics 30.6-7 (2011) pp. 506–519. 2011

The PPI affix dictionary (PPIAD) and BioMethod lexicon

Krallinger, M, AV Tendulkar, F Leitner, A Chatr-aryamontri, and A Valencia

BMC Bioinformatics 11 (2010) pp. 1–3. 2010

The FEBS Letters/BioCreative II.5 experiment: making biological information accessible

Leitner, F, A Chatr-Aryamontri, SA Mardis, A Ceol, M Krallinger, L Licata, L Hirschman, G Cesareni, and A Valencia

Nature Biotechnology 28.9 (2010) pp. 897–899. 2010

The FEBS Letters SDA corpus.

Leitner, Florian, Martin Krallinger, Gianni Cesareni, and Alfonso Valencia

FEBS Letters 584.19 (Oct. 2010) pp. 4129–4130. 2010

An Overview of BioCreative II.5.

Leitner, Florian, Scott A Mardis, Martin Krallinger, Gianni Cesareni, Lynette A Hirschman, and Alfonso Valencia

IEEE/ACM Transactions on Computational Biology and Bioinformatics 7.3 (June 2010) pp. 385–399. 2010

Evaluation of text-mining systems for biology: overview of the Second BioCreative community challenge.

Krallinger, M, A Morgan, L Smith, F Leitner, L Tanabe, J Wilbur, L Hirschman, and A Valencia

Genome Biology 9 Suppl 2 (2008) S1. 2008

Overview of the protein-protein interaction annotation extraction task of BioCreative II.

Krallinger, Martin, Florian Leitner, Carlos Rodriguez-Penagos, and Alfonso Valencia

Genome Biology 9 Suppl 2 (2008) S4. 2008

Introducing meta-services for biomedical information extraction.

Leitner, F, M Krallinger, C Rodriguez-Penagos, J Hakenberg, ..., C Sander, and A Valencia

Genome Biology 9 Suppl 2 (2008) S6. 2008

A text-mining perspective on the requirements for electronically annotated abstracts.

Leitner, Florian and Alfonso Valencia

FEBS Letters 582.8 (Apr. 2008) pp. 1178–1181. 2008

ProSAT: functional annotation of protein 3D structures.

Gabdoulline, Razif R, René Hoffmann, Florian Leitner, and Rebecca C Wade

Bioinformatics 19.13 (Sept. 2003) pp. 1723–1725. 2003

book chapters

BioCreative II.5 and the FEBS Letters Experiment on Structured Digital Abstracts

Leitner, Florian, Martin Krallinger, and Valencia Alfonso

Encyclopedia of Systems Biology pp. 101–106, 2013, Springer New York

BioCreative Meta-Server and Text-Mining Interoperability Standard

Leitner, Florian, Martin Krallinger, and Valencia Alfonso

Encyclopedia of Systems Biology pp. 106–110, 2013, Springer New York

Analysis of Biological Processes and Diseases Using Text Mining Approaches

Krallinger, Martin, Florian Leitner, and Alfonso Valencia

Methods in Molecular Biology pp. 341–382, 2010, Humana Press

Biological Knowledge Extraction

Leitner, Florian, Robert Hoffmann, and Alfonso Valencia

Bioinformatics for Systems Biology pp. 413–433, 2009, Humana Press

conference proceedings

Retrieval and Discovery of Cell Cycle Literature and Proteins by Means of Machine Learning, Text Mining and Network Analysis

Krallinger, Martin, Florian Leitner, and Alfonso Valencia

8th International Conference on Practical Applications of Computational Biology & Bioinformatics, 2014

Overview of the chemical compound and drug name recognition (CHEMDNER) task

Krallinger, Martin, Florian Leitner, Obdulia Rabal, Miguel Vazquez, Julen Oyarzabal, and Alfonso Valencia

BioCreative IV Challenge Evaluation Workshop, 2013

Mining cis-Regulatory Transcription Networks from Literature

Leitner, Florian, Martin Krallinger, Sushil Tripathi, Martin Kuiper, Astrid Lægneid, and Alfonso Valencia

Proceedings of the ISMB BioLINK SIG, 2013

Results of the BioCreative III Interaction Method Task

Krallinger, Martin, Miguel Vazquez, Florian Leitner, and Alfonso Valencia

Proceedings of the BioCreative III Challenge Evaluation Workshop, 2010

The BioCreative II.5 challenge overview

Krallinger, Martin, Florian Leitner, and Alfonso Valencia

Proceedings of the BioCreative II.5 Challenge Evaluation Workshop, 2009

BioCreative II.5: Evaluation and ensemble system performance

Mardis, Scott, Florian Leitner, and Lynette Hirschman

Proceedings of the BioCreative II.5 Challenge Evaluation Workshop, 2009

SOA-Based Integration of Text Mining Services

Starlinger, Johann, Florian Leitner, Alfonso Valencia, and Ulf Leser

Proceedings of the 2009 World Conference on Services, 2009

Assessment of the second BioCreative PPI task: automatic extraction of protein-protein interactions

Krallinger, Martin, Florian Leitner, and Alfonso Valencia

Proceedings of the second BioCreative Challenge Evaluation Workshop, 2007

Exploiting text mining of biological annotations to extract protein interactions for the Semantic web

Krallinger, Martin, Carlos Rodriguez-Penagos, Florian Leitner, and Alfonso Valencia

Seventh International Workshop on Network Tools and Applications in Biology, 2007