

# florian leitner

data scientist

## contact

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## languages

German native speaker

English mother tongue

Spanish fluent (r/w)

## computing

probabilistic  
programming

natural language  
processing

database administration

software engineering

Python, Scala, R, SQL,  
C, Perl, Java

## profile

*Bioinformatics and molecular biology.*

*Machine learning for data and text mining.*

*Query engine and information extraction development.*

*Distributed services and parallel high-performance computing.*

*Excellent communication, planning, and organization skills.*

## experience

- |           |   |                     |
|-----------|---|---------------------|
| 2014–now  | <b>Technical University of Madrid (UPM)</b><br>Juan de la Cierva research fellow (Data mining software development)<br>Development of an integrated text mining/information extraction system for neuro-biology with Scala (Factorie, Hadoop/Spark), Python (brat, SciKit-Learn) and R for data visualization. Teaching machine learning and text mining to students.   | Madrid, Spain       |
| 2013–2014 | <b>National Cancer Research Centre (CNIO)</b><br>Post-doc (Data mining & NLP software development)<br>Development of a large-scale text mining/information extraction pipeline in Java (UIMA), Scala (Hadoop/Spark), C (var. machine learning libraries) and Python (SciKit-Learn) for genome-wide transcription regulation interactions.   | Madrid, Spain       |
| 2006–2013 | <b>National Cancer Research Centre (CNIO)</b><br>PhD student (Bioinformatics software development)<br>Designer and lead of a dozen international research teams that implemented the BioCreative Meta-Server (Python/Django, Postgres, Java). Co- and main organizer of large, international scientific community challenges: BioCreative II (co), II.5 (main), III (co), and IV (co). Development of the BioCreative web site (www.biocreative.org) and team management interface (Python/Django, Postgres). Exploratory data analyses and evaluations in R. | Madrid, Spain       |
| 2003–2006 | <b>Institute for Molecular Pathology (IMP)</b><br>MSc student (Database administration and software/web development)<br>Data acquisition and import from biological resources (e.g., parser development) in Perl and LISP; Web-based data visualization (Apache Struts) for an in-hose bioinformatics framework ("Annotator"). Design and implementation of an indexing engine and the query interface with Apache Lucene.  | Vienna, Austria     |
| 2003–2003 | <b>CSO Lanifex GmbH</b><br>Consultant (Linux kernel and Firefox browser customization)<br>Development of a specialized VPN network for the Austrian National Bank (Linux kernel modifications and adapting the Mozilla framework as a GUI for the thin clients). Contributions to the Vienna United Nations intranet web-site (MySQL).  | Vienna, Austria     |
| 2002–2003 | <b>European Media Labs (EML)</b><br>Python/Java application developer<br>Development of a 3D visualization plug-in for annotations of protein structures (Java). Installation and administration of Python libraries for Structural Biology.  | Heidelberg, Germany |

2001–2002	<b>Novartis Research Institute</b> Web developer and database administration Development of a Perl-based framework for a large bioinformatics data pipeline; Non-Disclosure Agreement.	Vienna, Austria
1997–2000	<b>ProDesign Paragliders</b> Production and sales manager International production and sales management for a Tyrolean paraglider producer. Organization of marketing (sports) events. Contributions to the in-house management tool (Visual Basic).	Innsbruck, Austria

## education

2012	<b>PhD Bioinformatics, with distinction</b> Online assessment of protein interaction information extraction systems.	Autonomous University of Madrid (UAM), Spain
2006	<b>MSc Molecular Biology, with distinction</b> Integration of biological databases and mining for post-translational modifications.	Vienna University, Austria

## accomplishments

2014	<b>Machine Learning</b> completed with 100+/100 total score	Stanford/Coursera MOOC
2013	<b>Special Award - Premio Extraordinario</b> for my thesis work	Autonomous University of Madrid (UAM)
2012	<b>Speed Reading</b> accredited final reading speed: 2000 words/minute	Programa Integral de Lectura
2012	<b>Natural Language Processing</b> completed with 88/100 total score	Stanford/Coursera MOOC
2009	<b>Main Conference Organizer</b> three-day conference with nearly 100 participants	BioCreative, CNIO, Madrid
2009	<b>Services Cup</b> 3 <sup>rd</sup> place behind competitors from SAP and IBM	IEEE Services-I World Conference

## communication skills

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

# publications

## journal articles

BioC: a minimalist approach to interoperability for biomedical text processing

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

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

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

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

Bioinformatics (2012) bts435. 2012

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

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

Database 2012 (2012) bas017. 2012

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

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

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

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

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

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

The FEBS Letters SDA corpus.

Florian Leitner, Martin Krallinger, Gianni Cesareni, Alfonso Valencia

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

An Overview of BioCreative II.5.

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

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

The PPI affix dictionary (PPIAD) and BioMethod lexicon

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

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

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

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

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

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

Florian Leitner, Alfonso Valencia

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

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

Martin Krallinger, Florian Leitner, Carlos Rodríguez-Penagos, Alfonso Valencia

Genome Biology 9 Suppl 2 (2008) S4. 2008

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

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

Genome Biology 9 Suppl 2 (2008) S1. 2008

Introducing meta-services for biomedical information extraction.

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

Genome Biology 9 Suppl 2 (2008) S6. 2008

ProSAT: functional annotation of protein 3D structures.

Razif R Gabdoulline, René Hoffmann, Florian Leitner, 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

Florian Leitner, Martin Krallinger, Valencia Alfonso

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

### BioCreative Meta-Server and Text-Mining Interoperability Standard

Florian Leitner, Martin Krallinger, Valencia Alfonso

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

### Analysis of Biological Processes and Diseases Using Text Mining Approaches

Martin Krallinger, Florian Leitner, Alfonso Valencia

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

### Biological Knowledge Extraction

Florian Leitner, Robert Hoffmann, 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

Martin Krallinger, Florian Leitner, Alfonso Valencia

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

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

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

*BioCreative IV Challenge Evaluation Workshop*, 2013

### Mining cis-Regulatory Transcription Networks from Literature

Florian Leitner, Martin Krallinger, Sushil Tripathi, Martin Kuiper, Astrid Lógreid, Alfonso Valencia

*Proceedings of the ISMB BioLINK SIG*, 2013

### Results of the BioCreative III Interaction Method Task

Martin Krallinger, Miguel Vazquez, Florian Leitner, Alfonso Valencia

*Proceedings of the BioCreative III Challenge Evaluation Workshop*, 2010

### The BioCreative II.5 challenge overview

Martin Krallinger, Florian Leitner, Alfonso Valencia

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

### SOA-Based Integration of Text Mining Services

Johann Starlinger, Florian Leitner, Alfonso Valencia, Ulf Leser

*Proceedings of the 2009 World Conference on Services*, 2009

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

Martin Krallinger, Carlos Rodríguez-Penagos, Florian Leitner, Alfonso Valencia

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

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

Martin Krallinger, Florian Leitner, Alfonso Valencia

*Proceedings of the second BioCreative Challenge Evaluation Workshop*, 2007