

Pavel Senin

Data Science Software Engineer

AREAS OF EXPERTISE

Data analytics
Bioinformatics
Temporal data mining
Machine learning, NLP
Software engineering
Software metrology
Software process analysis

TECHNICAL SKILLS

Full SDLC, legacy wrapping
Java, R, Python, C/C++
SQL, XML, Perl, `bash`
DBA, ORM & persistence
deeplearning4j, Spark, BUPC
SOA, REST, MVC, n-tier
HTML, CSS, JavaScript, D3.js
Arduino & sensors
Kanban & Lean

SOFTWARE PROJECTS

GrammarViz 3.0 🐱

- *time series pattern mining*
- *discr. param. optimization*

SAX-VSM 🐱

- *time series classification*
- *behaviors discovery*

JMotif-R 🐱

- *time series mining toolkit*

JMotif-SAX 🐱

- *time series discretization*

JMotif-GI 🐱

- *grammatical inference*

Hackystat 🐱

- *software metrology*

PERSONAL DETAILS

3, Allée des Oliviers,
Castanet-Tolosan,
31320, France.
Cell. +33 6 42 51 18 94
senin@hawaii.edu
http://seninp.github.io

PERSONAL SUMMARY

Looking for a research-oriented position with a practical bent. A goal-oriented, forward thinking researcher with excellent organizational and interpersonal skills.

EXPERIENCE

Advanced Engineering Consultant

Altran Sud-Ouest

current

Toulouse, France

Working on spatio-temporal mining and root cause analysis for Airbus; participating in predictive maintenance capability development at Liebherr Aerospace.

Research Associate, 2016–2017

Los Alamos National Laboratory

(Research Technologist, 2007–2010)

PO Box 1663

Worked on high-throughput comparative analyses of microbiome for biosurveillance. Contributed a metagenome comparative toolkit to R&D 100 award winning EDGE platform. Participated in DOE Exascale Computing Project. Developed a fragment recruiting technique for pioneering single-cell genome sequencing project.

Graduate student/Research assistant

University of Hawai'i at Mānoa *ICS CSDL & RCUH*

2005 – 2015

Honolulu, HI

Proposed a novel technique for characteristic recurrent behaviors discovery and behavior-based software process analysis using software telemetry. Proposed a novel technique for spatio-temporal anomaly discovery based on algorithmic (Kolmogorov) complexity. Developed a pioneering technique for SAX discretization parameters optimization based on grammatical compression. Assembled the first transgenic plant genome (Carica Papaya) and optimized the cost of its finishing.

Bioinformatics Software Engineer

INRIA/INRA

2010 – 2015

Rennes/Toulouse, France

Took a part in Life Sciences research projects conducted by French premier research institutions. Designed and implemented high-throughput pipelines for sequencing data acquisition and analysis including genomic and transcriptomic data assembly, annotation, variant and ncRNA discovery and pathway analysis. Worked on structural motif discovery in GPCRs, mating disruption, and vector control.

EDUCATION

PhD, Computer Science (Software process analysis)

University of Hawai'i at Mānoa

2015

Honolulu, HI, USA

MS, Computer Science (Capstone on MCMC simulation)

University of Hawai'i at Mānoa

2007

Honolulu, HI, USA

MS, ABD, Appl. Mathematics (Num. optimization)

Rostov State University (SFedU)

2002

Rostov-na-Donu, Russia

SELECTED PUBLICATIONS

[scholar profile](#) 

GrammarViz 3.0: Interactive Discovery of Variable-length Time Series Patterns. Senin, P., Lin, J., Wang, X., Oates, T., Gandhi, S., Boedihardjo, A.P., Chen, C., Frankenstein, S. *ACM Trans. Knowl. Discov. Data*, 2018.

STAVIS 2.0: Mining Spatial Trajectories via Motifs. Chen, C., Boedihardjo, A.P., Jenkins, B.S., Ellison, C.L., Lin, J., Senin, P., Oates, T. *International Symposium on Spatial and Temporal Databases*, 2017

Time series anomaly discovery with grammar-based compression.

Senin, P., Lin, J., Wang, X., Oates, T., Gandhi, S., Boedihardjo, A.P., Chen, C., Frankenstein, S. *In Proc. EDBT*, 2015.