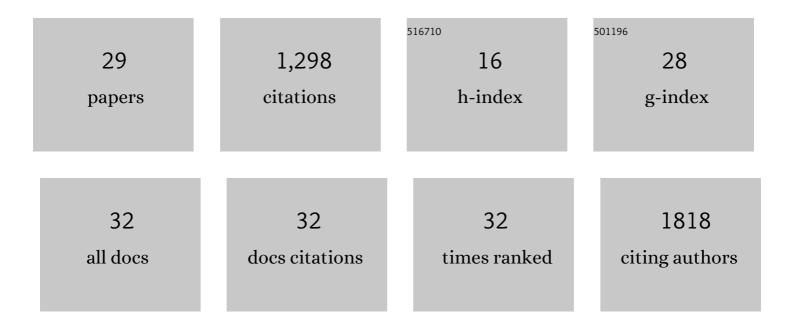
## BĤrbel FinkenstĤdt

List of Publications by Year in descending order

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RÃMREL FINKENSTÂMT

#	Article	IF	CITATIONS
1	3 â€ <sup>2</sup> -5 â€ <sup>2</sup> crosstalk contributes to transcriptional bursting. Genome Biology, 2021, 22, 56.	8.8	11
2	Telemonitored Human Circadian Temperature Dynamics During Daily Routine. Frontiers in Physiology, 2021, 12, 659973.	2.8	8
3	Identifying the recurrence of sleep apnea using a harmonic hidden Markov model. Annals of Applied Statistics, 2021, 15, 1171-1193.	1.1	2
4	A spatio-temporal model to reveal oscillator phenotypes in molecular clocks: Parameter estimation elucidates circadian gene transcription dynamics in single-cells. PLoS Computational Biology, 2021, 17, e1009698.	3.2	2
5	Scalable Bayesian Inference for Coupled Hidden Markov and Semi-Markov Models. Journal of Computational and Graphical Statistics, 2020, 29, 238-249.	1.7	16
6	Tele-Monitoring of Cancer Patients' Rhythms during Daily Life Identifies Actionable Determinants of Circadian and Sleep Disruption. Cancers, 2020, 12, 1938.	3.7	17
7	Filtering and inference for stochastic oscillators with distributed delays. Bioinformatics, 2019, 35, 1380-1387.	4.1	17
8	Predictability of individual circadian phase during daily routine for medical applications of circadian clocks. JCI Insight, 2019, 4, .	5.0	25
9	Hidden Markov models for monitoring circadian rhythmicity in telemetric activity data. Journal of the Royal Society Interface, 2018, 15, 20170885.	3.4	43
10	Bayesian inference on stochastic gene transcription from flow cytometry data. Bioinformatics, 2018, 34, i647-i655.	4.1	28
11	Relevance of a Mobile Internet Platform for Capturing Inter- and Intrasubject Variabilities in Circadian Coordination During Daily Routine: Pilot Study. Journal of Medical Internet Research, 2018, 20, e204.	4.3	26
12	ReTrOS: a MATLAB toolbox for reconstructing transcriptional activity from gene and protein expression data. BMC Bioinformatics, 2017, 18, 316.	2.6	1
13	Inferring transcriptional logic from multiple dynamic experiments. Bioinformatics, 2017, 33, 3437-3444.	4.1	1
14	Asymmetry between Activation and Deactivation during a Transcriptional Pulse. Cell Systems, 2017, 5, 646-653.e5.	6.2	13
15	Time-Series Transcriptomics Reveals That <i>AGAMOUS-LIKE22</i> Affects Primary Metabolism and Developmental Processes in Drought-Stressed Arabidopsis. Plant Cell, 2016, 28, 345-366.	6.6	92
16	A stochastic transcriptional switch model for single cell imaging data. Biostatistics, 2015, 16, 655-669.	1.5	29
17	Network balance <i>via</i> CRY signalling controls the <i>Arabidopsis</i> circadian clock over ambient temperatures. Molecular Systems Biology, 2013, 9, 650.	7.2	78
18	Quantifying intrinsic and extrinsic noise in gene transcription using the linear noise approximation: An application to single cell data. Annals of Applied Statistics, 2013, 7, .	1.1	29

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#	Article	IF	CITATIONS
19	A hierarchical model of transcriptional dynamics allows robust estimation of transcription rates in populations of single cells with variable gene copy number. Bioinformatics, 2013, 29, 1519-1525.	4.1	6
20	Inference on periodicity of circadian time series. Biostatistics, 2013, 14, 792-806.	1.5	50
21	A temporal switch model for estimating transcriptional activity in gene expression. Bioinformatics, 2013, 29, 1158-1165.	4.1	14
22	<i>Arabidopsis</i> Defense against <i>Botrytis cinerea</i> : Chronology and Regulation Deciphered by High-Resolution Temporal Transcriptomic Analysis  Â. Plant Cell, 2012, 24, 3530-3557.	6.6	337
23	Dynamic Analysis of Stochastic Transcription Cycles. PLoS Biology, 2011, 9, e1000607.	5.6	206
24	Using a Single Fluorescent Reporter Gene to Infer Half-Life of Extrinsic Noise and Other Parameters of Gene Expression. Biophysical Journal, 2010, 98, 2759-2769.	0.5	22
25	Bayesian inference of biochemical kinetic parameters using the linear noise approximation. BMC Bioinformatics, 2009, 10, 343.	2.6	97
26	Reconstruction of transcriptional dynamics from gene reporter data using differential equations. Bioinformatics, 2008, 24, 2901-2907.	4.1	58
27	Bayesian inference for dynamic transcriptional regulation; the Hes1 system as a case study. Bioinformatics, 2007, 23, 2596-2603.	4.1	52
28	Edgeworthian economies. Proceedings in Applied Mathematics and Mechanics, 2007, 7, 1041305-1041306.	0.2	0
29	Common structure in panels of short ecological time-series. Proceedings of the Royal Society B: Biological Sciences, 2000, 267, 2459-2467.	2.6	18