cases	doc_1		doc_2		decision	id
	authors	<ul> <li>Jie Ren</li> <li>Peter Liu</li> <li>Emily Fertig</li> <li>Jasper Snoek</li> <li>Ryan Poplin</li> </ul>	authors	<ul> <li>Mark A. DePristo</li> <li>Peter J. Liu</li> <li>Joshua V. Dillon</li> <li>Balaji Lakshminarayanan</li> <li>Ryan Poplin</li> <li>Jie Ren</li> <li>Jasper Snoek</li> <li>Emily Fertig</li> </ul>	DUPLICATES 1	
		Mark A. DePristo	title	Likelihood Ratios for Out-of-Distribution Detection		
		• J. S. Dillon	publication_date	2019-06-07 00:00:00		
		Balaji Lakshminarayanan	source	SupportedSources.PAPERS_WITH_CODE		
	title	Likelihood Ratios for Out-of-Distribution	journal			5G 152
		Detection Detection	volume			
	publication_date   2019-06-07 00:00:00		doi		DUPLICATES	ES  133
	source	SupportedSources.OPENALEX	urls	<ul> <li>https://arxiv.org/pdf/1906.02845v2.pdf</li> <li>https://github.com/google-research/google-research/tree/master/genomics_ood</li> <li>http://papers.nips.cc/paper/9611-likelihood-ratios-for-out-of-distribution-detection.pdf</li> </ul>	h t that he	
	journal	Neural Information Processing Systems				
	volume	32				
	doi	None	id	id-2815129506705936336		
	urls	https://openalex.org/W2970946347	abstract	Discriminative neural networks offer little or no performance guarantees when deployed on data not generated by the same process as the training distribution. On such out-of-distribution (OOD) inputs, the prediction may not only be erroneous, but confidently so, limiting the safe deployment of classifiers in real-world applications. One such		
	id	id2737037315583430677		challenging application is bacteria identification based on genomic sequences, which holds the promise of early detection of diseases, but requires a model that can output low confidence predictions on OOD genomic sequences from new bacteria that were not present in the training data. We introduce a genomics dataset for OOD detection that allows other researchers to benchmark progress on this important problem. We investigate deep generative model based approaches for OOD detection and observe that the likelihood score is heavily affected by population level background statistics. We propose a likelihood ratio method for deep generative models which effectively corrects for		
	abstract					
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				these confounding background statistics. We benchmark the OOD detection performance of the proposed method against existing approaches on the genomics dataset and show that our method achieves state-of-the-art performance. We demonstrate the generality of the proposed method by showing that it significantly improves OOD detection when applied to deep generative models of images.		
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