

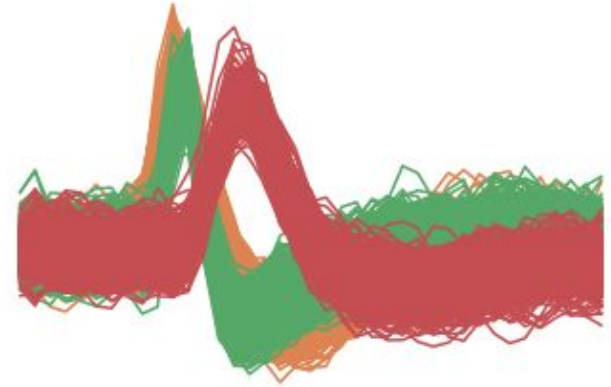
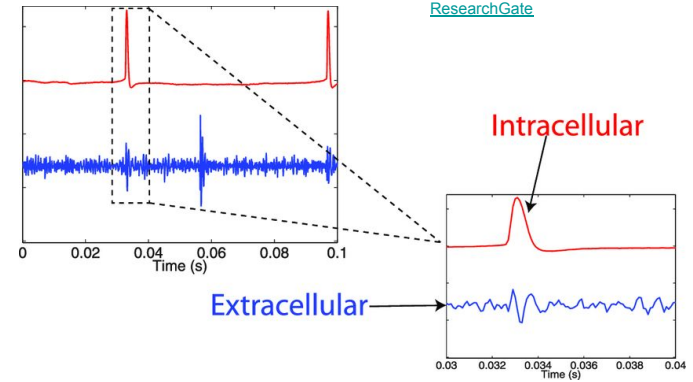
EN.601.482/682 Deep Learning

Automatic Neural Spike Sorting using an Ensemble of Autoencoders

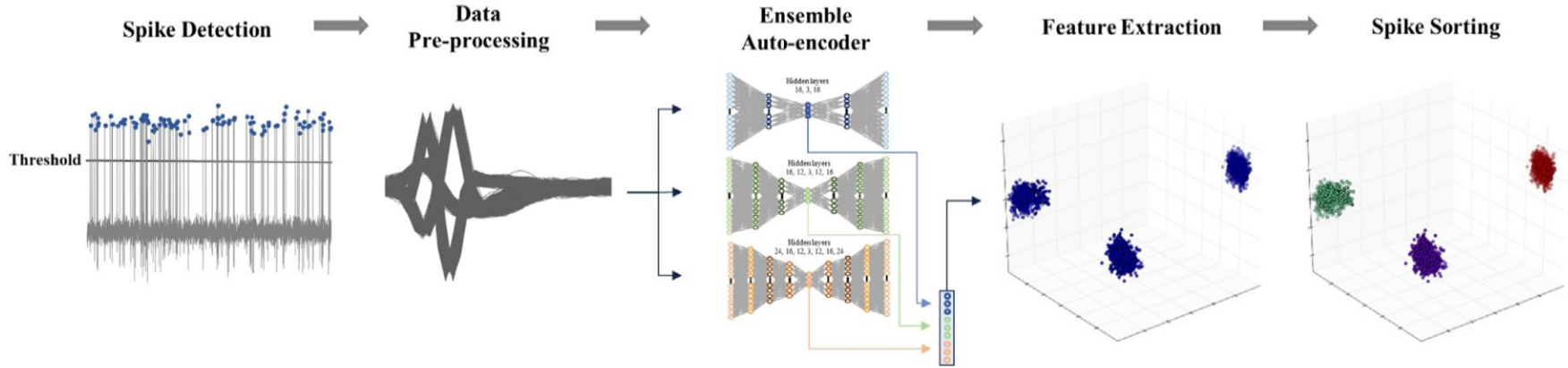
Paul Adkisson, Jacopo Teneggi, Giorgio Di Salvo, and Spencer Loggia

Neural Spike Sorting is an Important Bottleneck in Neuroscience and Applications

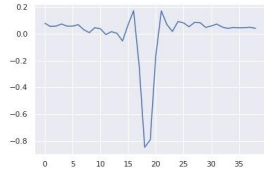
- Single Unit Activity is the Gold Standard
- Extracellular voltage recordings are noisy
- Spikes have a characteristic shape.
- Current manual methods are time-consuming, slow, and prone to error.
- Large need for accurate, robust, and automatic spike sorting algorithms



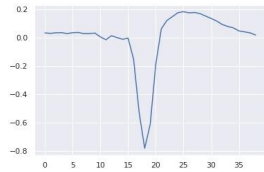
Spike Sorting Pipeline



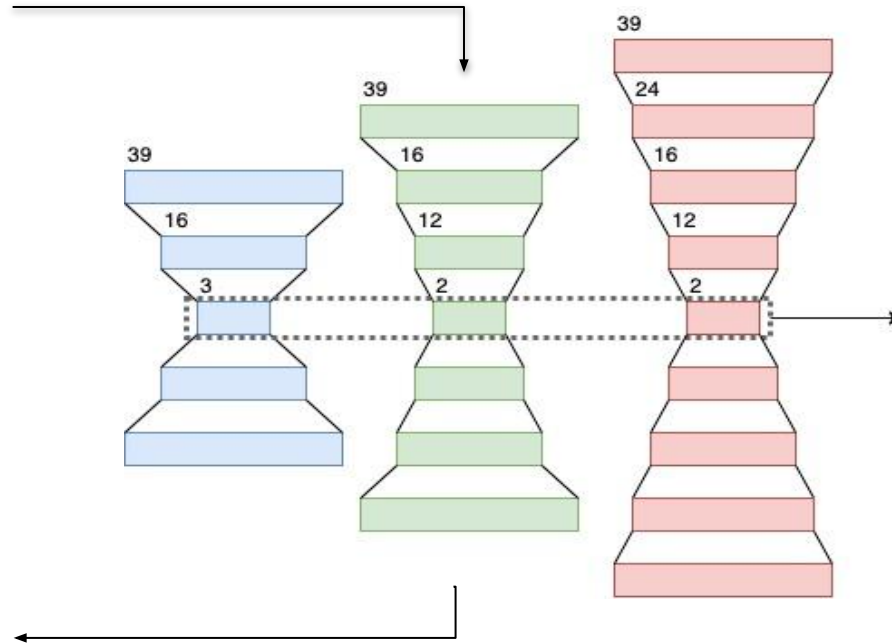
v0 Ensemble of Autoencoders: Architecture



original



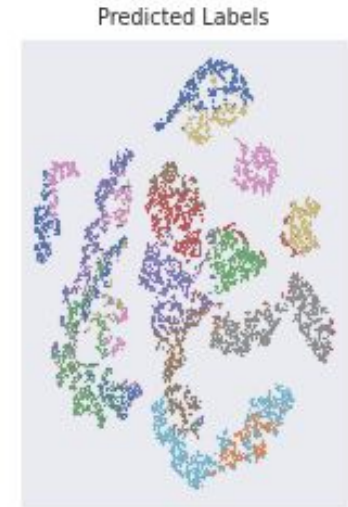
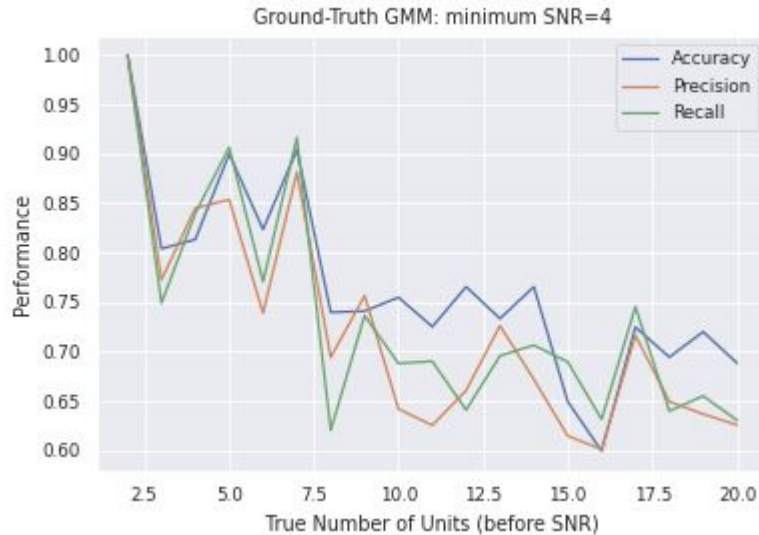
reconstructed



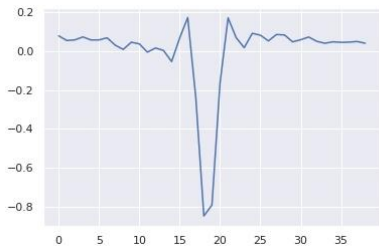
cluster
spiking units



v0 Ensemble of Autoencoders: Results

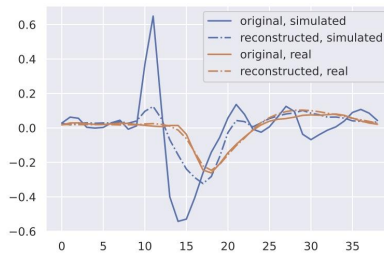
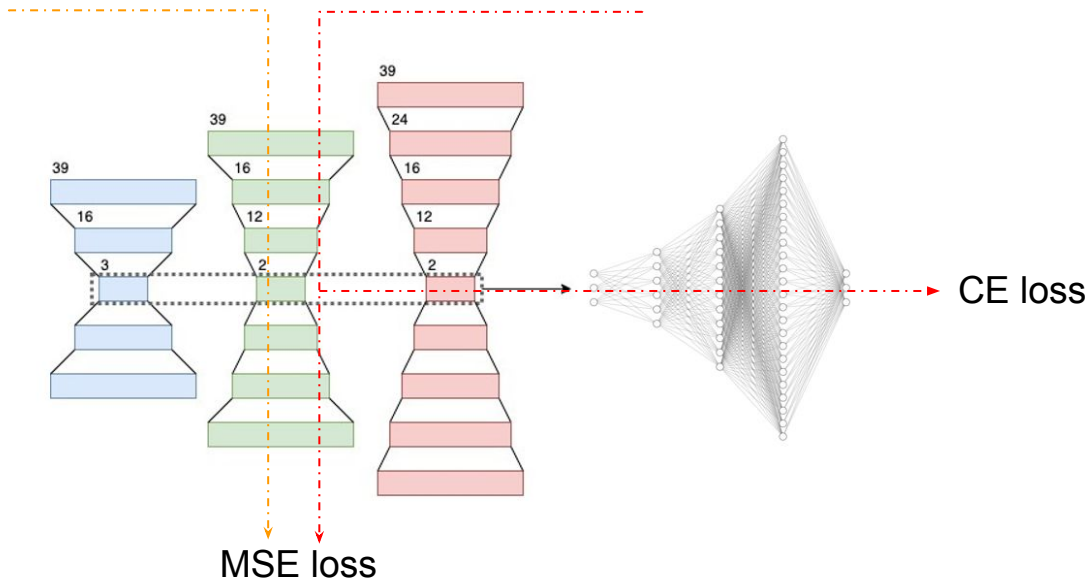


v1 Architecture



1: unsupervised learning (real spikes)

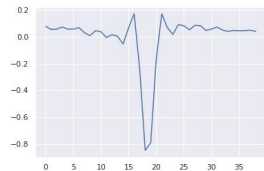
2: supervised learning (simulated spikes)



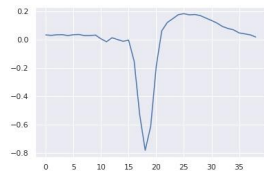
v1: Semi-Supervised Convolutional AE Ensemble



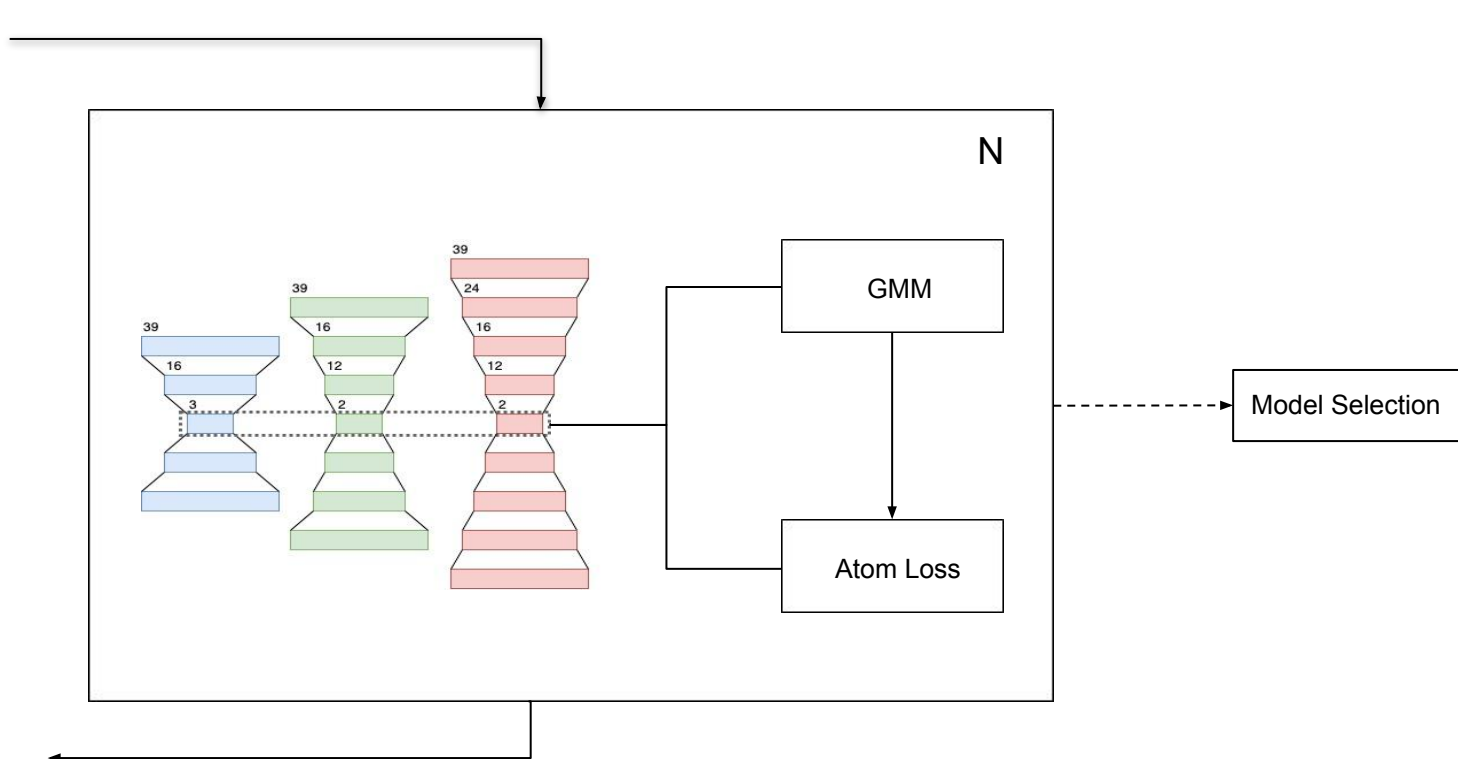
v2 Architecture



original



reconstructed



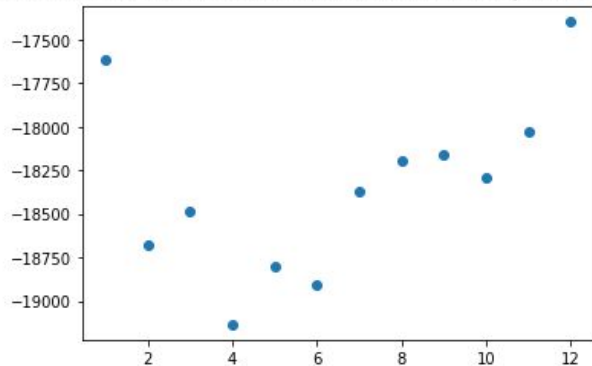
v2: Unsupervised End2End Embedding and Clustering



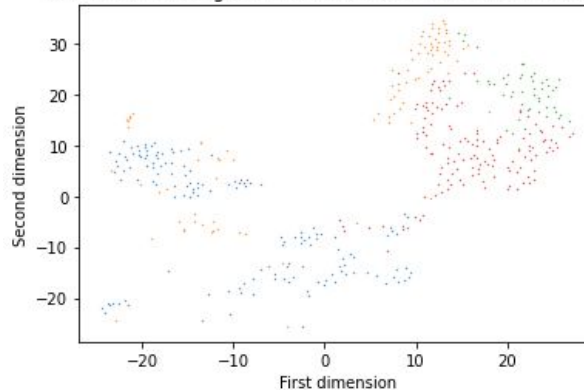
v0 Real Data

Fit to channel 4 of the ALM dataset

V0 BIC for Different Numbers of Theoretical Source Neurons, Real Data Channel 4

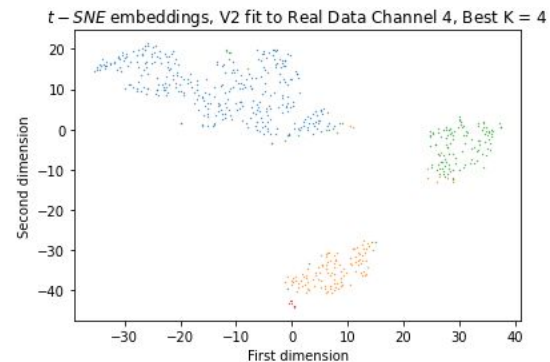
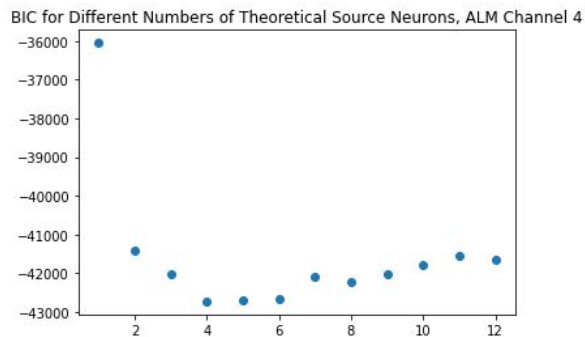
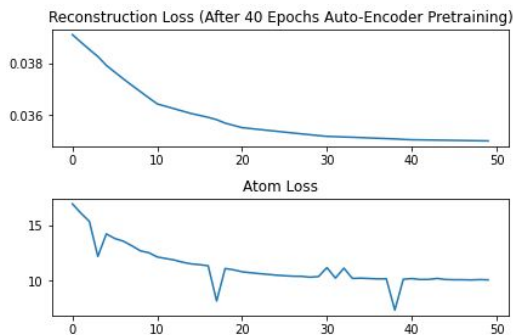


t -SNE embeddings, V0 fit to Real Data Channel 4, Best K = 4



v2 Real Data

Fit to channel 4 of the ALM dataset



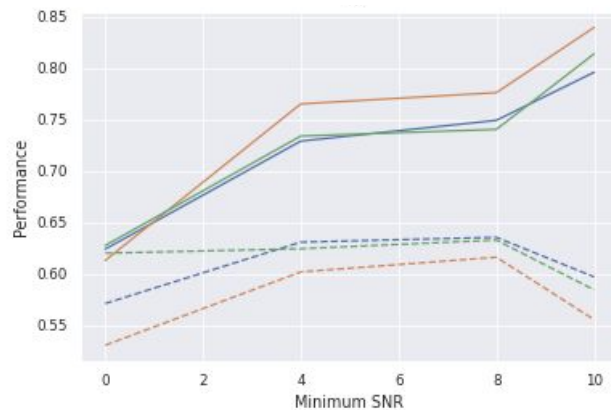
Supplemental Figures



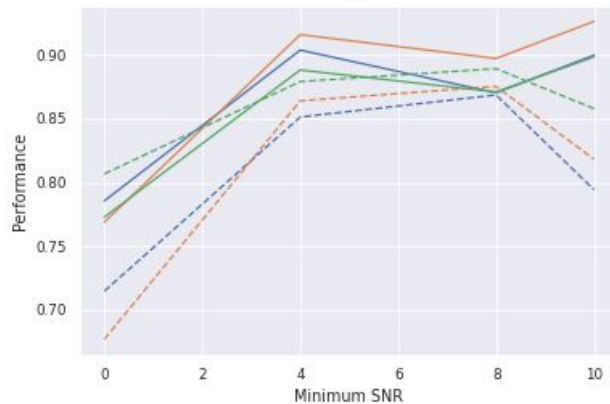
Performance Increases with Minimum SNR



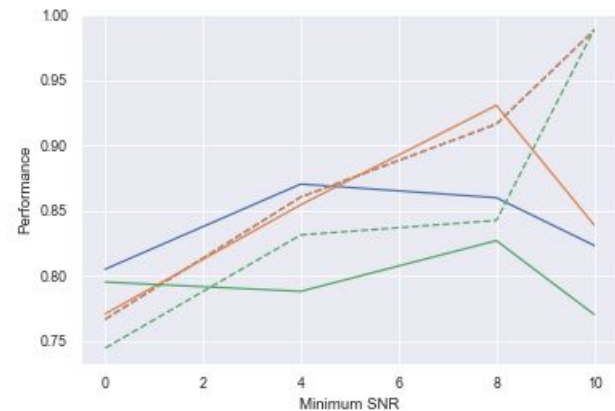
V0



V1



V2



SpikeForest Validation with minimum SNR = 4

		<u>HerdngSpikes2</u>	<u>IronClust</u>	<u>IRClust</u>	<u>KiloSort</u>	<u>KiloSort2</u>	<u>Klusta</u>	<u>MountainSort4</u>	<u>SpykingCircus</u>	<u>Tridesclous</u>	<u>Waveclus</u>
+	PAIRED_BOYDEN		0.44	0.54*	0.47	0.61*	0.32*	0.42	0.55	0.25	
+	PAIRED_CRCNS_HC1		0.48	0.36*	0.31*	0.44*	0.48*	0.46	0.53*	0.49	
+	PAIRED_ENGLISH	0.25*	0.62		0.67	0.7*		0.54	0.61*	0.23	
+	PAIRED_KAMPFF	0.66	0.82	0.84*	0.68	0.85		0.72	0.86	0.33	
+	PAIRED_MEA64C_YGER	0.82	0.78	0.82*	0.81	0.8*	0.64*	0.81	0.84	0.82	
+	PAIRED_MONOTRODE		0.37				0.37	0.38*	0.3*	0.36	0.42
+	SYNTH_BIONET		0.62	0.54	0.56	0.58*		0.56	0.49*	0.37	
+	SYNTH_MAGLAND		0.85	0.75	0.78	0.68*	0.54	0.87	0.81	0.67	
+	SYNTH_MEAREC_NEURONEXUS		0.75		0.87	0.73*	0.34	0.81	0.71	0.64	
+	SYNTH_MEAREC_TETRODE		0.64	0.38	0.66	0.18*	0.28	0.7	0.56	0.51	
+	SYNTH_MONOTRODE		0.7				0.07*	0.8	0.29	0.58	0.7
+	SYNTH_VISAPY	0.76	0.87					0.74	0.91	0.81	
+	HYBRID_JANELIA	0.56	0.76	0.62	0.77	0.73		0.63	0.76	0.67	
+	MANUAL_FRANKLAB		0.56	0.32	0.45	0.5	0.59	0.64	0.51	0.06	

* Indicates an incomplete or failed sorting on a subset of results and quantities are computed from imputed values. N/A indicates that no ground-truth units were above the SNR threshold.

