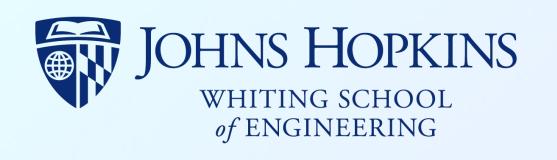
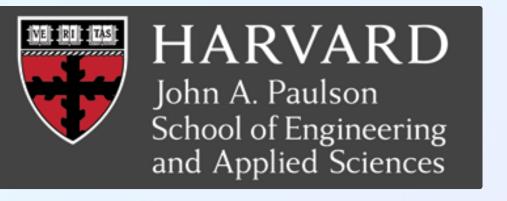
VESICLE: Volumetric Evaluation of Synaptic Interfaces using Computer Vision at Large Scale





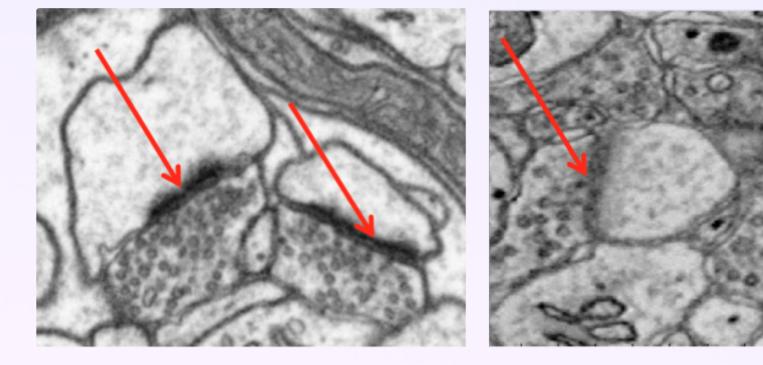
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- Challenge

- Large high-resolution volumes of neural tissue offer new frontiers for brain mapping
- This field promises rapid advances in biofidelic algorithms and healthcare
- Synapses are an integral part of these circuits and represent the communication point between cells
- Current methods are insufficent for highthroughput anisotropic, non-poststained data



Caffe

Isotropic, poststained FIBSEM data

VESICLE-CNN

Anisotropic, non-poststained SEM data (XY slice, in imaging plane)

Ciresan's N3



e) (XZ cross-section)

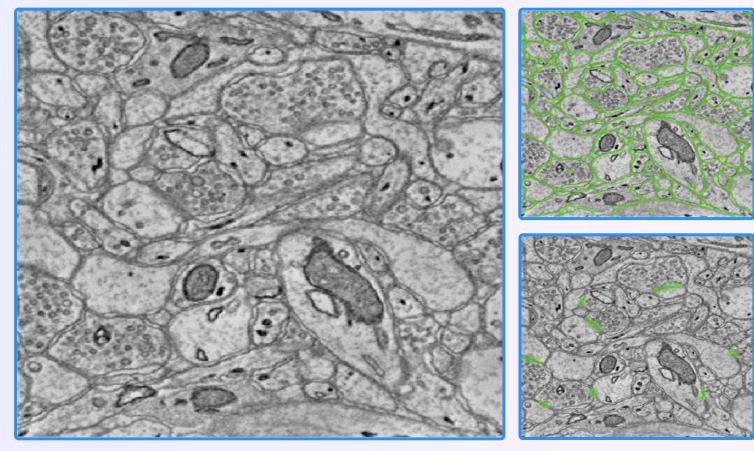


Pixel subsampling restricted to

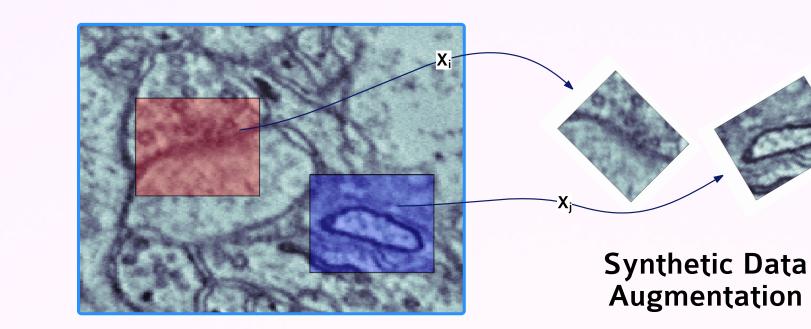
membrane priors

Our methods explicitly leverage

- biological context
- We provide two different approaches (performance/scalability tradeoffs)
 - VESICLE-CNN: deep learning classifier
 - VESICLE-RF: lightweight Random Forest approach



Raw Image data (left), High probability membrane pixels (top right), True Synapses (bottom right)



Tile extraction

We adopt and re-implement the pixel-level convolutional neural network classification approach of [3] suitably adapted for synapse detection.

VESICLE-RF

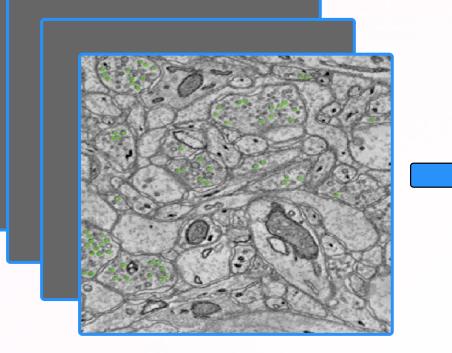
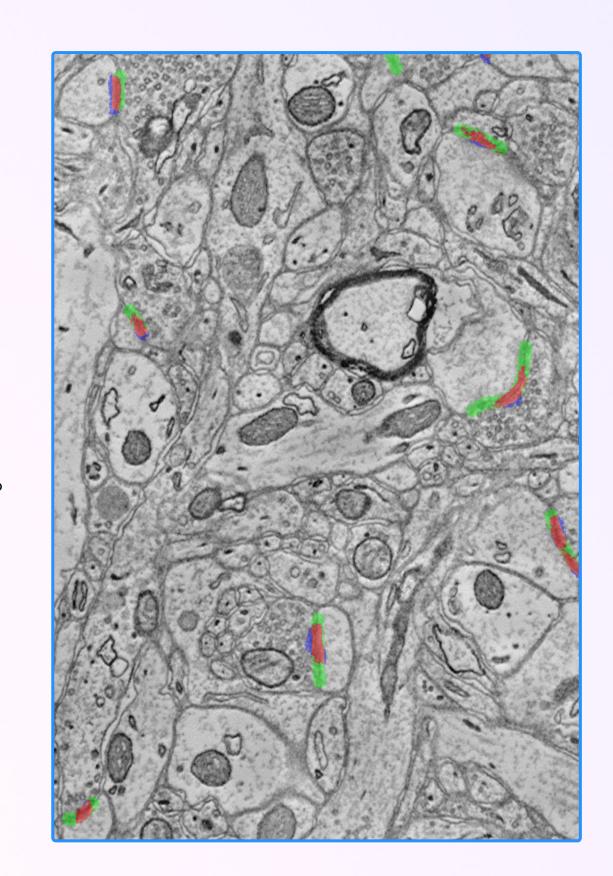


Table 1: Description of features used in VESICLE-RF; data transforms are summarized using different kernel bandwidths: $\theta_0 : [5, 5, 1], \theta_1 : [15, 15, 3], \theta_2 = [25, 25, 5], \theta_3 = [101, 101, 5], \theta_4 = \text{minimum vesicle distance.}$

>	Data Transform	Box Kernel
	Intensity	$ heta_0, heta_1$
	Local Binary Pattern	θ_0
	Image Gradient Magnitude	$ heta_1, heta_2$
	Vesicles	$ heta_2, heta_3, heta_4$
	Structure Tensor	$ heta_1, heta_2$

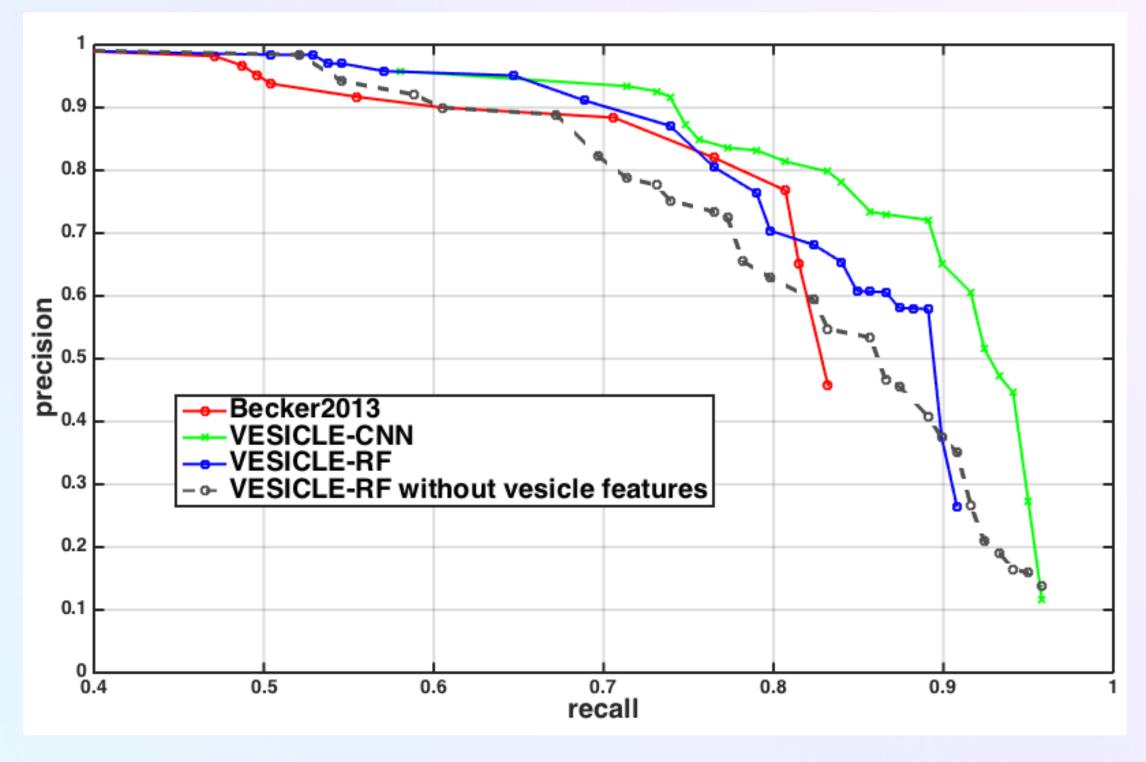
We leverage biological context to compute image transformations. One such channel identifies neurotransmitter-containing vesicles, which provide a strong indication of synaptic connections. These channels are summarized into ten features, using box kernels of different sizes.

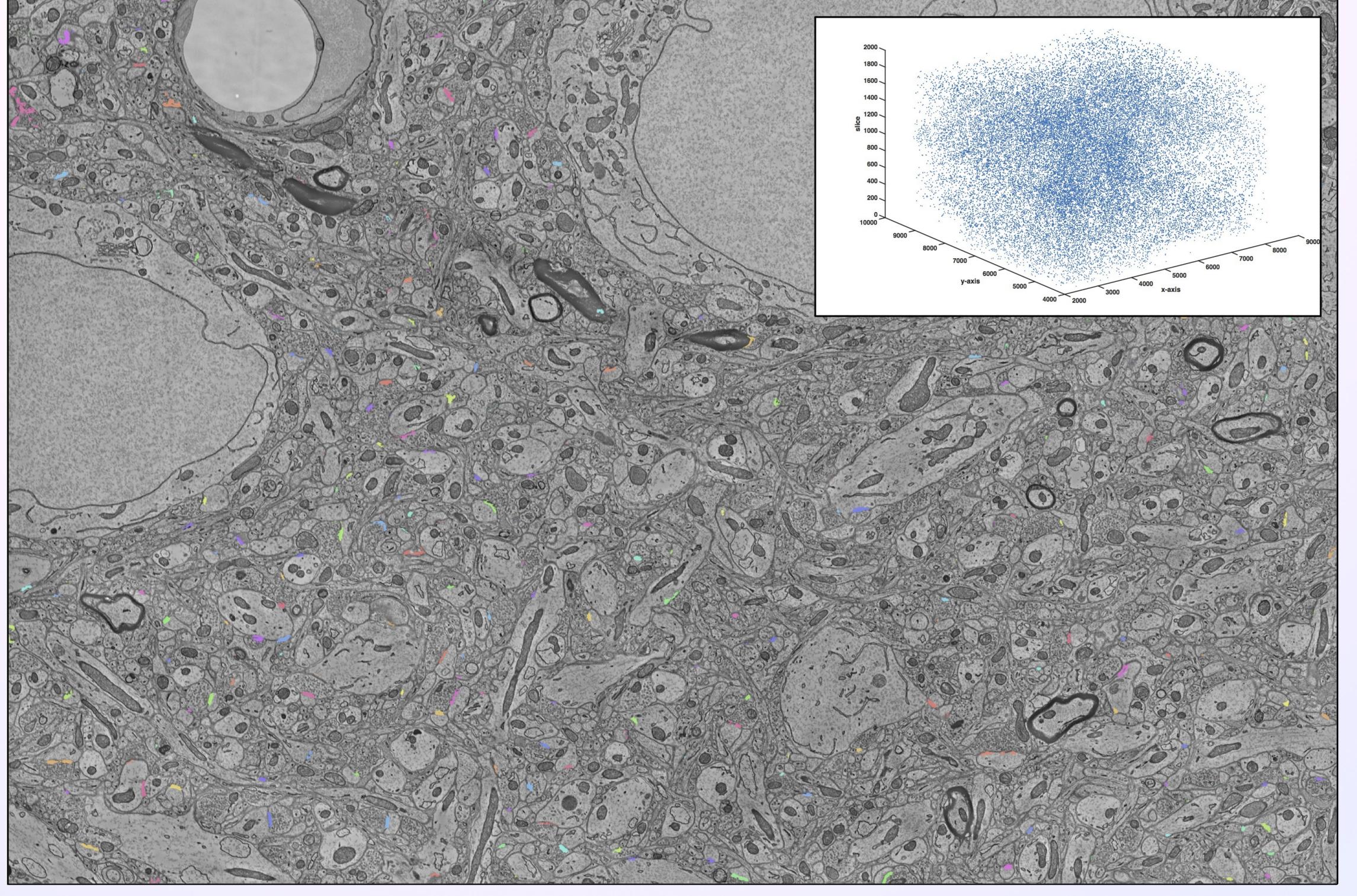


Classifier probabilities are thresholded and grouped into contiguous objects. Precision-recall curves are computed by sweeping over thresholds, synapse size and persistence limits.



- Our classifiers provide state of the art performance
- Found ~50,000 synapses in 60,000 cubic microns (220 GB on disk) of electron microscopy data
- Proof of concept scalability test detected 11.6 million synapses in a 20 teravoxel poststained data volume





VESICLE-RF and VESICLE-CNN significantly outperform prior state-of-the art, particularly at high recall rates. The choice of method and operating point depends on application and speed/performance tradeoffs.

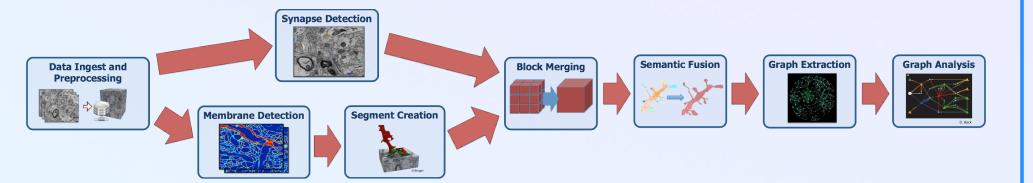
Visualization of large scale synapse detection results; we found a total of 50,000 putative synapses in our volume. An XY slice showing detected synapses is shown, and a point cloud of the synapse centroids are also visualized (inset).

Code and data are open source, and available at: openconnecto.me/vesicle

The mission of the NeuroData team is to enable data-driven neuroscience.

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Overall Images-to-Graphs Computer Vision Pipeline



[1] Carlos Becker, Karim Ali, Graham Knott, and Pascal Fua. Learning context cues for synapse segmentation. IEEE Transactions on Medical Imaging, 32(10):1864-1877, 2013. ISSN 02780062. doi: 10.1109/TMI.2013.2267747.

[2] William Gray Roncal, Dean M Kleissas, Joshua T Vogelstein, Priya Manavalan, Kunal Lillaney, Michael Pekala, Randal Burns, R Jacob Vogelstein, Carey E Priebe, Mark A Chevillet, and Gregory D Hager. An Automated Images-to-Graphs Framework for High Resolution Connectomics. Frontiers in neuroinformatics 2015, pages 1-13.

[3] DC Dan Ciresan, Alessandro Giusti, Luca M LM Gambardella, and Jürgen Schmidhu- ber. Deep neural networks segment neuronal membranes in electron microscopy im- ages. In Advances in neural information processing systems, pages 2843–2851, 2012.

[4] Davi Bock, Wei-chung Allen Lee, Aaron M Kerlin, Mark L Andermann, Greg Hood, Arthur W Wetzel, Sergey Yurgenson, Edward R Soucy, Hyon Suk Kim, and R Clay Reid. Network anatomy and in vivo physiology of visual cortical neurons. Nature, 471 (7337):177–182, 2011. ISSN 0028-0836. doi: 10.1038/nature09802.

The authors thank Bobby Kasthuri, Daniel Berger, and Jeff Lichtman for providing electron microscopy data and truth labels, and Lindsey Fernandez for helpful discussions on algorithm development and comparison metrics. This work is partially supported by JHU Applied Physics Laboratory Internal Research and Development funds, by NIH NIBIB 1RO1EB016411-01, NSF grants OIA-1125087 and IIS 1447344.