

1Automated curation of CNMF-E-extracted ROI spatial footprints and 2calcium traces using open-source AutoML tools

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17Abstract

18In vivo 1-photon calcium imaging is an increasingly prevalent method in behavioural neuroscience.
19Numerous analysis pipelines have been developed to improve the reliability and scalability of pre-
20processing and ROI extraction for these large calcium imaging datasets. Despite these advancements
21in pre-processing methods, manual curation of the extracted spatial footprints and calcium traces of
22neurons remains important for quality control. Here, we propose an additional semi-automated
23curation step for sorting spatial footprints and calcium traces from putative neurons extracted using
24the popular CNMF-E algorithm. We used the automated machine learning tools TPOT and
25AutoSklearn to generate classifiers to curate the extracted ROIs trained on a subset of human-labeled
26data. AutoSklearn produced the best performing classifier, achieving an F1 score > 92% on the
27ground truth test dataset. This automated approach is a useful strategy for filtering ROIs with
28relatively few labeled data points, and can be easily added to pre-existing pipelines currently using
29CNMF-E for ROI extraction.

301 Introduction

31Advances in one-photon (1p) miniaturized fluorescence microscopy in terms of utility, cost, and
32ease-of-use have increased the accessibility and popularity of *in vivo* calcium imaging in freely
33behaving rodents (Cai et al., 2016; Ghosh et al., 2011; Hamel et al., 2015; Jacob et al., 2018).
34Consequently, researchers are able to track the activity of neuronal populations across days, weeks,
35or even months (Gonzalez et al., 2019; Rubin et al., 2015). Concurrent with the growing usage of 1p
36microendoscopy in neuroscience, there is an increasing demand for high-throughput software that
37accurately and efficiently processes the very large raw calcium imaging datasets now being
38produced. To address this challenge, a number of algorithms and analysis pipelines have been

39 developed to automate the extraction of cells and calcium activity traces across time in a robust
40 manner—a necessary step for downstream analyses (Pnevmatikakis, 2019).

41

42 Motion correction, source extraction, and cell registration (across multiple recording sessions) are
43 important steps in pre-processing raw 1p calcium imaging data. Source extraction, the task of
44 identifying the locations and activity of neurons in the imaged field of view (FOV), is arguably the
45 most challenging of these steps is arguably the most challenging of these steps, as evidenced by the
46 number of different algorithms published with the aim of improving this critical step. Nevertheless,
47 two main methods of source extraction have been widely adopted in the field: principal component
48 analysis/independent component analysis (PCA/ICA) (Mukamel et al., 2009) and the more recent
49 extended constrained non-negative matrix factorization for microendoscopic data (CNMF-E) (Zhou
50 et al., 2018). CNMF-E explicitly models background signals present in 1p microendoscopic
51 recordings, and, therefore results in more accurate signal detection from neurons compared to
52 PCA/ICA (Zhou et al., 2018).

53

54 Our lab has successfully applied CNMF-E to recordings from our open-source Compact Head-
55 mounted Endoscope (CHEndoscope) in order to identify neuron locations (or spatial footprints) and
56 extract their calcium activity traces from freely-behaving mice performing different behavioural
57 tasks. CNMF-E has proven to be a reliable tool across multiple imaging sessions and experimental
58 paradigms conducted in the lab with minimal parameter tuning in our hands (Jacob et al., 2018).
59 However, like PCA/ICA, CNMF-E may still produce some false-positives in the output of detected
60 cells (i.e., non-neuronal spatial footprints or calcium traces), which can be filtered out of the final
61 dataset manually. We initially found success in filtering CNMF-E-extracted spatial footprints and
62 traces by adding a manual curation step that involved visual inspection of each ROI and calcium
63 trace (previously described in (Jacob et al., 2018)). While this type of manual curation can reduce the
64 number of false-positives in CNMF-E's output, visual inspection of potentially tens of thousands of
65 extracted cells can be time-consuming, and this method is not free from human error. Here, we
66 propose an automated machine learning (AutoML) approach built on top of the CNMF-E algorithm's
67 outputs to filter out potential false-positives. We implemented a semi-automated classification tool to
68 limit the amount of manual curation required during pre-processing, without completely removing
69 the ability to fine-tune the process with human-labeled datasets.

70

71 The main outputs of CNMF-E's source extraction algorithm are: 1) the extracted calcium traces
72 representing cellular activity, and, 2) the spatial footprint of putative neurons. As mentioned
73 previously, manual curation of these outputs involves identifying both aberrant traces that do not
74 have stable baseline fluorescence (Resendez et al., 2016), transient durations inconsistent with the
75 expressed calcium indicator (e.g., GCAMP6f) (Badura et al., 2014), and/or spatial footprints that are
76 not consistent with the shape and size of neurons in the brain region being recorded (Resendez et al.,
77 2016). We trained and validated our classifiers on a dataset of 14 000 manually curated spatial
78 footprints and traces output from CNMF-E. The final model chosen was then used to automate the
79 curation of ROIs from other recording sessions. From the two AutoML libraries, we chose the best
80 performing model to train on the full training set to evaluate on the test set. We find our model can
81 accurately predict whether a cell would be included or excluded at a rate of 92%.

82The potential time savings of manually curating thousands of cells makes this approach a method
83worth employing as part of a typical 1p calcium imaging pipeline. While our AutoML-based curation
84pipeline was primarily developed to be used with CHEndoscope data, our model takes the output of
85CNMF-E and as a result, allows this method to be readily applied to data acquired using other 1p
86miniature endoscopes.

872 **Methods**

88**Dataset preparation and pre-processing**

89

90The dataset used for model training was acquired from multiple hippocampal CA1 recordings
91captured across different mice and recording sessions using methods described in Jacob et al. 2018.
92From these recordings, we used CNMF-E (Zhou et al., 2018) to extract spatial footprints and calcium
93traces of 14 000 ROIs. We then manually reviewed and labeled these ROIs as neuronal (included for
94further analysis) or artefact (excluded from analysis). The labels were generated by two human expert
95raters that inspected the calcium transients and spatial footprints based on previously reported
96criteria:

97 1. fast rise and slow decay of calcium transients with stable baseline fluorescence (Resendez et
98 al., 2016).

99 2. calcium transient durations consistent with GCaMP6f (or appropriate GCaMP variant)
100 (Badura, Sun, Giovannucci, Lynch, & Wang, 2014).

101 3. spatial footprints consistent with appropriate neuronal shape and size (Resendez et al., 2016).

102Interrater agreement for the dataset was 87% across the two raters on a subset of the data (1073
103putative ROIs extracted from CNMF-E) (Figure 1).

104Spatial footprints consisted of the maximum projection of the identified cell from all frames in the
105video. We found that location of the footprint in the FOV was not important in our labelling criteria
106(compared to shape and size of footprint), we cropped the spatial footprints to remove empty space.
107Each spatial footprint was reduced to an 80x80 pixel image centered on the peak intensity of the
108footprint. Furthermore, recordings were of varying lengths, so all trace data was cropped at 500
109frames (equivalent to 100s of recording at 5fps). The 2 dimensional footprints were reduced to a 1
110dimensional vector (6400 pixels) and concatenated to the trace data.

111

112We aggregated the labeled ROIs into a dataset split into training and test sets, which comprised 80%
113(~11 000 ROIs) and 20% (~3 000 ROIs) of the data, respectively.

114

115**Model optimization and selection**

116

117We used two automated machine learning (AutoML) methods, TPOT (Olson et al., 2016; Olson &
118Moore, 2019) and AutoSklearn (Feurer et al., 2019) that are based on the popular Python machine
119learning toolbox, scikit-learn (Pedregosa et al. 2011) to select optimal classification models. While
120other AutoML tools exist that may outperform the ones we chose (Truong et al., 2019), TPOT and
121AutoSklearn are both free open-source, and easy to use, making them accessible for labs to
122incorporate into their existing analysis pipelines.

123

124The key advantage of AutoML tools such as TPOT and AutoSklearn is that they do the extensive
125work of finding the best type(s) of data transformation and models to build a pipeline for classifying

126the input data, as well as the hyperparameters associated with these steps. TPOT is a tree-based
127optimization tool that builds and optimizes machine learning pipelines using genetic programming
128(Olson et al., 2016; Olson & Moore, 2019). TPOT generates pipelines of pre-processing steps and
129classification models in order to maximize classification performance while prioritizing simpler
130pipelines. AutoSklearn performs algorithm selection and hyperparameter tuning using Bayesian
131optimization, meta-learning and ensemble construction (Feurer et al., 2019) and as a result, the final
132classifier is an ensemble of many different model types and their associated hyperparameters. We
133primarily used default TPOT and AutoSklearn parameters, with a max evaluation time for a single
134pipeline of 10 minutes, and a total search time of 2 days.

135

136During training, we used 10-fold cross-validation using stratified folds that preserved the relative
137proportions of “include” and “exclude” labels (i.e., during each run of training, 9 of 10 folds were
138used for training, and the 10th fold was used to test the performance of the model). This process was
139repeated for all 10 folds, resulting in an averaged performance metric for the data. We optimized the
140models to maximize the F1 score, the harmonic average of precision and recall, where high precision
141indicates a low false positive rate, and high recall indicates a low false negative rate. In our dataset, a
142true positive is an extracted ROI that both the trained model and a “ground truth” human scorer
143define as suitable to be included for further analysis (i.e., it satisfies the three selection criteria listed
144above). A true negative is an extracted ROI that is excluded for further analysis by both the model
145and our ground truth scoring.

1463 **Results**

147To determine the efficacy of an AutoML approach for classification of CNMF-E extracted ROIs, we
148tested the ability of TPOT and AutoSklearn to build classifiers that can label the pre-processed spatial
149footprints and calcium traces of putative ROIs. Both TPOT and AutoSklearn were trained on 11 000
150labeled ROIs in the training set split into 10 folds for cross-validation, repeated 5 times. The best
151models obtained during training were used to determine the F1 score on the test set. Table 1 reports
152the performance of the best models obtained by TPOT and AutoSklearn across the training folds and
153on the test set.

154Next we assessed the transferability of the best classifier pipelines identified by TPOT and
155AutoSklearn using fewer samples. We used the top performing classifier pipelines and
156hyperparameters chosen by TPOT and AutoSklearn and trained the initialized pipelines using
157datasets of increasing ROI number. The training set size ranged from 150 to 10 000 ROIs. Using a
158change point analysis algorithm (PELT, Killick et al. 2012), we determined that AutoSklearn and
159TPOT classifiers approached a maximal F1 score with 719 and 1000 labeled ROIs, respectively
160(Figure 2). The pipelines found using our much larger labeled dataset may be easily incorporated
161into other pipelines with minimal computational effort to train and finetune on CNMF-E extracted
162ROIs from other 1p experiments, using fewer labeled ROIs.

163To examine the classifier performance in terms of false positives and false negatives, we created
164confusion matrices to visualize the rate of true positives, true negatives, false positives and false
165negatives from the TPOT and AutoSklearn predictions compared to ground truth. We found that the
166classifier built with Autosklearn (0.922 F1, Table 1) performs better in terms of both reducing false
167positives and false negatives (Figure 3).

168

169 To further assess the nature of the classification errors, we looked at the class confidences or
170 probabilities of the test set predictions from the trained TPOT and AutoSklearn models (Figure 4).
171 Class probabilities indicate the classifier’s certainty (using confidence score for TPOT and class
172 probability for AutoSklearn) that a sample belongs to a particular class label. We tested whether
173 mislabeled ROIs were also those which the classifiers expressed less confidence in classifying. We
174 examined the size of the difference between certainty scores (true positives versus false positives,
175 true negatives versus false negatives) in TPOT and AutoSklearn using Cohen’s d (Cohen, 2013;
176 Sawilowsky, 2009) (Table 2). The AutoSklearn classifier—which outperformed the TPOT classifier
177 based on F1 scores— showed large differences in certainty scores when labeling ROIs as positive
178 ($d=1.36$) or negative ($d=2.34$). By contrast, the TPOT classifier was relatively less confident on both
179 types of classification (positive $d=0.63$, negative $d=1.68$). In other words, the AutoSklearn classifier
180 was more certain in applying labels to ROIs than was the TPOT classifier. This indicates that false
181 negatives and false positives in the higher performing AutoSklearn classifier may arise from “edge-
182 cases” ROIs in the dataset which the classifier was not as certain about the label. In contrast, the
183 poorer performance of the TPOT classifier may simply be due to poor generalization on the test set.

184 To investigate the nature of the false positives and false negatives from the best TPOT and
185 AutoSklearn models, we looked at the underlying spatial footprints and calcium traces for mislabeled
186 ROIs from both AutoML tools (Figure 5). Representative examples of excluded ROIs from the
187 ground truth dataset show that some cells may be excluded (i.e., true negatives) because of poor trace
188 data and/or poor spatial footprints, which possibly represent non-neuronal imaging artefacts and/or
189 ROIs representing areas of background fluorescence. While some false positives from AutoSklearn
190 shared similar features with true negative ROIs, others were more ambiguous. Upon inspection, these
191 ROIs sometimes were high-quality spatial footprints with poor-quality calcium traces, or vice-versa,
192 or were composed of spatial footprints and calcium traces of true neuronal-origin mixed with
193 additional non-neuronal noise. These examples represent “edge-cases” which may be difficult to
194 judge even by a human rater.

1954 Discussion

196 Automated curation of ROIs provides a fast, accurate method for classifying neural data generated in
197 1p calcium imaging experiments. We show that AutoML tools such as the open source TPOT and
198 AutoSklearn packages provide an easy way to build effective classifiers for ROIs extracted from the
199 widely used CNMF-E algorithm. Spatial footprints and calcium traces from CNMF-E can be used to
200 train these models with minimal data preprocessing. Furthermore, it may be possible to apply the top
201 performing classifiers generated from this work to other experimental datasets taken from different
202 1p imaging setups, while requiring relatively few labeled samples. Other analyses pipelines such as
203 MIN1PIPE (Lu et al. 2018) have been developed to improve source extraction by reducing false
204 positive ROIs without increasing the rate of false negatives. However, given the more widespread
205 adoption of CNMF-E, the approach described here prevents labs from having to adopt entirely new
206 analysis pipelines. Our approach provides a balance between the need to manually review the output
207 of CNMF-E ROIs to maximize the number of detected cells, while still allowing some further
208 automation of the otherwise laborious curation process.

209 An AutoML approach to reviewing these traces may be useful for curating traces from labeled data
210 of the extracted ROIs from CNMF-E and can be implemented on top of pre-existing analysis
211 pipelines without much need to adapt the software. However, there are a number of limitations to this
212 approach. Firstly, we emphasize the automated aspect of this machine learning classifier approach
213 and little need for hand-tuning, but we recognize that the best models still make errors. Cases in
214 which the best performing classifier generated by AutoSklearn failed to detect true positives or true

215negatives were further reviewed and were typically seen to be edge cases where it may be difficult
216for a human reviewer to make a judgment. Similarly, we found that a second expert scorer looking at
217the same data may not make the exact same judgments on such edge cases (having an interrater
218reliability score of 87%). While the AutoML classifiers were trained on the data that had relatively
219little preprocessing beyond cropping and downsampling, future work could address whether feature
220engineering over the spatial footprints and trace data could further improve accuracy and reduce
221training time for model selection and hyperparameter tuning. Better curation of a training dataset for
222the models may help reduce ambiguous cases that make it difficult for a classifier to make accurate
223predictions.

224In conclusion, we present here a demonstration and benchmark of an AutoML approach for curation
225of CNMF-E extracted ROIs. The methods described here can provide a flexible, free open-source,
226and easy-to incorporate curation step for other researchers using CNMF-E for source extraction of
227their 1p datasets, while requiring few changes to their existing analysis pipelines.

2285 **References**

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2776 **Conflict of Interest**

278*The authors declare that the research was conducted in the absence of any commercial or financial*
279*relationships that could be construed as a potential conflict of interest.*

2807 **Author Contributions**

281LT, PF, SJ contributed to the study design. AJ designed and constructed the CHEndoscopes. AR and
282AM conducted surgeries, behavior experiments, CNMF-E processing, and manual ROI labelling. LT
283performed all analyses using automated machine learning pipelines. LT, AM, AR, AJ performed the
284statistical analyses and wrote the paper. All authors discusses and commented on the manuscript.

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2939 **Acknowledgments**

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295 were used to perform this research.

296 **Data Availability Statement**

297 The datasets and code generated for this study can be found in the cnmfe-reviewer GitHub repository
298 [<https://github.com/jf-lab/cnmfe-reviewer>].

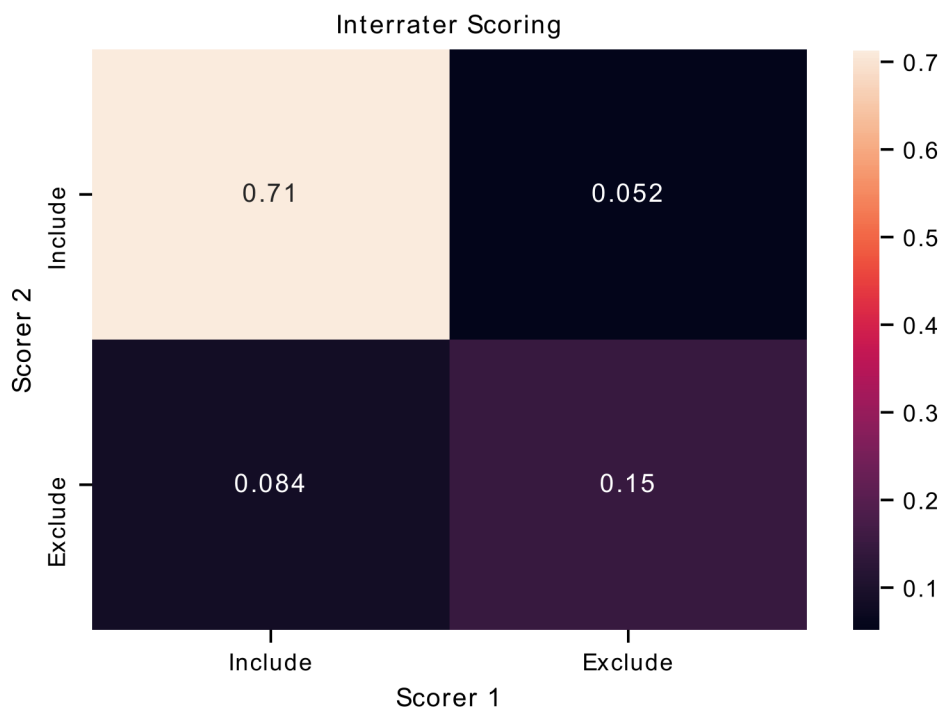
299

300 Figures

301 **Figure 1. Interrater agreement of ROI labels.** A confusion matrix comparing the manually
302 reviewed labels (include of exclude) for putative ROIs extracted from CNMF-E determined by two
303 different raters. Each cell of the matrix is annotated with the proportion of ROIs.

304

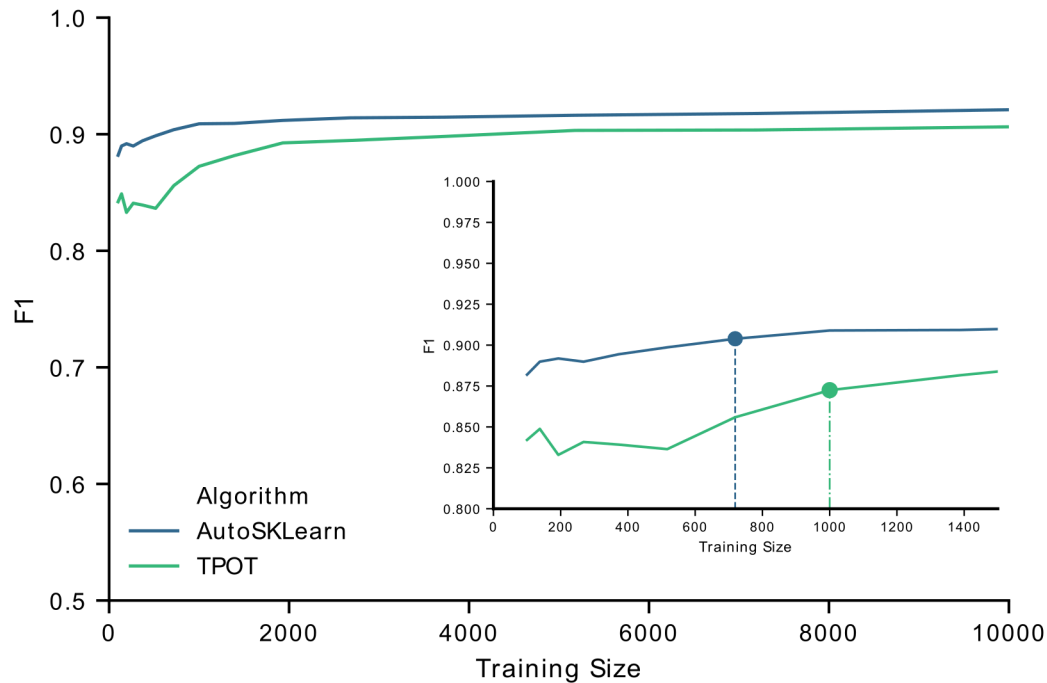
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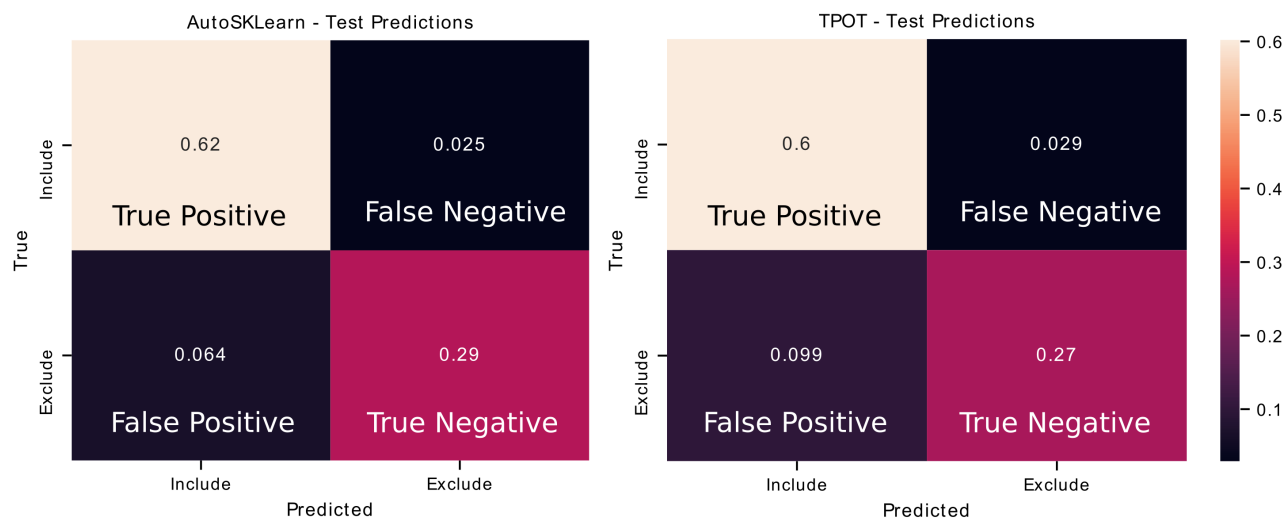
306 **Figure 2. F1 score performance with increasing training size.** Graph of the F1 test scores versus
307 the number of training samples used to train the best models output by AutoSklearn (blue) and TPOT
308 (green). (Inset) A graph of the same plot with a smaller range of training sizes and the change point is
309 marked on each algorithm type.

310

311

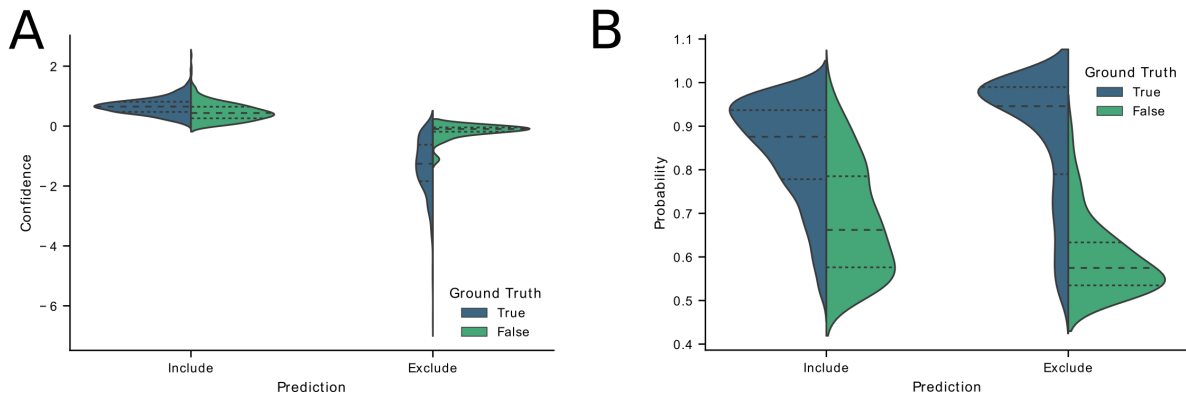


312 **Figure 3. Confusion matrices of AutoML tools: TPOT and AutoSklearn.** Each cell in the matrix
313 is annotated with the proportion of ROIs labeled as Include or Exclude according to the predicted and
314 true labels. Colors indicate the relative proportions of the labels where lower proportions are darker
315 in color and higher proportions are lighter in color. The confusion matrices were made from
316 predictions on the test set from the best models output by TPOT (left) and AutoSklearn (right).



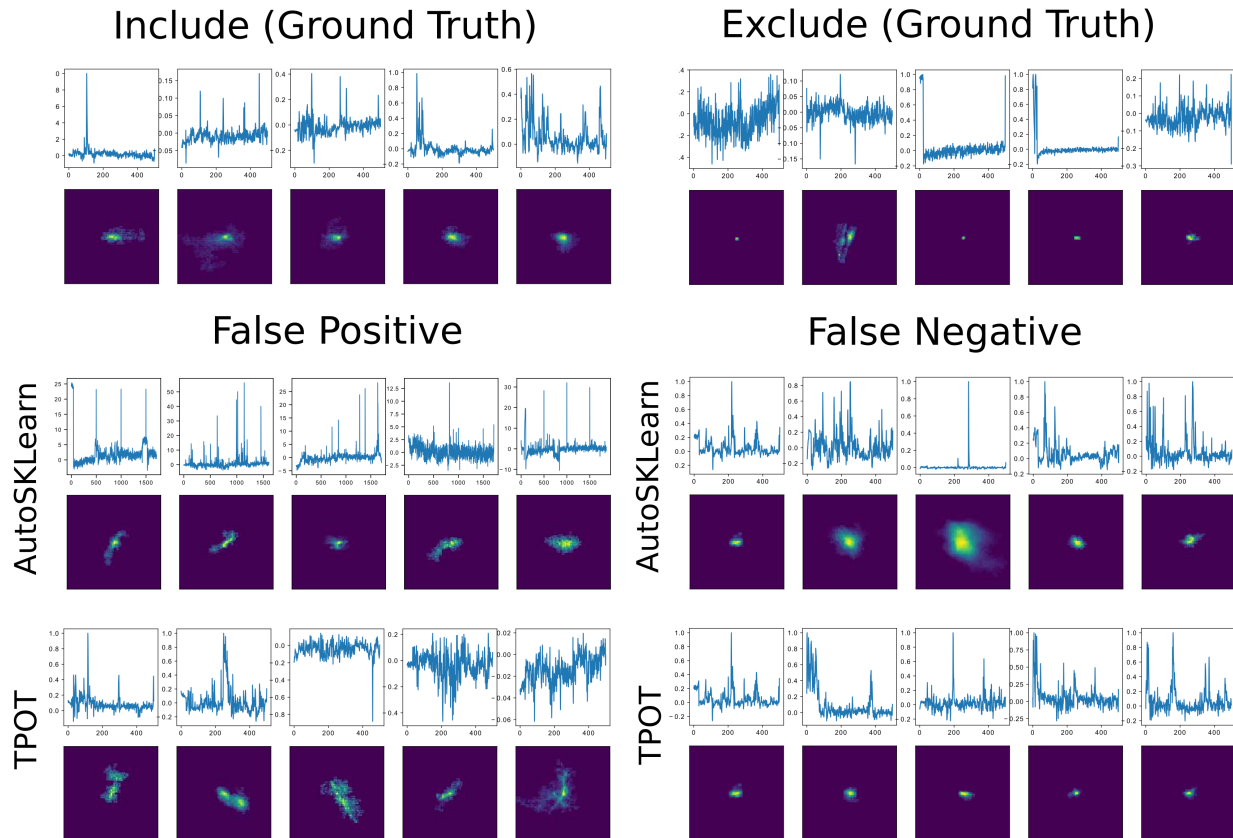
318

319 **Figure 4. Classifier confidence (TPOT) and class probabilities (AutoSklearn) on predicted false**
320 **positives and false negatives.** Violin plots of the distribution of (A) TPOT classifier confidence or
321 (B) AutoSklearn class probabilities on predicted ROI labels (Include or Exclude) in the test set. Each
322 half of the violin plot is the distribution of values for labels that were correct (True, left/blue) or
323 incorrect (False, right/green) based on the ground truth labels.



325

326 **Figure 5. Representative false positives and negatives compared to ground truth ROIs.** Example
327 calcium traces (top) and spatial footprints (bottom) from ground truth ROIs labeled as Include (left)
328 or Exclude (right). Example calcium traces (top) and spatial footprints (bottom) of false positive and
329 false negative ROIs predicted from the AutoSklearn (middle row) or TPOT (bottom row) classifiers.



331 **Tables**

332 **Table 1. Mean F1 scores of AutoML methods on training cross-validation and final F1 scores**
 333 **on the test set.**

334

	TPOT		AutoSklearn	
	Training CV (10-fold, 5x)	Test	Training CV (10-fold, 5x)	Test
F1 Score	0.906	0.904	0.917	0.922

335

336 **Table 2. Cohen’s *d* of certainty scores between predicted labels that were correct or incorrect**
 337 **compared to ground truth in TPOT or AutoSklearn.**

338

	Include (Positive)		Exclude (Negative)	
	TPOT	AutoSklearn	TPOT	AutoSklearn
Cohen’s <i>d</i>	0.63	1.36	1.68	2.34

339