Overcoming the Domain Gap in Contrastive Learning of Neural Action Representations

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Abstract

A fundamental goal in neuroscience is to understand the relationship between neural activity and behavior. For example, the ability to extract behavioral intentions from neural data, or neural decoding, is critical for developing effective brain machine interfaces. Although simple linear models have been applied to this challenge, they cannot identify important non-linear relationships. Thus, a self-supervised means of identifying non-linear relationships between neural dynamics and behavior, in order to compute neural representations, remains an important open problem. To address this challenge, we generated a new multimodal dataset consisting of the spontaneous behaviors generated by fruit flies, Drosophila melanogastera popular model organism in neuroscience research. The dataset includes 3D markerless motion capture data from six camera views of the animal generating spontaneous actions, as well as synchronously acquired two-photon microscope images capturing the activity of descending neuron populations that are thought to drive actions. Standard contrastive learning and unsupervised domain adaptation techniques struggle to learn neural action representations (embeddings computed from the neural data describing action labels) due to large inter-animal differences in both neural and behavioral modalities. To overcome this deficiency, we developed simple yet effective augmentations that close the inter-animal domain gap, allowing us to extract behaviorally relevant, yet domain agnostic, information from neural data. This multimodal dataset and our new set of augmentations promise to accelerate the application of self-supervised learning methods in neuroscience.

1 Introduction

Recent technological advances have enabled large-scale simultaneous recordings of neural activity and behavior in animals including rodents, macaques, humans and the vinegar fly, *Drosophila melanogaster* [1, 2, 3, 4, 5, 6]. In parallel, recent efforts have been made it possible to perform markerless predictions of 2D and 3D animal poses [7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17]. Video and pose data have been used to segment and cluster temporally related behavioral information [18, 19, 20, 21, 22]. To capture a similarly low dimensional representation of neural activity, most efforts have focused on the application of recurrent state space models [23, 24, 25], or variational autoencoders [26, 4]. By contrast, there has been relatively limited work aimed at extracting behavioral information from neural data [27, 28, 29] and most efforts have focused on identifying linear relationships between these two modalities using simple correlation analysis, or generalized linear models [30, 31, 32]. However, *neural action representations*—the mapping of behavioral information within neural data—which are particularly crucial for brain-machine interfaces and closed-loop experimentation [33, 34] are highly nonlinear. Therefore, devising a systematic approach for uncovering complex non-linear relationships between behavioral and neural modalities remains an important challenge.

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Contrastive learning is one promising approach to address this gap. It has been used to extract information from multimodal datasets in a self-supervised way, for modalities including audio, speech, and optical flow [35, 36, 37, 38, 39, 40]. Contrastive learning also has been applied to unimodal datasets, including the study of human motion sequences [41, 42, 43], medical imaging [44, 45], video understanding [46, 47], and pose estimation [48, 49]. Thus, contrastive learning holds great promise for application in neuroscience.

One of the largest barriers to applying contrastive learning to behavioral-neural multimodal datasets is the fact that their statistics (e.g., neuron locations and sizes, body part lengths and ranges of motion) often differ dramatically across animals. This makes it difficult to train models that can generalize across subjects. We confront this domain gap when comparing neural imaging datasets from two different flies (**Supplementary Fig. S3; Supplementary Videos 1-2**). Although multimodal domain adaptation methods for downstream tasks such as action recognition exist [35], they assume supervision in the form of labeled source data. However, labeling behavioral-neural datasets requires expensive and arduous manual labor by trained scientists, and thus often leaving the vast majority of data unlabeled. Similarly, it is non-trivial to generalize few-shot domain adaptation methods to multimodal tasks [50, 51]. Thus, the field of neuroscience needs new computational approaches that can extract information from ever-increasing amounts of unlabeled multimodal datasets that also suffer from extensive domain gaps across subjects.

Here, we address this challenge by extracting domain agnostic action representations from neural data. We measure representation quality using an action recognition task, in which we apply a linear classification head and transfer our pretrained weights to classify action labels. Therefore, we call our representations *neural action representations*. To best reflect real world conditions, during the unsupervised pre-training phase, we assume access to the paired behavioral-neural data for all domains but without any action labels. Then, we show that a strong domain gap exists across data taken from different animals, rendering standard contrastive methods ineffective. To address this challenge, we propose a set of simple augmentations that can perform domain adaptation and extract useful representations. We find that the resulting model outperforms baseline approaches, including linear models, previous neural representation learning approaches and common domain adaptation techniques. Finally, to accelerate the uptake and development of these and other self-supervised methods in neuroscience, we will release our new multimodal *Drosophila* behavioral-neural dataset along with associated dense action labels for spontaneously-generated behaviors

2 Methods

2.1 **Problem Definition**

We assume a paired set of data $\mathcal{D}_s = \{(\mathbf{b}_i^s, \mathbf{n}_i^s)\}_{i=1}^{n_s}$, where \mathbf{b}_i^s and \mathbf{n}_i^a represent the behavioral and neural information respectively, with n_s being the number of samples for animal $s \in S$. We quantify behavioral information \mathbf{b}_i^s as a set of 3D poses corresponding to a set of frames i from animal *s*, and neural information \mathbf{n}_i^s as a set of two-photon microscope images capturing the activity of neurons. We assume that the two modalities are always synchronized (paired), and therefore describe the same set of events. Our goal is to learn a parameterized image encoder function f_n , which maps a set of neural images \mathbf{n}_i^s to a low-dimensional representation. We aim for our learned representation to be representative of the underlying behavioral label, while being modality-agnostic and not representative of the underlying animal identity information *s*, and therefore effectively removing the domain gap across animals and modalities. We assume that we are not given behavioral labels during unsupervised training.

2.2 Contrastive Representation Learning

For each input pair $(\mathbf{b}_{\mathbf{i}}^{s}, \mathbf{n}_{\mathbf{i}}^{s})$, we first draw a random view $(\mathbf{b}_{\mathbf{i}}^{s}, \tilde{\mathbf{n}}_{\mathbf{i}}^{s})$ with a sampled transformation function $t_n \sim \mathcal{T}_n$ and $t_b \sim \mathcal{T}_b$, where \mathcal{T}_n and \mathcal{T}_b represent a family of stochastic image transformation functions for behavioral and neural data, respectively. Next, the encoder functions f_b and f_n transform input data into low-dimensional vectors \mathbf{h}_b and \mathbf{h}_n , followed by non-linear projection functions g_b and g_n , which further transform data into the vectors \mathbf{z}_b and \mathbf{z}_n . During training, we sample a minibatch of N input pairs $(\mathbf{b}_{\mathbf{i}}^{s}, \mathbf{n}_{\mathbf{i}}^{s})$, and train with the symmetric loss function

$$\mathcal{L}_{NCE} = -\sum_{i=1}^{N} \log \frac{\exp\left(\left\langle \mathbf{z}_{b}^{i}, \mathbf{z}_{n}^{i} \right\rangle / \tau\right)}{\sum_{k=1}^{N} \exp\left(\left\langle \mathbf{z}_{b}^{i}, \mathbf{z}_{n}^{k} \right\rangle / \tau\right)} + \log \frac{\exp\left(\left\langle \mathbf{z}_{n}^{i}, \mathbf{z}_{b}^{i} \right\rangle / \tau\right)}{\sum_{k=1}^{N} \exp\left(\left\langle \mathbf{z}_{n}^{i}, \mathbf{z}_{b}^{k} \right\rangle / \tau\right)}$$
(1)

where $\langle \mathbf{z}_b^i, \mathbf{z}_n^i \rangle$ is the cosine similarity between behavioral and neural modalities and $\tau \in \mathbb{R}^+$ is the temperature parameter. The loss function maximizes the mutual information between two modalities [52]. The symmetric version of the contrastive loss function was previously used in multimodal self-supervised learning [45, 53]. An overview of our method for learning f_n is shown in **Supplementary** Fig S2. Although standard contrastive learning bridges the gap between different modalities, it does not bridge the gap between different animals, a fundamental challenge that we address in this work through augmentations described in the following section.

Swapping Augmentation: Given a set of consecutive 3D poses \mathbf{b}_{i}^{s} , for each $k \in \mathbf{i}$, we stochastically replace \mathbf{b}_{k}^{s} with one of its nearest pose neighbors in the set of domains $\mathcal{D}_{S/s}$, where S is the set of all animals. To do so, we first randomly select a domain $\hat{s} \in S/s$ and define a probability distribution $\mathbf{P}_{\mathbf{b}_{i}^{s}}^{\hat{s}}$ over the domain $\mathcal{D}_{\hat{s}}$ with respect to \mathbf{b}_{k}^{s} ,

$$\mathbf{P}_{\mathbf{b}_{k}^{\hat{s}}}^{\hat{s}}(\mathbf{b}_{l}^{\hat{s}}) = \frac{\exp(-\|\mathbf{b}_{l}^{\hat{s}} - \mathbf{b}_{k}^{s}\|_{2})}{\sum_{\mathbf{b}_{m}^{\hat{s}} \in \mathcal{D}_{\hat{s}}} \exp(-\|\mathbf{b}_{m}^{\hat{s}} - \mathbf{b}_{k}^{s}\|_{2})}.$$
(2)

We then replace each 3D pose \mathbf{b}_k^s by first uniformly sampling a new domain \hat{s} , and then sampling from the above distribution $\mathbf{P}_{\mathbf{b}_k^s}^s$, therefore resulting in $\mathbf{\tilde{b}}_k^s \sim \mathbf{P}_{\mathbf{b}_k^s}^s$. In practice, we calculate the distribution \mathbf{P} only over the first \mathbf{N} nearest neighbors of \mathbf{b}_k^s , in order to sample from a distribution of the most similar poses. We empirically set \mathbf{N} to 128. Swapping augmentation reduces the identity information in the behavioral data without perturbing it to the extent that semantic action information is lost. Each transformed behavioral sample $\mathbf{\tilde{b}}_i^s$ is composed of multiple domains. This forces the behavioral encoding function f_b to leave identity information out, therefore merging multiple domains in the latent space. Swapping augmentation is similar to synonym replacement augmentation used in natural language processing [54], where randomly selected words in a sentence are replaced by their synonyms. To the best of our knowledge, we are the first to use swapping augmentation in the context of time-series analysis or for domain adaptation.

Neural Calcium Imaging Data Augmentation: Our neural data was obtained using two-photon microscopy and calcium imaging. The resulting images are only a function of the underlying neural activity, and have temporal properties that differ from the true neural activity. For example, calcium signals from a neuron change much more slowly than the neuron's actual firing rate. Consequently, a single neural image \mathbf{n}_t includes decaying information concerning neural activity from the recent past, and thus carries information about previous behaviors. This makes it harder to decode the current behavioral state. We aimed to prevent this overlap of ongoing and previous actions. Specifically, we wanted to teach our network to be invariant with respect to past behavioral information by augmenting the set of possible past actions. To do this, we generated new data $\tilde{\mathbf{n}}_i^s$, that included previous neural activity \mathbf{n}_k^s . To mimic calcium indicator decay dynamics, given a neural data sample \mathbf{n}_i^s of multiple frames, we sample a new neural frame \mathbf{n}_k^s from the same domain, where $k \notin \mathbf{i}$. We then convolve \mathbf{n}_k^s with the temporally decaying calcium convolutional kernel \mathcal{K} , therefore creating a set of images from a single frame \mathbf{n}_k^s , which we then add back to the original data sample \mathbf{n}_i^s . This results in $\tilde{\mathbf{n}}_i^s = \mathbf{n}_i^s + \mathcal{K} * \mathbf{n}_k^s$ where * denotes the convolutional operation. In the Appendix, we explain calcium dynamics and our calculation of the kernel \mathcal{K} in more detail.

3 Experiments

In this section we introduce a new dataset consisting of *Drosophila melanogaster* neural and behavioral recordings as well as the set of downstream evaluation metrics.

3.1 Dataset

Motion Capture and Two-photon Dataset (MC2P): We acquired data from tethered adult female flies, (*Drosophila melanogaster*). This dataset consists of neural activity recorded using a two-photon microscope [55] from the axons of descending neurons passing through the animal's cervical connective. It also includes behavioral data recorded using multi-view infrared cameras (**Supplementary Fig. S1; Supplementary Videos 1-2**). Specifically, behavioral video data of size 480×960 pixels were acquired at 100 frames-per-second (fps) using a six circular camera network with the animal at its center. The neural data was recorded using a two-photon microscope, yielding images of 480×736 pixels at 16 fps. Eight animals and 133 trials were recorded, resulting in 8.2 hours of recordings with 2,975,000 behavioral and 476,000 neural frames. The dataset includes manual and dense action labels of eight behaviors: *forward walking, pushing, hindleg grooming, abdominal grooming, rest*,

foreleg grooming, antennal grooming, and *eye grooming.* We report the statistics of our dataset in **Supplementary Fig. S5**. See the Appendix for more details.

3.2 Evaluation

To evaluate our unsupervised pretrained neural encoder f_n , we froze its parameters and trained a randomly initialized linear classification layer with with SGD. To compare data efficiency, for each setting we evaluated image encoders with 50% and 100% of the data. We report aggregated results over 4-fold cross-validation evaluations and report the average in each task. We evaluated models on the following tasks:

Single-Animal Action Recognition: We performed action recognition on a single domain by training and testing on the same animal. We repeated the same experiment on each of four animals, and report the mean accuracy.

Multi-Animal Action Recognition: We evaluated models on their ability to reduce the domain gap. We trained the linear classifier on N-1 animals and tested on the left-out one, leaving each animal out one at a time.

Identity Recognition: We classified animal identity from among the eight animals. We sampled 1000 random data-points uniformly across animals and applied 4-fold cross validation. In the case that the learned representations are domain (subject) invariant, we expect that the linear classifier will not be able to detect the domain of the representations, resulting in a lower identity recognition accuracy.

4 Results

We present action recognition results from neural imaging data in **Table 1** and identity recognition task results in **Table S2**. For the supervised baseline, we trained an MLP with manually annotated action labels using cross-entropy loss, with the raw neural data as input, and show the results in the "Raw" section of **Table 1**. For the "Self-Supervised" section, before using the proposed augmentations, the contrastive method SimCLR performed worse than convolutional and recurrent regression-based methods including the current state-of-art BehaveNet [27]. Although domain adaptation methods MMD (Maximum Mean Discrepancy) and GRL (Gradient Reversal Layer) close the domain gap and lower identity recognition accuracy, they do not position semantically similar points near one another (**Supplementary Fig. S4**). As a result, domain adaptation-based methods suffer less from the domain gap problem, they do not produce as discriminative representations as contrastive learning based methods. The same trend is observed in Table **Table S2**. Our proposed set of augmentations close the domain gap, while significantly improving the action recognition baseline for self-supervised methods, for both single-animal and multi-animal tasks. We include detailed information about the baselines in the Appendix.

5 Conclusion

We introduced an unsupervised neural action representation framework. We extended previous methods by establishing set of augmentations that we show overcomes the multimodal domain gap in our Drosophila behavioral-neural dataset. Finally, we will share in order to dataset to accelerate the application of self-supervised learning methods in neuroscience. In future work, we aim to extend our work for domain generalization.

Tasks	$\rightarrow \rightarrow$	Single-	• Animal ↑	Multi-	Animal ↑
Percentage of Data		0.5	1.0	0.5	1.0
Random Guess		16.6	16.6	16.6	16.6
Neural (Linear) Neural (MLP)	Raw	29.3 -	32.5	18.4 18.4	18.4 18.4
SimCLR [56]	Self-Supervised	54.3	57.6	46.9	50.6
Regression (Recurr.)		53.6	59.7	49.4	51.2
Regression (Conv.)		52.6	59.6	50.6	55.8
BehaveNet [27]		54.6	60.2	50.5	56.8
Ours		57.9	63.3	54.8	61.9
SimCLR [56] + MMD	Domain Ada.	53.6	57.8	50.1	53.1
SimCLR [56] + GRL		53.5	56.3	49.9	52.3
Regression (Conv.) + MMD		54.5	60.7	52.6	55.4
Regression (Conv.) + GRL		55.5	60.2	51.8	55.7

Table 1: Action Recognition Accuracy. Single- and multi-animal action recognition results on the MC2P dataset. Behavioral and Neural MLP results for the single-animal task are removed because single animals often do not have enough labels for every action.

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Checklist

- 1. For all authors...
 - (a) Do the main claims made in the abstract and introduction accurately reflect the paper's contributions and scope? [Yes]
 - (b) Did you describe the limitations of your work? [Yes] Please see the Conclusion section.
 - (c) Did you discuss any potential negative societal impacts of your work? [Yes] Please see the Broader Impact Statement Section.
 - (d) Have you read the ethics review guidelines and ensured that your paper conforms to them? [Yes]
- 2. If you are including theoretical results...
 - (a) Did you state the full set of assumptions of all theoretical results? [N/A]
 - (b) Did you include complete proofs of all theoretical results? [N/A]
- 3. If you ran experiments...
 - (a) Did you include the code, data, and instructions needed to reproduce the main experimental results (either in the supplemental material or as a URL)? [Yes] We include instructions to download and use our dataset in the supplementary materials.
 - (b) Did you specify all the training details (e.g., data splits, hyperparameters, how they were chosen)? [Yes] Please see the appendix, particularly the implementation details section.
 - (c) Did you report error bars (e.g., with respect to the random seed after running experiments multiple times)? [Yes] We use cross-validation and report the mean accuracy. Please see the appendix, the implementation details section.
 - (d) Did you include the total amount of compute and the type of resources used (e.g., type of GPUs, internal cluster, or cloud provider)? [Yes] Please see the appendix, the implementation details section.
- 4. If you are using existing assets (e.g., code, data, models) or curating/releasing new assets...
 - (a) If your work uses existing assets, did you cite the creators? [N/A]
 - (b) Did you mention the license of the assets? [Yes] We include the license of our dataset in the supplementary material.
 - (c) Did you include any new assets either in the supplemental material or as a URL? [Yes] We include instructions to download and using our dataset in the supplementary materials.
 - (d) Did you discuss whether and how consent was obtained from people whose data you're using/curating? [N/A]
 - (e) Did you discuss whether the data you are using/curating contains personally identifiable information or offensive content? [N/A]
- 5. If you used crowdsourcing or conducted research with human subjects...
 - (a) Did you include the full text of instructions given to participants and screenshots, if applicable? [N/A]
 - (b) Did you describe any potential participant risks, with links to Institutional Review Board (IRB) approvals, if applicable? [N/A]
 - (c) Did you include the estimated hourly wage paid to participants and the total amount spent on participant compensation? [N/A]