

Decoding context

In the file `DecodingDataRead.m`, we first took the binarized calcium activity and took the sum of events in 3 s bins (60 frames). We then restricted analysis to:

- (1) times when the mouse was running, and
- (2) when the mouse was in context "1" or "2," representing two different cue configurations in the maze.

Finally, only activity from place cells were used. The resulting pre-processed data was saved for each mouse in a subfolder under the name `binned_activity_decode.mat`.

```
rootdir = "";
folders = ["M119"+filesep "M120"+filesep "M292"+filesep "M319"+filesep ...
    "M231"+filesep "M314"+filesep "M316"+filesep "M318"+filesep "M210"+filesep];
cohort = ["D1", "D1", "D1", "D1", "G1", "G1", "G1", "G1", "D1"];
sessions = ["early", "trained", "grouping"];
```

Estimate SVM performance for each animal & each condition.

We saved each run as a separate `.mat` file manually for comparison later. The resulting `validation_accuracy` scores were put into excel tables for glme analysis and ease of comparison.

For panel D, the `ablate_percent` and `ablation` strategy were varied.

```
ablate_percent=0.50;
ablation = 'descend';

test_accuracy = nan(length(folders),3);
validation_accuracy = nan(length(folders),3);
s_max = length(sessions);

weights = cell(length(folders),3);
corrs = cell(length(folders),3);

parfor f = 1:length(folders)
    for s = 1:s_max
        try
            A=load(folders(f)+"binned_activity_decode_"+sessions(s)+".mat");

            ds = 10; % how many samples to downsample

            N_cells = size(A.a_use,2);
            N_cells_use = round(ablate_percent*N_cells);
            idx_cells_use = [];
            if strcmp(ablation,'random')
                % shuffle the cells
                subset_cells = randperm(N_cells);
                idx_cells_use = subset_cells(1:N_cells_use);
                corrs{f,s} = A.corr_coef(idx_cells_use);
```

```

elseif strcmp(ablation, 'ascend')
    % sort the cells by increasing corr coef (most remap are
    % first)
    [corr_temp,idx_cells_use] =
topkrows(A.corr_coef,N_cells_use,'ascend');
    corrs{f,s} = corr_temp;

elseif strcmp(ablation,'descend')
    [corr_temp,idx_cells_use] =
topkrows(A.corr_coef,N_cells_use,'descend');
    corrs{f,s} = corr_temp;
elseif strcmp(ablation,'None')
    idx_cells_use = 1:N_cells_use;
    corrs{f,s} = A.corr_coef(idx_cells_use);
end

a_use_sub = A.a_use(1:ds:end,idx_cells_use);
context_use_sub = A.context_use(1:ds:end);

% % reshuffle context
% shuffle_context_ind = randperm(size(context_use_sub,1));
% context_use_sub = context_use_sub(shuffle_context_ind);

hpartition =
cvpartition(context_use_sub,'Holdout',0.25,'Stratify',true);

X_train = a_use_sub(training(hpartition),:);
Y_train = context_use_sub(training(hpartition));

classificationSVM = fitcsvm(...
    X_train, ...
    Y_train, ...
    'KernelFunction', 'rbf', ...
    'PolynomialOrder', [], ...
    'KernelScale', 'auto', ...
    'BoxConstraint', 1, ... % usually 1
    'Standardize', true);
    %'ScoreTransform','sign');

% k-fold partitioning validation
partitionedModel = crossval(classificationSVM, 'Kfold', 20);
[validationPredictions, validationScores] =
kfoldPredict(partitionedModel);
validationAccuracy = 1 - kfoldLoss(partitionedModel, 'LossFun',
'ClassifError');

validation_accuracy(f,s) = validationAccuracy;

% test set on hold out
X_test = a_use_sub(test(hpartition),:);

```

```

Y_test = context_use_sub(test(hpartition));

[testPredictions,testScores] = predict(classificationSVM,X_test);

testAccuracy = 1 - loss(classificationSVM,X_test,Y_test);

rocObj_test = rocmetrics(Y_test, testScores,[1,2]);

test_accuracy(f,s) = testAccuracy;

% comparing SVM weights to remapping metric
weights{f,s} = classificationSVM.Beta;

display("Completed "+ folders(f)+"binned_activity_decode_"+sessions(s)
+ ".mat")

    catch e
        display("Skipping "+ folders(f)+"binned_activity_decode_"+sessions(s)
+ ".mat")
    end
end
end
end

```

```

"Completed M292\binned_activity_decode_early.mat"
"Completed M120\binned_activity_decode_early.mat"
"Completed M319\binned_activity_decode_early.mat"
"Completed M316\binned_activity_decode_early.mat"
"Completed M119\binned_activity_decode_early.mat"
"Completed M231\binned_activity_decode_early.mat"
"Completed M292\binned_activity_decode_trained.mat"
"Completed M292\binned_activity_decode_grouping.mat"
"Completed M316\binned_activity_decode_trained.mat"
"Completed M119\binned_activity_decode_trained.mat"
"Completed M319\binned_activity_decode_trained.mat"
"Completed M120\binned_activity_decode_trained.mat"
"Completed M314\binned_activity_decode_early.mat"
"Completed M316\binned_activity_decode_grouping.mat"
"Completed M318\binned_activity_decode_early.mat"
"Completed M119\binned_activity_decode_grouping.mat"
"Skipping M210\binned_activity_decode_early.mat"
"Completed M231\binned_activity_decode_trained.mat"

```

```
"Completed M120\binned_activity_decode_grouping.mat"
"Completed M319\binned_activity_decode_grouping.mat"
"Completed M231\binned_activity_decode_grouping.mat"
"Completed M210\binned_activity_decode_trained.mat"
"Skipping M210\binned_activity_decode_grouping.mat"
"Completed M314\binned_activity_decode_trained.mat"
"Completed M318\binned_activity_decode_trained.mat"
"Completed M318\binned_activity_decode_grouping.mat"
"Completed M314\binned_activity_decode_grouping.mat"
```

Stats for Panel B

```
clear;
datat = readtable("decoder_results_deltas_repeat.xlsx");
WithinSubjectData =
table(categorical({'All','PC','NonPC','All','PC','NonPC'}),categorical({'D','D','D',
'G','G','G'}),VariableNames=["CellSets","Tasks"]);

rm = fitrm(datat,'Score1-Score6 ~ 1','WithinDesign',WithinSubjectData);
ranova(rm,'WithinModel','CellSets+Tasks')
```

ans = 6×8 table

	SumSq	DF	MeanSq	F	pValue	pValueGG
1 (Intercept)	35.2169	1	35.2169	2.2641e+03	4.7363e-10	4.7363e-10
2 Error	0.1089	7	0.0156	1	0.5000	0.5000
3 (Intercept):CellSets	0.0907	2	0.0453	11.0551	0.0013	0.0084
4 Error(CellSets)	0.0574	14	0.0041	1	0.5000	0.5000
5 (Intercept):Tasks	0.0060	1	0.0060	8.9293	0.0203	0.0203
6 Error(Tasks)	0.0047	7	6.7139e-04	1	0.5000	0.5000

```
rm.multcompare('Tasks','by','CellSets')
```

ans = 6×8 table

	CellSets	Tasks_1	Tasks_2	Difference	StdErr	pValue	Lower
1	All	D	G	0.0165	0.0064	0.0361	0.0014
2	All	G	D	-0.0165	0.0064	0.0361	-0.0316
3	NonPC	D	G	0.0162	0.0107	0.1729	-0.0090
4	NonPC	G	D	-0.0162	0.0107	0.1729	-0.0414

	CellSets	Tasks_1	Tasks_2	Difference	StdErr	pValue	Lower
5	PC	D	G	0.0343	0.0106	0.0143	0.0092
6	PC	G	D	-0.0343	0.0106	0.0143	-0.0594

```
rm.multcompare('CellSets', 'by', 'Tasks')
```

```
ans = 12x8 table
```

	Tasks	CellSets_1	CellSets_2	Difference	StdErr	pValue	Lower
1	D	All	NonPC	0.1045	0.0223	0.0055	0.0389
2	D	All	PC	0.0251	0.0088	0.0564	-7.8038e-04
3	D	NonPC	All	-0.1045	0.0223	0.0055	-0.1701
4	D	NonPC	PC	-0.0794	0.0278	0.0561	-0.1612
5	D	PC	All	-0.0251	0.0088	0.0564	-0.0510
6	D	PC	NonPC	0.0794	0.0278	0.0561	-0.0023
7	G	All	NonPC	0.1042	0.0243	0.0089	0.0326
8	G	All	PC	0.0429	0.0150	0.0565	-0.0013
9	G	NonPC	All	-0.1042	0.0243	0.0089	-0.1758
10	G	NonPC	PC	-0.0613	0.0326	0.2141	-0.1573
11	G	PC	All	-0.0429	0.0150	0.0565	-0.0871
12	G	PC	NonPC	0.0613	0.0326	0.2141	-0.0347

Stats for Panel D, inset

The reported beta values are the interaction terms between the percentage "slope" and each task type.

```
clear;
datat = readtable("decoder_results_deltas_repeat_ablate.xlsx");
percents = [zeros(9,1); repmat(25,9,1); repmat(50,9,1)]/100;
cohorts = repmat(datat.Cohort,3,1);
animals = repmat(datat.Animal,3,1);
DU_scores = [datat.Score1; datat.Score5; datat.Score9];
DS_scores = [datat.Score3; datat.Score7; datat.Score11];
GU_scores = [datat.Score2; datat.Score6; datat.Score10];
GS_scores = [datat.Score4; datat.Score8; datat.Score12];

grand_tasks =
reordercats(categorical([repmat("DU",27,1); repmat("DS",27,1); repmat("GU",27,1); repmat("GS",27,1)]),["DU","DS","GU","GS"]);
grand_scores = [DU_scores; DS_scores; GU_scores; GS_scores];
grand_percents = repmat(percents,4,1);
grand_animals = repmat(animals,4,1);
grand_cohorts = repmat(cohorts,4,1);
```

```
grand_table =
table(grand_animals,grand_cohorts,grand_percents,grand_tasks,grand_scores);

grand_glme = fitglme(grand_table,'grand_scores ~ 1 + grand_percents*grand_tasks +
(1|grand_animals)')
```

grand_glme =
Generalized linear mixed-effects model fit by PL

Model information:

Number of observations	102
Fixed effects coefficients	8
Random effects coefficients	9
Covariance parameters	2
Distribution	Normal
Link	Identity
FitMethod	MPL

Formula:

grand_scores ~ 1 + grand_percents*grand_tasks + (1 | grand_animals)

Model fit statistics:

AIC	BIC	LogLikelihood	Deviance
-417.7	-391.45	218.85	-437.7

Fixed effects coefficients (95% CIs):

Name	Estimate	SE	tStat	DF	pValue	Lower	Upper
{'(Intercept)'	0.89465	0.024998	35.789	94	1.4748e-56	0.84501	0.94429
{'grand_percents'	-0.11178	0.021694	-5.1524	94	1.4149e-06	-0.15485	-0.06871
{'grand_tasks_DS'	0.0013544	0.009902	0.13678	94	0.89149	-0.018306	0.020971
{'grand_tasks_GU'	-0.026374	0.010266	-2.5692	94	0.011767	-0.046757	0.013988
{'grand_tasks_GS'	-0.028085	0.010266	-2.7358	94	0.0074402	-0.048467	0.012297
{'grand_percents:grand_tasks_DS'	-0.012929	0.03068	-0.42141	94	0.67442	-0.073846	0.047988
{'grand_percents:grand_tasks_GU'	-0.017113	0.031625	-0.54112	94	0.58971	-0.079904	0.045678
{'grand_percents:grand_tasks_GS'	-0.08602	0.031625	-2.7201	94	0.0077758	-0.14881	0.07677

Random effects covariance parameters:

Group: grand_animals (9 Levels)

Name1	Name2	Type	Estimate
{'(Intercept)'	{'(Intercept)'	{'std'}	0.071993

Group: Error

Name	Estimate
{'sqrt(Dispersion)'	0.02301