

Better-Than-Chance Classification for Signal Detection

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Abstract

[TODO]

1 Introduction

A common workflow in neuroimaging consists of fitting a classifier, and estimating its predictive accuracy using cross validation. Given that the cross validated accuracy is a random quantity, it is then common to test if the cross validated accuracy is significantly better than chance using a permutation test. Examples in the neuroscientific literature include Golland and Fischl [2003], Pereira et al. [2009], Varoquaux et al. [2016], and especially the recently popularized *multivariate pattern analysis* (MVPA) framework of Kriegeskorte et al. [2006]. This practice is also observed in very high profile publications in the genetics literature: Golub et al. [1999], Slonim et al. [2000], Radmacher et al. [2002], Mukherjee et al. [2003], Juan and Iba [2004], Jiang et al. [2008].

To fix ideas, we will adhere to a concrete example. In Gilron et al. [2016], the authors seek to detect brain regions which encode differences between vocal and non-vocal stimuli. Following the MVPA workflow, the localization problem is cast as a supervised learning problem: if the type of the stimulus can be predicted from the spatial activation pattern significantly better than chance, then a region is declared to encode vocal/non-vocal information. We call this an *accuracy test*, a.k.a. *class prediction* in Simon et al. [2003], or *pattern discrimination* in Pereira et al. [2009].

This same signal detection task can be also approached as a two-group multivariate test. Inferring that a region encodes vocal/non-vocal information, is essentially inferring that the spatial distribution of brain activations is different given a vocal/non-vocal stimulus. As put in Pereira et al. [2009]:

... the problem of deciding whether the classifier learned to discriminate the classes can be subsumed into the more general question as to whether there is evidence that the underlying distributions of each class are equal or not.

A practitioner may then call upon a two-group location test such as Hotelling’s T^2 [Anderson, 2003]. Alternatively, if the size of a brain region is too large compared to the number of observations, so that the spatial covariance cannot be fully estimated, then a high dimensional version of Hotelling’s test can be called upon, such as in Schäfer and Strimmer [2005] or Srivastava [2013]. For brevity, and in contrast to *accuracy tests*, we will call these two-sample multivariate tests simply *location tests*, also termed *class comparisons* in Simon et al. [2003].

At this point, it becomes unclear which is preferable: a location test or an accuracy test? The former with a heritage dating back to Hotelling [1931], and the latter being extremely popular, as the 959 citations¹ of Kriegeskorte et al. [2006] suggest.

The comparison between location and accuracy tests was precisely the goal of Ramdas et al. [2016], who compared the T^2 location test to the accuracy of *Fisher’s linear discriminant analysis* classifier (LDA). By comparing the rates of convergence of the powers to 1, Ramdas et al. [2016] concluded that accuracy and location tests are rate equivalent. Judging by convergence rates alone, not much is (asymptotically) lost by using an accuracy test.

Asymptotic relative efficiency measures (ARE) are typically used by statisticians to compare between test statistics with similar rates [van der Vaart, 1998]. The ARE between Hotelling’s T^2 (location) test and Fisher’s LDA (accuracy) test in Ramdas et al. [2016] is lower bounded by $\sqrt{2\pi} \approx 2.5$. This means that Fisher’s LDA requires at least 2.5 more samples to achieve the same (asymptotic) power than the T^2 test. In this light, the accuracy test is remarkably inefficient compared to the location test. For comparison, the t-test is only 1.04 more (asymptotically) efficient than Wilcoxon’s rank-sum test [Lehmann, 2009], so that an ARE of 2.5 is strong evidence in favor of the location test.

Before discarding accuracy tests as inefficient, we recall that Ramdas et al. [2016] analyzed a *half-sample* holdout. The authors conjectured that a leave-one-out approach, which makes more efficient use of the data, may have better performance. Also, the analysis in Ramdas et al. [2016] is asymptotic. This eschews the discrete nature of the accuracy statistic, which will be shown to have crucial impact. Since typical sample sizes in neuroscience are not large, we seek to study which test is to be preferred in finite samples?

¹GoogleScholar. Accessed on Aug 4, 2016.

66 Our conclusion will be quite simple: *location tests almost always have more*
 67 *power than accuracy tests.*

68 The main argument for our statement rests upon the observation that
 69 with typical sample sizes, the accuracy test statistic is highly discrete. Dis-
 70 crete test statistics are known to be conservative [Hemerik and Goeman,
 71 2014], since they are insensitive to mild perturbations of the data, and they
 72 cannot exhaust the permissible false positive rate. The degree of discretiza-
 73 tion is governed by the number of samples. In our neuroscience example
 74 from Gilron et al. [2016], the classification is performed based on 40 trials,
 75 so that the test statistic may assume only 40 possible values. This number
 76 of examples is not unusual if considering this is the number of subjects, or
 77 the number of trial-repeats in an neuroimaging study.

78 The discretization effect is aggravated if the test statistic is highly concen-
 79 trated. For an intuition consider the usage of a the *resubstitution accuracy*
 80 as a test statistic. This statistic simply means that the accuracy is not cross
 81 validated. If the data is high dimensional, the resubstitution accuracy will
 82 be very high due to over fitting [McLachlan, 1976, Theorem 1]. In an extreme
 83 case, the resubstitution accuracy will be 1 for the observed data, but also for
 84 any permutation. The concentration of resubstitution accuracy near 1, and
 85 its discreteness, render this test completely useless, with a power of 0.

86 To compare the power of accuracy tests and location tests in finite sam-
 87 ples, we perform a simulation study of a battery of test statistics. The main
 88 findings are reported in Section 4, and the intuition for our findings is pro-
 89 vided in Section 6, but first, the problem’s setup.

90 2 Problem setup

91 Let $y \in \mathcal{Y}$ be a class encoding. Let $x \in \mathcal{X}$ be a p dimensional feature vector.
 92 In our vocal/non-vocal example we have $\mathcal{Y} = \{-1, 1\}$ and p , the number of
 93 voxels in a brain region so that $\mathcal{X} = \mathbb{R}^{27}$.

94 Given n pairs of (x_i, y_i) , typically assumed i.i.d., a location test amounts
 95 to testing whether $x|y = 1$ has the the same distribution as $x|y = -1$.
 96 I.e., we test if the multivariate voxel activation pattern has the same dis-
 97 tribution when given a vocal stimulus, as when given a non-vocal stimulus.
 98 An accuracy test amounts to learning a predictive model $\hat{f}(x)$ from some
 99 assumed model class $\hat{f} \in \mathcal{F}$. The prediction accuracy, denoted $T_{\hat{f}}^{acc}$, is de-
 100 fined as the probability of a given classifier \hat{f} of making a correct prediction
 101 $T_{\hat{f}}^{acc} := Prob(\hat{f}(x) = y)$ when given a randomly drawn data point, (x, y) .
 102 A statistically significant “better than chance” estimate of $T_{\hat{f}}^{acc}$ is evidence

103 that the classes are distinct.

104 2.1 Candidate Tests

105 The design of a permutation test using the prediction accuracy, requires the
106 following design choices:

- 107 1. How to estimate accuracy?
- 108 2. Is the statistic cross validated or not?
- 109 3. For a K-fold cross validated test statistic: should the data be refolded
110 in each permutation?
- 111 4. Permute labels of features?
- 112 5. For a K-fold cross validated test statistic: should the data folding bal-
113 anced (a.k.a. stratified)?
- 114 6. How many folds?

115 We will now address these questions while bearing in mind that unlike the
116 typical supervised learning setup, we are not interested in an unbiased esti-
117 mate of the prediction error, but rather in the mere detection of a difference
118 between two groups.

119 **How to estimate accuracy?** Given a predictor \hat{f} , a natural test statis-
120 tic is some estimate of its accuracy $T_{\hat{f}}^{acc}$. Complicating matters: very low
121 accuracies, even 0, is evidence that the classes are separated, and we only
122 need to invert the predictions. We can thus consider $|T_{\hat{f}}^{acc} - 0.5|$ as the test
123 statistic. This, however, implies that if the classes are identical, random
124 guessing has 0.5 accuracy. This is not true if the classes are not balanced.
125 For unbalanced data the chance level is the probability of the minority class,
126 we denote by \hat{p}_{min} [Golland et al., 2005, Sec 4.1]. This suggests the following
127 test statistic $|T_{\hat{f}}^{acc} - \hat{p}_{min}|$. Since we will be aggregating these statistics over
128 random data sets where \hat{p}_{min} may vary, it seems appropriate to standard-
129 ize the scale of this statistic. We thus also consider the z-scored accuracy:
130 $|T_{\hat{f}}^{acc} - \hat{p}_{min}| / \sqrt{\hat{p}_{min}(1 - \hat{p}_{min})}$.

131 **Cross validate or not?** Were we interested in an unbiased estimator of
132 the prediction error, there is no question that some independent validation
133 is in order. Since we are merely interested in detecting a difference between
134 classes, a biased error estimate is not an issue provided that bias is consistent
135 over all permutations. The underlying intuition is that if the exact same
136 computation is performed over all permutations, then a permutation test
137 will be “fair”, i.e., will not inflate the false positive rate. We will thus be
138 considering both cross validated accuracies, and resubstitution accuracies as
139 our test statistics, a.k.a. *resubstitution classification*.

140 **Refolding?** The standard practice in neuroimaging is to refold the data
141 after each permutation [Pereira et al., 2009]. This is imperative if permuting
142 labels while aiming at balanced data folds. This is not, however, imperative
143 in general. For simplicity, we will adhere to the standard practice of refolding
144 the data within each permutation.

145 **Permute labels of features?** While seemingly identical, the compound-
146 ing of permutations with data foldings renders these two approaches distinct.
147 As an example, consider balanced (stratified) K-fold cross validation where
148 the initial data folding is balanced. After a label permutation, the original
149 folds will probably not be balanced. If the *features* are permuted, then the
150 labels conserve their original fold assignments, and the original folds are bal-
151 anced after each permutation. Since we only report results while refolding
152 the data in each permutation, then the only difference between permuting
153 labels and permuting features seems to be a computational one. We thus
154 adhere to the more common, albeit computationally less efficient practice of
155 permuting labels.

156 **Balanced folding?** As already implied, a standard practice when cross
157 validating is to constrain the data folds to be balanced (i.e. stratified). This
158 is well justified when aiming at unbiased accuracy estimation. This also
159 simplifies matter when aiming at signal detection, as can be seen from the
160 above discussion of the appropriate test statistic. On the other hand, it
161 may complicate matters, as can be seen from the above discussion on label
162 versus feature permutation. We will report results with both balanced and
163 unbalanced data foldings, only to discover, it does not really matter.

164 **How many folds?** Different authors suggest different rules for the num-
165 ber of folds. We will be varying the number of folds. This will affect the
166 concentration of permutation distribution of the estimated accuracy, which

will have a crucial effect on the conservativeness of the accuracy test. Our intuition suggests that since more folds imply a less concentrated estimate, then leave-one-out should be the less conservative, and 2-fold should be the most conservative.

The of tests we will be comparing is collected for convenience in Table 1.

Name	Basis	CV	Accuracy	Parameters
Hotelling	Hotelling	—	—	shrink=FALSE
Hotelling.shrink	Hotelling	—	—	shrink=TRUE
lda.CV.1	LDA	TRUE	accuracy	—
lda.CV.2	LDA	TRUE	z-accuracy	—
lda.noCV.1	LDA	FALSE	accuracy	—
lda.noCV.2	LDA	FALSE	z-accuracy	—
sd	SD	—	—	—
svm.CV.1	SVM	TRUE	accuracy	cost=1e1
svm.CV.2	SVM	TRUE	accuracy	cost=1e-1
svm.CV.3	SVM	TRUE	z-accuracy	cost=1e1
svm.CV.4	SVM	TRUE	z-accuracy	cost=1e-1
svm.noCV.1	SVM	FALSE	accuracy	cost=1e1
svm.noCV.2	SVM	FALSE	accuracy	cost=1e-1
svm.noCV.3	SVM	FALSE	z-accuracy	cost=1e1
svm.noCV.4	SVM	FALSE	z-accuracy	cost=1e-1

Table 1: This table enumerates the various test statistics we will be studying. Three are location tests: Hotelling, Hotelling.shrink, and sd. *Hotelling* is the classical two-group T^2 statistic. *Hotelling.shrink* is a high dimensional version with the regularized covariance in Schäfer and Strimmer [2005]. *sd* is another high dimensional version of the T^2 , from Srivastava et al. [2013]. The rest of the tests are variations of the linear SVM, and Fisher’s LDA, with varying accuracy measures, cross validated or not, and varying tuning parameters. For example, *svm.CV.4* is a linear SVM, with *libsvm*’s cost parameter set at 0.1, using the cross validated z-scored accuracy ($|T_f^{acc} - \hat{p}_{max}| / \sqrt{\hat{p}_{max}(1 - \hat{p}_{max})}$, see Section 2.1). Another example is *lda.noCV.1*, which is Fisher’s LDA, returning the resubstitution accuracy, without cross validation, and without z-scoring.

172

3 Controlling the False Positive Rate

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Figure 1 demonstrates that all of the tests considered conserve the desired 0.05 false positive rate, up to varying levels of conservatism. This can be seen from the fact that the probability of rejection is no larger than 0.05 in the absence of any effect, encoded by a red circle. This is true, in particular

177

178 if: (a) the folds are balanced or not, (b) the tuning parameters of some test
 179 statistic are varied, (d) the number of folds is varied. We also observe that
 180 the most conservative tests are the resubstitution accuracy measures. We
 181 return to this matter in the Discussion.

Figure 1: The power of a permutation test with various test statistics. The power on the x axis. Effect are color and shape coded. The various statistics on the y axis. Their details are given in Table 1. Effects vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). Simulation details in Appendix B. Cross-validation was performed with balanced (stratified) and unbalanced data folding. See sub-captions.



182 4 Power

183 Having established that all of the tests in our battery control the false positive
 184 rate, it remains to be seen if they have similar power— especially when
 185 comparing the power of location tests to accuracy tests. From the simulation
 186 results reported in Appendix C we collect the following insights:

- 187 1. Location tests have more power than accuracy tests in all our configurations.
 188
- 189 2. The conservativeness decays as the sample grows (Figures 6a, 6b and
 190 7a), supporting the statement that discretization is responsible for
 191 power loss.

- 192 3. The power may increase or decrease with the number of folds (Figure 3).
- 193 4. The z-scoring of the accuracies was introduced to deal with unbalanced
194 foldings. If the z-scoring has any effect at all, it merely kills power.
195 There is really no reason to use it.
- 196 5. Both accuracy and location tests are inappropriate for scale alternatives
197 (Figure 5a). This was to be expected and is reported mostly as a sanity
198 check.
- 199 6. The presence of heavy tails (Figure 5b) may reduce power, but does
200 not quantitatively change results.
- 201 7. Balanced folding typically has no effect. It increased power only for
202 the z-scored statistics (Figure 1). This is surprising given they were
203 precisely designed to deal with the presence of imbalance.
- 204 8. Varying the accuracy test’s tuning parameter, such as the cost (i.e.
205 margins) has no effect on the power of the test.
- 206 9. Correlation between coordinates, mimicking temporal correlation in
207 fMRI data, has no effect on conclusions, since all test statistics account
208 for this correlation (Figure 7b).

209 The major insight from simulations is that the use of accuracy tests for
210 signal detection is underpowered compared to location tests. We now verify
211 this finding on a neuroimaging dataset.

212 5 Neuroimaging Example

213 Figure 2 is an application of both a location and an accuracy test to the data
214 of Pernet et al. [2015]. The authors of Pernet et al. [2015] collected fMRI
215 data while subjects were exposed to the sounds of human speech (vocal),
216 and other non-vocal sounds. Each subject was exposed to 20 sounds of each
217 type, totaling in $n = 40$ trials in each scan. The study was rather large and
218 consisted of about 200 subjects. The data was kindly made available by the
219 authors at the OpenfMRI website².

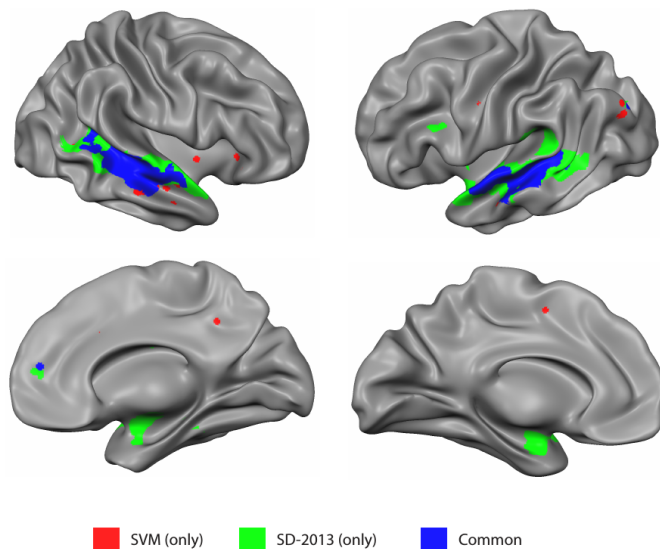
220 We perform group inference using within-subject permutations using the
221 pipeline of Stelzer et al. [2013], which was also reported in Gilron et al. [2016].
222 For completeness, the pipeline is described in Appendix A. To demonstrate

²<https://openfmri.org/>

our point, we compare the *sd* location test with the *svm.cv.1* accuracy test (see Table 1 for the definition of these statistics).

In agreement with our simulation results, the location test (*sd*) discovers more brain regions when compared to an accuracy test (*svm.cv.1*). The former discovers 1,232 regions, while the latter only 441, as depicted in Figure 2. We emphasize that both test statistics were compared with the same permutation scheme, and the same error controls, so that any difference in detections is due to their different power.

Having established that accuracy tests are underpowered both in simulation and in application, we wish to identify the conditions under which this will occur, and discuss implications on the practice of accuracy tests.



*Figure 2: Brain regions encoding information discriminating between vocal and non-vocal stimuli. Map reports the centers of 27-voxel sized spherical regions, as discovered by an accuracy test (*svm.cv.1*), and a location test (*sd*). *svm.cv.1* was computed using 5-fold cross validation, and a cost parameter of 1. Region-wise significance was determined using the permutation scheme of Stelzer et al. [2013], followed by region-wise $FDR \leq 0.05$ control using the Benjamini-Hochberg procedure [Benjamini and Hochberg, 1995]. Number of permutations equals 400. The location test detect 1,232 regions, and the accuracy test 441, 399 of which are common to both. For the details of the analysis see Appendix A and Gilron et al. [2016].*

234 6 Discussion

235 We have set out to understand which of the tests is more powerful: the ac-
236 curacy test or the location test. Using simulations, we have concluded that
237 the location tests are preferable. Their high dimensional versions such as
238 Srivastava [2013] and Schäfer and Strimmer [2005] are preferable for typical
239 neuroimaging problems such as MVPA. We attribute this to several phe-
240 nomena: (a) Discretization introduced in finite samples by the accuracy test
241 statistic. (b) Inefficient use of the data for the validation holdout set. In our
242 high dimensional setup, we also confirmed that high-dimensional versions of
243 the T^2 test, such as Srivastava [2013] or Schäfer and Strimmer [2005] are
244 preferable over the original T^2 .

245 The sensitivity of the power to the number of folds suggests that most
246 of the power is lost due to the discretization and not to the holdout. The
247 degree of discretization is governed by the sample size. For this reason, an
248 asymptotic analysis such as Ramdas et al. [2016] may uncover the holdout
249 inefficiency, but will not uncover the discretization effect. The practical ad-
250 vice for the practitioner, is that for the purpose of signal detection, there
251 is typically a multivariate test (be it a location test or other), that is more
252 powerful than an accuracy test. There is also a good chance that it would
253 be easier to implement, since no validation will be involved.

254 6.1 Neyman-Pearson Classification

255 [TODO]

256 6.2 A good accuracy test

257 In Section 6.6 we discuss cases where an accuracy test cannot replace a
258 location test. For such cases we collect some conclusions from our simulations
259 on the best practices for accuracy tests.

- 260 1. The conservativeness due to discretization decreases with sample size.
- 261 2. Cross validating the accuracy statistic increases power in moderate
262 sample sizes. The power loss due to the holdout inefficiency is smaller
263 than the power loss due to the concentration of the resubstitution ac-
264 curacy. For large sample sizes, discretization and concentration have
265 weaker effects, and the cross validated accuracy may be replaced with
266 the computationally more efficiency resubstitution accuracy.

- 267 3. Permuting features is easier than permuting labels. It allows to preserve
268 balanced folds after a permutation without refolding, thus reducing
269 computational complexity.
- 270 4. There is no gain in z-scoring the accuracy scores.
- 271 5. Cross validated accuracy with balanced folds has more power than un-
272 balanced folds. We currently have no intuition to offer for this phe-
273 nomenon.
- 274 6. It is unclear what is the effect of the number of folds. More folds in-
275 crease power by reducing the number of holdout samples. On the other
276 hand, it increases the concentration of the accuracy statistic. Com-
277 pounded with the discreteness of the accuracy statistic, this decreases
278 power.
- 279 7. The value of the tuning parameters of a classifier have little to no
280 effect.

281 6.3 Related Literature

282 Olivetti et al. [2012] and Olivetti et al. [2014] also looked into a similar
283 problem as we do, namely, what is the preferred accuracy test? They propose
284 a new test they call an *independence test*, and demonstrate by simulation that
285 it has more power than other accuracy tests, and can deal with non-balanced
286 data sets. We did not include this test in the battery we compared, but we
287 note the following: (a) The independence test of Olivetti et al. [2012] relies on
288 a discrete test statistic. This means that in the cases that the accuracy test is
289 called upon for discriminating populations, it will probably be underpowered
290 compared to location tests. (b) In contrast with the underlying motivation
291 of Olivetti et al. [2012]’s independence test, we did not find that balancing
292 the data folds is crucial for an accuracy test.

293 Golland et al. [2005] study accuracy tests using simulation, real neu-
294 roimaging and genetic data, a theoretical analysis of the concentration of
295 the permutation p-value around. Their theoretical results formalize our in-
296 tuition on the effect of the concentration of the permutation p-value: The
297 finite Vapnik–Chervonenkis (VC) dimension requirement (Sec 4.3) prevents
298 the permutation p-value from concentrating. Their simulation study shows
299 that imbalance of the original data set may severely inflate the false alarm
300 rates (Sec 3). Like us, they find that if the original data set is balanced, then
301 the resubstitution error (and also the leave-one-out), are very conservative.
302 A fact we attribute to discretization and concentration. Golland et al. [2005]

also study the effect of the balance of the original data set, and find that if the original data set is highly unbalanced (governed by their p parameter), then the permutation tests can severely inflate the false positive rates.

6.4 Non-linear predictors

It may be argued that accuracy tests permits the separation between classes in high dimensions, such as in *reproducing kernel Hilbert spaces* (RKHS) by using non-linear predictors. This is immaterial since group tests can also be performed in higher dimensions (e.g. Gretton et al. [2012], or Heller et al. [2012]).

6.5 Ease of implementation

A very important point is the ease of implementation. The need for cross validation of the accuracy test greatly increases its computational complexity. Moreover, anyone who has actually implemented tests with discrete statistics, will attest they are considerably harder to implement. This is because their unforgiveness to the type of inequality. Indeed, mistakenly replacing a weak inequality with a strong inequality in one’s program may considerably change the results. This is not the case for continuous test statistics.

6.6 Reservations

Some reservations to the generality of our findings are in order. Firstly, not all accuracy tests are concerned with signal detection. Indeed, it is possible that the purpose of the test is not to detect a difference between classes, but to actually test the performance of a particular classifier. Examples include brain decoding for machine interfaces, and clinical diagnosis, where the presence of a medical condition is “predicted” from imaging data. [e.g. Olivetti et al., 2012, Wager et al., 2013]

Secondly, not all signals are manifested in a shift of the null distribution. Our focus on location tests is misleading. Perhaps Simon et al. [2003]’s *class comparison* is a more appropriate name, in that it does not only imply a shift alternative. Indeed, one may consider signal, i.e. effects, as a change in scale, such as the *spiked covariance* model. In this case, other-than-Hotelling type tests are appropriate [e.g. Nadler, 2008]. Tests have been proposed even when the nature of the difference between populations is left unspecified [e.g. Gretton et al., 2012]. The fact that in our neuroimaging example (Section 5) some brain regions were detected with the accuracy test, and not the location test, is consistent with this observation.

338 The reservation to the reservation is that the far greater power of the
339 location test, certainly in our example, does serve as an empirical evidence
340 that changes in location are a prevalent phenomenon.

341 **6.7 Epilogue**

342 Given all the above, we find the popularity of accuracy tests quite puzzling.
343 We believe this is due to a reversal of the inference cascade. Researchers
344 first fit a classifier, and then ask if the classes are any different. Were they
345 to start by asking if classes are any different, and only then try to classify,
346 then location tests would naturally arise as the preferred method. As put by
347 Ramdas et al. [2016]:

348 The recent popularity of machine learning has resulted in the ex-
349 tensive teaching and use of prediction in theoretical and applied
350 communities and the relative lack of awareness or popularity of
351 the topic of Neyman-Pearson style hypothesis testing in the com-
352 puter science and related “data science” communities.

353 And more simply by Frank Harrell in the `CrossValidated` Q&A site³:

354 ... your use of proportion classified correctly as your accuracy
355 score. This is a discontinuous improper scoring rule that can be
356 easily manipulated because it is arbitrary and insensitive.

³[http://stats.stackexchange.com/questions/17408/
how-to-assess-statistical-significance-of-the-accuracy-of-a-classifier](http://stats.stackexchange.com/questions/17408/how-to-assess-statistical-significance-of-the-accuracy-of-a-classifier).

References

- T. W. Anderson. *An Introduction to Multivariate Statistical Analysis*. Wiley-Interscience, Hoboken, NJ, 3 edition edition, July 2003. ISBN 978-0-471-36091-9.
- Y. Benjamini and Y. Hochberg. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *JOURNAL-ROYAL STATISTICAL SOCIETY SERIES B*, 57:289–289, 1995.
- R. Gilron, J. Rosenblatt, O. Koyejo, R. A. Poldrack, and R. Mukamel. Quantifying spatial pattern similarity in multivariate analysis using functional anisotropy. *arXiv:1605.03482 [q-bio]*, May 2016.
- P. Golland and B. Fischl. Permutation tests for classification: towards statistical significance in image-based studies. In *IPMI*, volume 3, pages 330–341. Springer, 2003.
- P. Golland, F. Liang, S. Mukherjee, and D. Panchenko. Permutation Tests for Classification. In P. Auer and R. Meir, editors, *Learning Theory*, number 3559 in Lecture Notes in Computer Science, pages 501–515. Springer Berlin Heidelberg, June 2005. ISBN 978-3-540-26556-6 978-3-540-31892-7. doi: 10.1007/11503415_34.
- T. R. Golub, D. K. Slonim, P. Tamayo, C. Huard, M. Gaasenbeek, J. P. Mesirov, H. Coller, M. L. Loh, J. R. Downing, M. A. Caligiuri, C. D. Bloomfield, and E. S. Lander. Molecular Classification of Cancer: Class Discovery and Class Prediction by Gene Expression Monitoring. *Science*, 286(5439):531–537, Oct. 1999. ISSN 0036-8075, 1095-9203. doi: 10.1126/science.286.5439.531.
- A. Gretton, K. M. Borgwardt, M. J. Rasch, B. Schölkopf, and A. Smola. A Kernel Two-sample Test. *J. Mach. Learn. Res.*, 13:723–773, Mar. 2012. ISSN 1532-4435.
- R. Heller, Y. Heller, and M. Gorfine. A consistent multivariate test of association based on ranks of distances. *Biometrika*, page ass070, Dec. 2012. ISSN 0006-3444, 1464-3510. doi: 10.1093/biomet/ass070.
- J. Hemerik and J. Goeman. Exact testing with random permutations. *arXiv:1411.7565 [math, stat]*, Nov. 2014.
- H. Hotelling. The Generalization of Student’s Ratio. *The Annals of Mathematical Statistics*, 2(3):360–378, Aug. 1931. ISSN 0003-4851, 2168-8990. doi: 10.1214/aoms/1177732979.

- 392 W. Jiang, S. Varma, and R. Simon. Calculating confidence intervals for
393 prediction error in microarray classification using resampling. *Statistical*
394 *Applications in Genetics and Molecular Biology*, 7(1), 2008.
- 395 L. Juan and H. Iba. Prediction of tumor outcome based on gene expression
396 data. *Wuhan University Journal of Natural Sciences*, 9(2):177–182, Mar.
397 2004. ISSN 1007-1202, 1993-4998. doi: 10.1007/BF02830598.
- 398 N. Kriegeskorte, R. Goebel, and P. Bandettini. Information-based functional
399 brain mapping. *Proceedings of the National Academy of Sciences of the*
400 *United States of America*, 103(10):3863–3868, July 2006. ISSN 0027-8424,
401 1091-6490. doi: 10.1073/pnas.0600244103.
- 402 E. L. Lehmann. Parametric versus nonparametrics: two alternative method-
403 ologies. *Journal of Nonparametric Statistics*, 21(4):397–405, 2009. ISSN
404 1048-5252. doi: 10.1080/10485250902842727.
- 405 G. J. McLachlan. The bias of the apparent error rate in discriminant analysis.
406 *Biometrika*, 63(2):239–244, Jan. 1976. ISSN 0006-3444, 1464-3510. doi:
407 10.1093/biomet/63.2.239.
- 408 S. Mukherjee, P. Tamayo, S. Rogers, R. Rifkin, A. Engle, C. Campbell,
409 T. R. Golub, and J. P. Mesirov. Estimating dataset size requirements
410 for classifying DNA microarray data. *Journal of Computational Biology:*
411 *A Journal of Computational Molecular Cell Biology*, 10(2):119–142, 2003.
412 ISSN 1066-5277. doi: 10.1089/106652703321825928.
- 413 B. Nadler. Finite sample approximation results for principal component
414 analysis: A matrix perturbation approach. *The Annals of Statistics*, 36
415 (6):2791–2817, Dec. 2008. ISSN 0090-5364, 2168-8966. doi: 10.1214/
416 08-AOS618.
- 417 E. Olivetti, S. Greiner, and P. Avesani. Induction in Neuroscience with
418 Classification: Issues and Solutions. In G. Langs, I. Rish, M. Grosse-
419 Wentrup, and B. Murphy, editors, *Machine Learning and Interpretation*
420 *in Neuroimaging*, number 7263 in Lecture Notes in Computer Science,
421 pages 42–50. Springer Berlin Heidelberg, 2012. ISBN 978-3-642-34712-2
422 978-3-642-34713-9. doi: 10.1007/978-3-642-34713-9_6.
- 423 E. Olivetti, S. Greiner, and P. Avesani. Statistical independence for the
424 evaluation of classifier-based diagnosis. *Brain Informatics*, 2(1):13–19, Dec.
425 2014. ISSN 2198-4018, 2198-4026. doi: 10.1007/s40708-014-0007-6.

- 426 F. Pereira, T. Mitchell, and M. Botvinick. Machine learning classifiers and
427 fMRI: A tutorial overview. *NeuroImage*, 45(1, Supplement 1):S199–S209,
428 Mar. 2009. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2008.11.007.
- 429 C. R. Pernet, P. McAleer, M. Latinus, K. J. Gorgolewski, I. Charest, P. E. G.
430 Bestelmeyer, R. H. Watson, D. Fleming, F. Crabbe, M. Valdes-Sosa, and
431 P. Belin. The human voice areas: Spatial organization and inter-individual
432 variability in temporal and extra-temporal cortices. *NeuroImage*, 119:164–
433 174, Oct. 2015. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2015.06.050.
- 434 M. D. Radmacher, L. M. McShane, and R. Simon. A Paradigm for
435 Class Prediction Using Gene Expression Profiles. *Journal of Computa-*
436 *tional Biology*, 9(3):505–511, June 2002. ISSN 1066-5277. doi: 10.1089/
437 106652702760138592.
- 438 A. Ramdas, A. Singh, and L. Wasserman. Classification Accuracy as a Proxy
439 for Two Sample Testing. *arXiv:1602.02210 [cs, math, stat]*, Feb. 2016.
- 440 J. Schäfer and K. Strimmer. A Shrinkage Approach to Large-Scale Covariance
441 Matrix Estimation and Implications for Functional Genomics. *Statistical*
442 *Applications in Genetics and Molecular Biology*, 4(1), Jan. 2005. ISSN
443 1544-6115. doi: 10.2202/1544-6115.1175.
- 444 R. Simon, M. D. Radmacher, K. Dobbin, and L. M. McShane. Pitfalls in the
445 Use of DNA Microarray Data for Diagnostic and Prognostic Classification.
446 *Journal of the National Cancer Institute*, 95(1):14–18, Jan. 2003. ISSN
447 0027-8874, 1460-2105. doi: 10.1093/jnci/95.1.14.
- 448 D. K. Slonim, P. Tamayo, J. P. Mesirov, T. R. Golub, and E. S. Lander. Class
449 Prediction and Discovery Using Gene Expression Data. In *Proceedings of*
450 *the Fourth Annual International Conference on Computational Molecular*
451 *Biology*, RECOMB ’00, pages 263–272, New York, NY, USA, 2000. ACM.
452 ISBN 978-1-58113-186-4. doi: 10.1145/332306.332564.
- 453 M. S. Srivastava. On testing the equality of mean vectors in high dimension.
454 *Acta et Commentationes Universitatis Tartuensis de Mathematica*, 17(1):
455 31–56, June 2013. ISSN 2228-4699. doi: 10.12697/ACUTM.2013.17.03.
- 456 M. S. Srivastava, S. Katayama, and Y. Kano. A two sample test in high
457 dimensional data. *Journal of Multivariate Analysis*, 114:349–358, Feb.
458 2013. ISSN 0047-259X. doi: 10.1016/j.jmva.2012.08.014.
- 459 J. Stelzer, Y. Chen, and R. Turner. Statistical inference and multiple test-
460 ing correction in classification-based multi-voxel pattern analysis (MVPA):

- 461 Random permutations and cluster size control. *NeuroImage*, 65:69–82, Jan.
462 2013. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2012.09.063.
- 463 A. W. van der Vaart. *Asymptotic Statistics*. Cambridge University Press,
464 Cambridge, UK ; New York, NY, USA, Oct. 1998. ISBN 978-0-521-49603-
465 2.
- 466 G. Varoquaux, P. R. Raamana, D. Engemann, A. Hoyos-Idrobo, Y. Schwartz,
467 and B. Thirion. Assessing and tuning brain decoders: cross-validation,
468 caveats, and guidelines. working paper or preprint, June 2016.
- 469 T. D. Wager, L. Y. Atlas, M. A. Lindquist, M. Roy, C.-W. Woo, and E. Kross.
470 An fMRI-Based Neurologic Signature of Physical Pain. *New England Jour-*
471 *nal of Medicine*, 368(15):1388–1397, Apr. 2013. ISSN 0028-4793. doi:
472 10.1056/NEJMoa1204471.

473 A Analysis pipeline

474 Here is the analysis pipeline of Stelzer et al. [2013] we for the auditory data in
 475 Gilron et al. [2016]. Denoting by $i = 1, \dots, I$ the subject index, $v = 1, \dots, V$
 476 the voxel index, and $s = 1, \dots, S$ the permutation index. Since regions⁴ are
 477 centered around a unique voxel, the voxel index v also serves as a unique
 478 region index. Algorithm 1 computes a region-wise test statistic, which is
 479 compared to its permutation null distribution computed by Algorithm 2.

Algorithm 1: Compute a group parametric map.

Data: fMRI scans, and experimental design.
Result: Brain map of group statistics: $\{\bar{T}_v\}_{v=1}^V$

```

1 for  $v \in 1, \dots, V$  do
2   for  $i \in 1, \dots, I$  do
3      $T_{i,v} \leftarrow$  test statistic for subject  $i$  in a region centered at  $v$ .
4    $\bar{T}_v \leftarrow \frac{1}{I} \sum_{i=1}^I T_{i,v}$ .
```

Algorithm 2: Compute a permutation p-value map.

Data: fMRI scans of 20 subjects, experimental design.
Result: Brain map of permutation p-values: $\{p_v\}_{v=1}^V$

```

1 for  $s \in 1, \dots, S$  do
2   permute labels;
3    $\bar{T}_v^s \leftarrow$  parametric map
```

⁴*searchlight* or *sphere* in the MVPA parlance

482 B Simulation Details

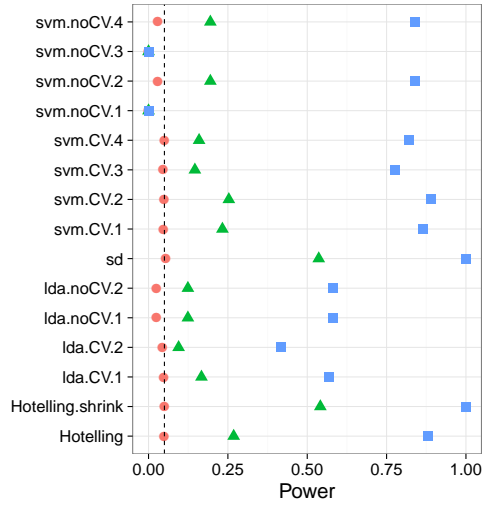
483 The following details are common to all the reported simulations, unless stated
484 otherwise in a figure’s caption. The R code for the simulations can be found
485 in [TODO].

486 Each simulation is based on 4,000 replications. In each replication, we
487 generate n i.i.d. samples from a shift model $\mathbf{x}_i = \mu \mathbf{y}_i^* + \eta_i$. Where $y_i^* = \{0, 1\}$
488 is the class of subject i in dummy coding. Recalling that $y_i = \{-1, 1\}$ is the
489 class in effect coding, then clearly $y_i = 2y_i^* - 1$. The noise is distributed as
490 $\eta_i \sim \mathcal{N}_p(0, \Sigma)$. The sample size $n = 40$. The dimension of the data is $p = 23$.
491 The covariance $\Sigma = I$. Effects, i.e. shifts μ , are equal coordinate p -vectors
492 with coordinates that vary over $\mu \in \{0, 1/4, 1/2\}$.

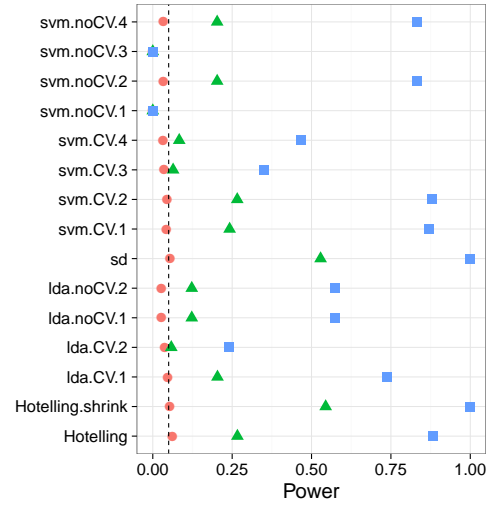
493 Having generated the data, we compute each of the test statistics in Ta-
494 ble 1. For test statistics that require data folding, we used 8 folds. We then
495 compute a permutation p-value by permuting the class labels, and recomput-
496 ing each test statistic. We perform 400 such permutations. We then reject
497 the $\mu_i = 0$ null hypothesis if the permutation p-value is smaller than 0.05.
498 The reported power is the proportion of replication where the permutation
499 p-value falls below 0.05.

C Simulation Results

Figure 3: Simulation details in Appendix B except the changes in the sub-captions.

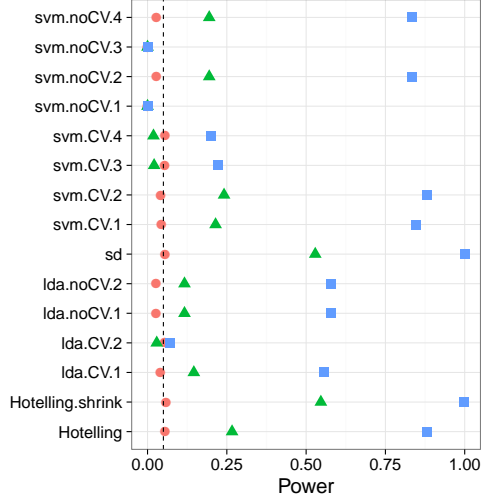


(a) 2-fold cross validation.
Balanced folding.

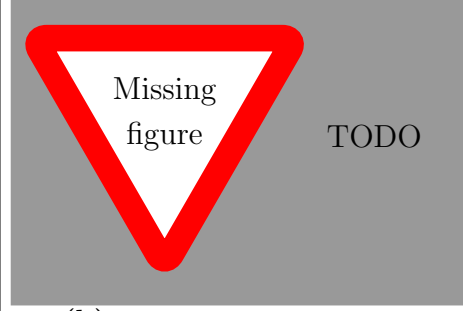


(b) 20-fold cross validation.
Balanced folding

Figure 4: *Simulation details in Appendix B except the changes in the sub-captions.*

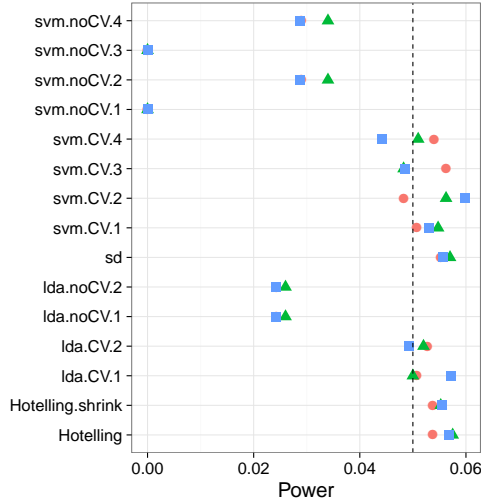


(a) **2-fold** cross validation.
Unbalanced folding.

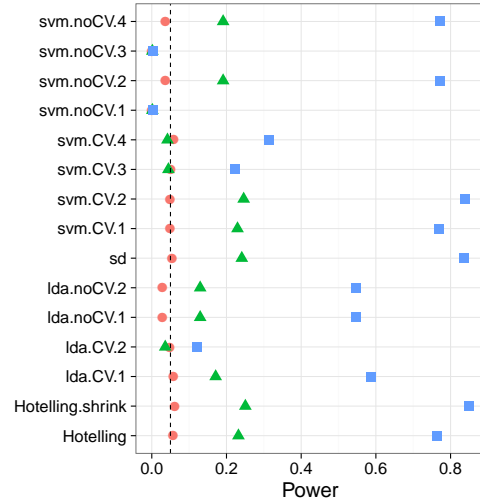


(b) **20-fold** cross validation.
Unbalanced folding.

Figure 5: *Simulation details in Appendix B except the changes in the sub-captions.*

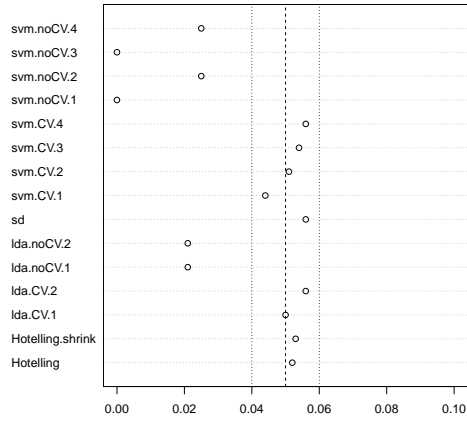


(a) **Scale Change:** $\mathbf{x}_i = \eta_i * \mu^{\mathbf{y}_i^*}$
so that the effect are a scale
change.

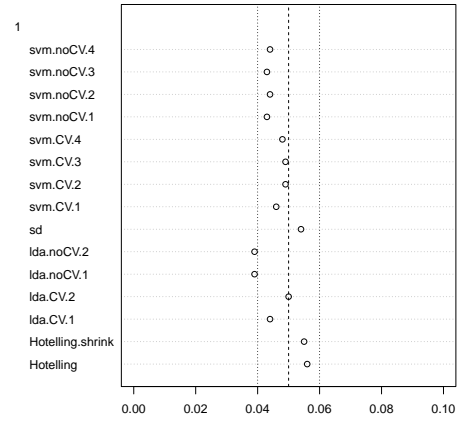


(b) **Heavytailed:** η_i is not
 p -variate Gaussian, but rather
 p -variate t , with $df = 3$.

Figure 6: *Simulation details in Appendix B except the changes in the sub-captions.*

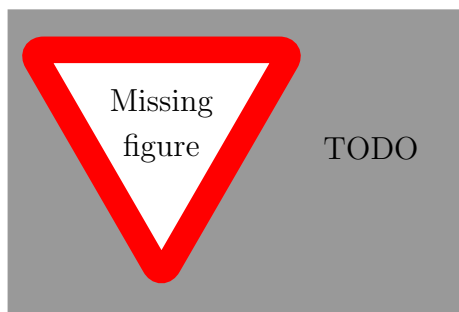


(a) **Low-Dimension:** False positive rates for $n = 40$.



(b) **High-Dimension:** False positive rates for $n = 400$.

Figure 7: Simulation details in Appendix B except the changes in the sub-captions.



(a) **High-Dimension, local alternative:** $n = 400$,
 $\mu \in \frac{\sqrt{40}}{\sqrt{400}} \times \{0, 1/4, 1/2\}$.



(b) **AR(1) dependence:**
 $\Sigma_{k,l} = \rho^{|k-l|}; \rho = 0.8$.