

# Better-Than-Chance Classification for Signal Detection

Jonathan Rosenblatt      Roei Gilron      Roy Mukamel

August 6, 2016

## 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 citations<sup>1</sup> 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?

---

<sup>1</sup>GoogleScholar. 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 be 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

173

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 website<sup>2</sup>.

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

---

<sup>2</sup><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 simulation study shows that the bal-  
296 ance of the original data has a strong impact on the bias of the permutation  
297 test. Their theoretical results formalize our intuition on the effect of the con-  
298 centration of the permutation p-value: The finite Vapnik–Chervonenkis (VC)  
299 dimension requirement [Golland et al., 2005, Sec 4.3] prevents the permuta-  
300 tion p-value from concentrating.

## 301 6.4 Non-linear predictors

302 It may be argued that accuracy tests permits the separation between classes  
303 in high dimensions, such as in *reproducing kernel Hilbert spaces* (RKHS) by  
304 using non-linear predictors. This is immaterial since group tests can also be  
305 performed in higher dimensions (e.g. Gretton et al. [2012], or Heller et al.  
306 [2012]).

## 307 6.5 Ease of implementation

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

## 315 6.6 Reservations

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

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

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

## 336 6.7 Epilogue

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

343       The recent popularity of machine learning has resulted in the ex-  
344       tensive teaching and use of prediction in theoretical and applied  
345       communities and the relative lack of awareness or popularity of  
346       the topic of Neyman-Pearson style hypothesis testing in the com-  
347       puter science and related “data science” communities.

348 And more simply by Frank Harrell in the `CrossValidated` Q&A site<sup>3</sup>:

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

---

<sup>3</sup>[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.

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

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



- 456 Random permutations and cluster size control. *NeuroImage*, 65:69–82, Jan.  
457 2013. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2012.09.063.
- 458 A. W. van der Vaart. *Asymptotic Statistics*. Cambridge University Press,  
459 Cambridge, UK ; New York, NY, USA, Oct. 1998. ISBN 978-0-521-49603-  
460 2.
- 461 G. Varoquaux, P. R. Raamana, D. Engemann, A. Hoyos-Idrobo, Y. Schwartz,  
462 and B. Thirion. Assessing and tuning brain decoders: cross-validation,  
463 caveats, and guidelines. working paper or preprint, June 2016.
- 464 T. D. Wager, L. Y. Atlas, M. A. Lindquist, M. Roy, C.-W. Woo, and E. Kross.  
465 An fMRI-Based Neurologic Signature of Physical Pain. *New England Jour-*  
466 *nal of Medicine*, 368(15):1388–1397, Apr. 2013. ISSN 0028-4793. doi:  
467 10.1056/NEJMoa1204471.

## 468 A Analysis pipeline

469 Here is the analysis pipeline of Stelzer et al. [2013] we for the auditory data in  
 470 Gilron et al. [2016]. Denoting by  $i = 1, \dots, I$  the subject index,  $v = 1, \dots, V$   
 471 the voxel index, and  $s = 1, \dots, S$  the permutation index. Since regions<sup>4</sup> are  
 472 centered around a unique voxel, the voxel index  $v$  also serves as a unique  
 473 region index. Algorithm 1 computes a region-wise test statistic, which is  
 474 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
```

---

<sup>4</sup>*searchlight* or *sphere* in the MVPA parlance

## 477 B Simulation Details

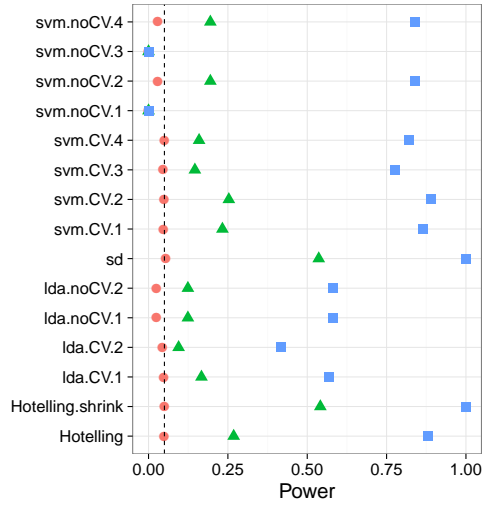
478 The following details are common to all the reported simulations, unless stated  
479 otherwise in a figure’s caption. The R code for the simulations can be found  
480 in [TODO].

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

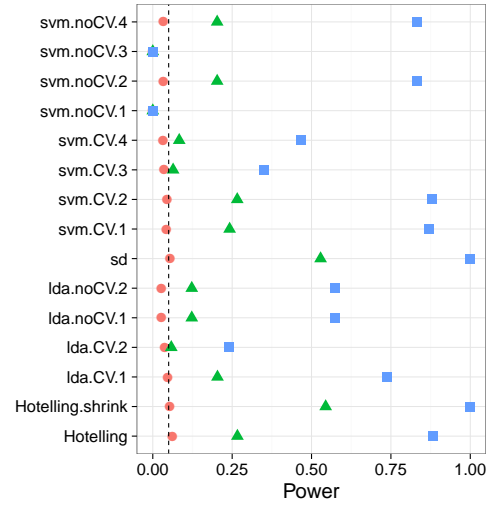
488 Having generated the data, we compute each of the test statistics in Ta-  
489 ble 1. For test statistics that require data folding, we used 8 folds. We then  
490 compute a permutation p-value by permuting the class labels, and recomput-  
491 ing each test statistic. We perform 400 such permutations.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

## C Simulation Results

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

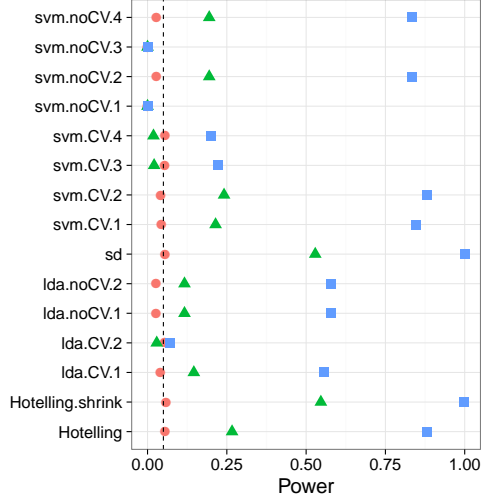


(a) 2-fold cross validation.  
Balanced folding.

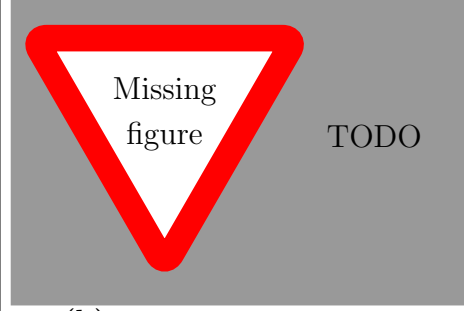


(b) 20-fold cross validation.  
Balanced folding

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

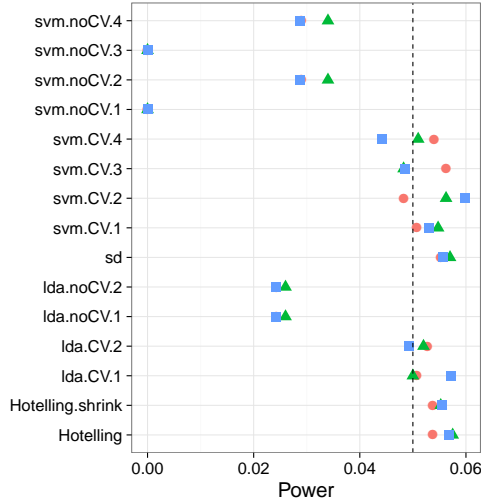


(a) **2-fold** cross validation.  
Unbalanced folding.

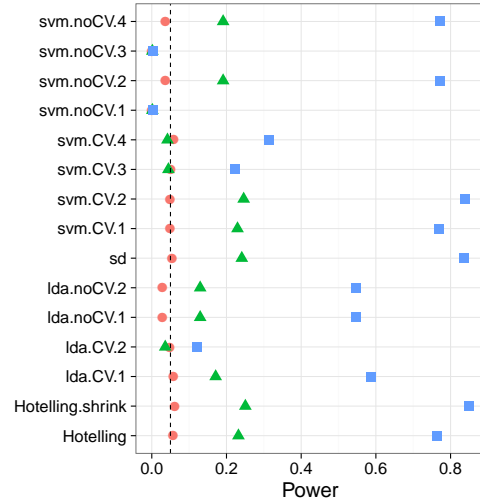


(b) **20-fold** cross validation.  
Unbalanced folding.

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

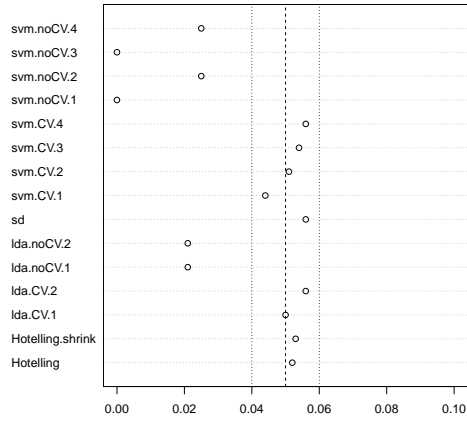


(a) **Scale Change:**  $\mathbf{x}_i = \eta_i * \mu^{\mathbf{y}_i^*}$   
so that the effect are a scale  
change.

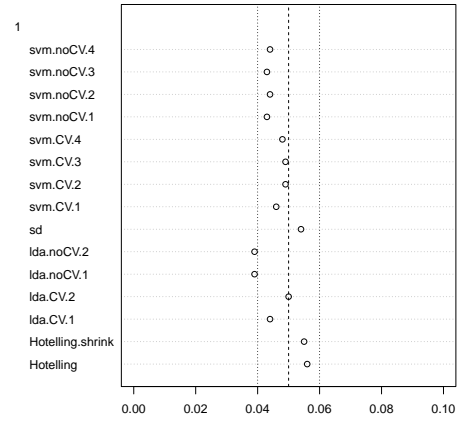


(b) **Heavytailed:**  $\eta_i$  is not  
 $p$ -variate Gaussian, but rather  
 $p$ -variate  $t$ , with  $df = 3$ .

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

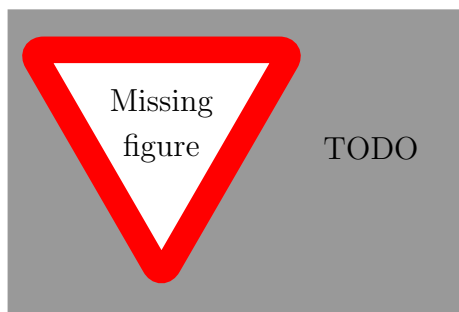


(a) **Low-Dimension:** False positive rates for  $n = 40$ .



(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:**  
 $\Sigma_{k,l} = \rho^{|k-l|}; \rho = 0.8$ .