

# 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*, or *pattern discrimination*.

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]:

26 ... the problem of deciding whether the classifier learned to dis-  
 27 criminate the classes can be subsumed into the more general ques-  
 28 tion as to whether there is evidence that the underlying distribu-  
 29 tions of each class are equal or not.

30 A practitioner may then call upon a two-group population test such as  
 31 Hotelling’s  $T^2$  [Anderson, 2003]. Alternatively, if the size of a brain re-  
 32 gion is large compared to the number of observations, so that the spatial  
 33 covariance cannot be fully estimated, then a high dimensional version of  
 34 Hotelling’s test can be called upon, such as in Schäfer and Strimmer [2005]  
 35 or Srivastava [2007]. For brevity, and in contrast to *accuracy tests*, we will  
 36 call any two-sample multivariate tests simply *population tests*, also termed  
 37 *class comparisons*. [TODO: rename to parameter test?]

38 At this point, it becomes unclear which is preferable: a population test or  
 39 an accuracy test? The former with a heritage dating back to Hotelling [1931],  
 40 and the latter being extremely popular, as the 959 citations<sup>1</sup> of Kriegeskorte  
 41 et al. [2006] suggest.

42 The comparison between location and accuracy tests was precisely the  
 43 goal of Ramdas et al. [2016], who compared the  $T^2$  population test to the  
 44 accuracy of *Fisher’s linear discriminant analysis* classifier (LDA). By com-  
 45 paring the rates of convergence of the powers to 1, Ramdas et al. [2016]  
 46 concluded that accuracy and population tests are rate equivalent.

47 Asymptotic relative efficiency measures (ARE) are typically used by statis-  
 48 ticians to compare between rate-equivalent test statistics [van der Vaart,  
 49 1998]. Ramdas et al. [2016] derive the asymptotic power functions of the  
 50 two test statistics, which allows to compute the ARE between Hotelling’s  $T^2$   
 51 (location) test and Fisher’s LDA (accuracy) test. Theorem 14.7 of van der  
 52 Vaart [1998] relates asymptotic power functions to ARE. Using the results of  
 53 Ramdas et al. [2016] we deduce that the ARE is lower bounded by  $2\pi \approx 6.3$ .  
 54 This means that Fisher’s LDA requires at least 6.3 more samples to achieve  
 55 the same (asymptotic) power than the  $T^2$  test. In this light, the accuracy  
 56 test is remarkably inefficient compared to the population test. For compar-  
 57 ison, the t-test is only 1.04 more (asymptotically) efficient than Wilcoxon’s  
 58 rank-sum test [Lehmann, 2009], so that an ARE of 6.3 is strong evidence in  
 59 favor of the population test.

60 Before discarding accuracy tests as inefficient, we recall that Ramdas  
 61 et al. [2016] analyzed a *half-sample* holdout. The authors conjectured that a  
 62 leave-one-out approach, which makes more efficient use of the data, may have  
 63 better performance. Also, the analysis in Ramdas et al. [2016] is asymptotic.  
 64 This eschews the discrete nature of the accuracy statistic, which will be

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<sup>1</sup>GoogleScholar. Accessed on Aug 4, 2016.

65 shown to have crucial impact. Since typical sample sizes in neuroscience are  
66 not large, we seek to study which test is to be preferred in finite samples?  
67 Our conclusion will be quite simple: *population tests almost always have more*  
68 *power than accuracy tests.*

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

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

89 To compare the power of accuracy tests and population tests in finite sam-  
90 ples, we perform a simulation study of a battery of test statistics. We start  
91 with formalizing the problem in Section 2. The main findings are reported  
92 in Sections 4 and 5. A discussion follows in Section 6.

## 93 2 Problem setup

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

97 Given  $n$  pairs of  $(x_i, y_i)$ , typically assumed i.i.d., a population test amounts  
98 to testing whether  $x|y = 1$  has the the same distribution as  $x|y = -1$ . I.e.,  
99 we test if the multivariate voxel activation pattern has the same distribution  
100 when given a vocal stimulus, as when given a non-vocal stimulus.

An accuracy test amounts to learning a predictive model and testing if its  
predictions  $y|x$  are better than chance. Denoting a dataset by  $\mathcal{S} := (x_i, y_i)_{i=1}^n$ ,

the a predictor,  $\mathcal{A}_{\mathcal{S}}(x) : \mathcal{X} \rightarrow \mathcal{Y}$ , is the output of a learning algorithm  $\mathcal{A}$  when applied to the dataset,  $\mathcal{A} : \mathcal{S} \rightarrow \mathcal{A}_{\mathcal{S}}(x)$ . The accuracy of predictor  $\mathcal{A}_{\mathcal{S}}(x)$  is defined as the probability of  $\mathcal{A}_{\mathcal{S}}(x)$  making a correct prediction. Denoting by  $\mathcal{P}$  the probability measure of  $(x, y)$ , and by  $\mathcal{P}^n$  the same for the i.i.d sample  $\mathcal{S}$ , then

$$\mathcal{E}_{\mathcal{A}_{\mathcal{S}}(x)} := \mathcal{P}(\mathcal{A}_{\mathcal{S}}(x) = y). \quad (1)$$

The accuracy of an algorithm  $\mathcal{A}$  is defined as the average accuracy, over all possible data sets

$$\mathcal{E}_{\mathcal{A}} := \int_{\mathcal{S}} \mathcal{E}_{\mathcal{A}_{\mathcal{S}}} d\mathcal{P}^n(\mathcal{S}). \quad (2)$$

101 Denoting an estimate of  $\mathcal{E}_{\mathcal{A}_{\mathcal{S}}(x)}$  by  $\hat{\mathcal{E}}_{\mathcal{A}_{\mathcal{S}}(x)}$ , and  $\mathcal{E}_{\mathcal{A}}$  by  $\hat{\mathcal{E}}_{\mathcal{A}}$ , a statistically sig-  
 102 nificant “better than chance” estimate of either, is evidence that the classes  
 103 are distinct. In a typical application, the predictor is not fixed, so that  $\hat{\mathcal{E}}_{\mathcal{A}}$ ,  
 104 and not  $\hat{\mathcal{E}}_{\mathcal{A}_{\mathcal{S}}(x)}$ , will be used for the testing.

105 Two popular estimates of  $\hat{\mathcal{E}}_{\mathcal{A}}$  are the *resubstitution estimate*, and the  
 106 V-fold cross validation (CV) estimate [Hastie et al., 2003].

**Definition 1** (Resubstitution accuracy). The resubstitution accuracy estimator,  $\hat{\mathcal{E}}_{\mathcal{A}}^{resub}$ , is defined as

$$\hat{\mathcal{E}}_{\mathcal{A}}^{Resub} := \frac{1}{n} \sum_{i=1}^n \mathcal{I}\{\mathcal{A}_{\mathcal{S}}(x_i) = y_i\}, \quad (3)$$

107 where  $\mathcal{I}\{A\}$  is the indicator function of event  $A$ .

**Definition 2** (V-fold CV). Denoting by  $\mathcal{S}^v$  the  $v$ ’th partition of the dataset, and by  $\mathcal{S}^{(v)}$  its complement, so that  $\mathcal{S}^v \cup \mathcal{S}^{(v)} = \cup_{v=1}^V \mathcal{S}^v = \mathcal{S}$ , the V-fold CV accuracy estimator,  $\hat{\mathcal{E}}_{\mathcal{A}}^{Vfold}$ , is defined as

$$\hat{\mathcal{E}}_{\mathcal{A}}^{Vfold} := \frac{1}{V} \sum_{v=1}^V \frac{1}{|\mathcal{S}^v|} \sum_{i \in \mathcal{S}^v} \mathcal{I}\{\mathcal{A}_{\mathcal{S}^{(v)}}(x_i) = y_i\}, \quad (4)$$

## 108 2.1 Candidate Tests

109 The design of a permutation test using  $\hat{\mathcal{E}}_{\mathcal{A}}$ , requires the following design  
 110 choices:

- 111 1. Is  $\hat{\mathcal{E}}_{\mathcal{A}}$  cross validated or not?

112 2. For a V-fold cross validated test statistic:

113 (a) Should the data be refolded in each permutation?

114 (b) Should the data folding be balanced (a.k.a. stratified)?

115 (c) How many folds?

116 3. How to estimate  $\hat{\mathcal{E}}_{\mathcal{A}}$ ?

117 We will now address these questions while bearing in mind that unlike  
118 the typical supervised learning setup, we are not interested in an unbiased  
119 estimate of  $\mathcal{E}_{\mathcal{A}}$ , but rather in its mere departure from chance level.

120 **Cross validate or not?** Given our goal, a biased estimate of  $\hat{\mathcal{E}}_{\mathcal{A}}$  is not a  
121 problem provided that bias is consistent over all permutations. The under-  
122 lying intuition is that a permutation test will be unbiased, provided that the  
123 exact same computation is performed over all permutations. We will thus  
124 be considering both cross validated accuracies, and *resubstitution accuracies*,  
125 where the accuracy is evaluated on the training set and not on a holdout.

126 **Balanced folding?** The standard practice when cross validating is to con-  
127 strain the data folds to be balanced, i.e. stratified [e.g. Ojala and Garriga,  
128 2010]. This means that each fold has the same number of examples from  
129 each class. We will report results with both balanced and unbalanced data  
130 foldings, only to discover, it does not really matter.

131 **Refolding?** The standard practice in neuroimaging is to permute labels  
132 and refold the data after each permutation, so that the balance of the classes  
133 in each fold is preserved. We will adhere to this practice due to its popularity,  
134 even though it can be simplified by permuting features instead of labels, as  
135 done by Golland et al. [2005].

136 **How many folds?** Different authors suggest different rules for the number  
137 of folds. We will be varying the number of folds, and ultimately discover that  
138 the power *decreases with the number of folds*.

**How to estimate accuracy?** Low accuracies, even 0, are evidence that  
the classes are separated so that for our purposes, we should consider the  
departure from chance level  $|\hat{\mathcal{E}}_{\mathcal{A}} - 0.5|$  as candidate test statistic. For un-  
balanced classes, chance level is not 0.5, but rather the probability of  
the majority class, we denote by  $\hat{\pi}$ . This suggests the following test statistic

$|\hat{\mathcal{E}}_{\mathcal{A}} - \hat{\pi}|$ . Since we will be aggregating these statistics over random data sets where  $\hat{\pi}$  may vary, it seems appropriate to standardize the scale. We thus study, along with the naive accuracy estimate,  $\hat{\mathcal{E}}_{\mathcal{A}}$ , also the *z-scored accuracy* of algorithm  $\mathcal{A}$ :

$$\hat{\mathcal{Z}}_{\mathcal{A}} := \frac{|\hat{\mathcal{E}}_{\mathcal{A}} - \hat{\pi}|}{\sqrt{\hat{\pi}(1 - \hat{\pi})}}. \quad (5)$$

139 Table 1 collects an initial battery of tests we will be comparing.

| Name             | Algorithm | Accuracy       | Z-scored | Parameters |
|------------------|-----------|----------------|----------|------------|
| Hotelling        | Hotelling | —              | —        | —          |
| Hotelling.shrink | Hotelling | —              | —        | —          |
| sd               | SD        | —              | —        | —          |
| lda.CV.1         | LDA       | V-fold         | FALSE    | —          |
| lda.CV.2         | LDA       | V-fold         | TRUE     | —          |
| lda.noCV.1       | LDA       | Resubstitution | FALSE    | —          |
| lda.noCV.2       | LDA       | Resubstitution | TRUE     | —          |
| svm.CV.1         | SVM       | V-fold         | FALSE    | cost=10    |
| svm.CV.2         | SVM       | V-fold         | FALSE    | cost=0.1   |
| svm.CV.3         | SVM       | V-fold         | TRUE     | cost=10    |
| svm.CV.4         | SVM       | V-fold         | TRUE     | cost=0.1   |
| svm.noCV.1       | SVM       | Resubstitution | FALSE    | cost=10    |
| svm.noCV.2       | SVM       | Resubstitution | FALSE    | cost=0.1   |
| svm.noCV.3       | SVM       | Resubstitution | TRUE     | cost=10    |
| svm.noCV.4       | SVM       | Resubstitution | TRUE     | cost=0.1   |

Table 1: This table collects the various test statistics we will be studying. Three are population 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 from 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 implemented with the *svm* R function [Meyer et al., 2015], the cost parameter set at 0.1, and using the cross validated z-scored accuracy in Eq. 5. Another example is *lda.noCV.1*, which is Fisher’s LDA, returning the resubstitution accuracy.

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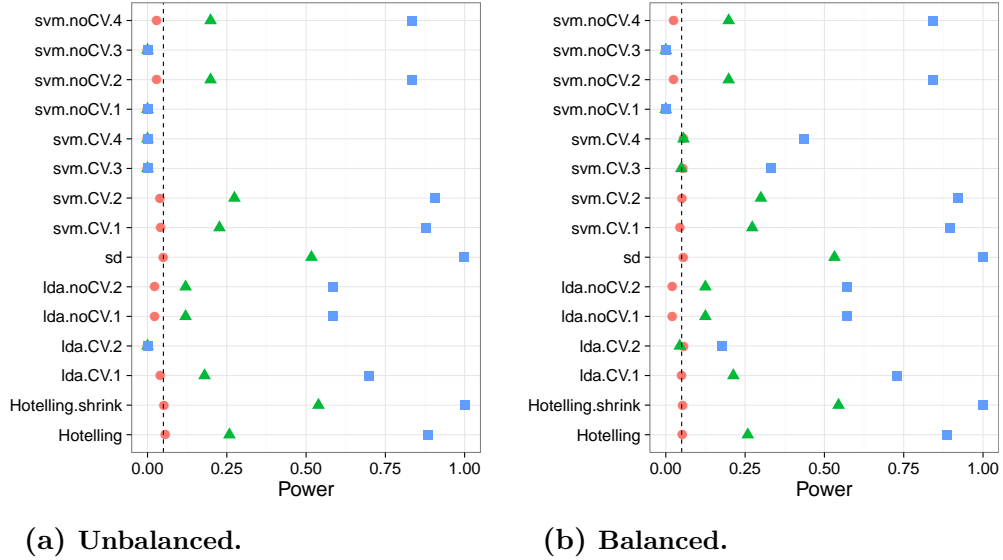
### 3 Controlling the False Positive Rate

Our simulation show 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 if:

- (a) The folds are balanced or not (Figures 1,6 and 7)
- (b) The tuning parameters are varied (cost=10 versus cost=0.1).
- (c) The number of folds is varied (Figures 6 and 7).
- (d) The noise is heavytailed (Figure 8b).
- (e) The problem is high or low dimensional (Figure 9.)
- (f) The noise is correlated (Figure 10b).

We also observe that the most conservative tests are the resubstitution accuracy statistics. We 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 and unbalanced data folding. See sub-captions.



## 155 4 Power

156 Having established that all of the tests in our battery control the false pos-  
157 itive rate, it remains to be seen if they have similar power– especially when  
158 comparing population tests to accuracy tests. From the simulation results  
159 reported in Appendix C we collect the following insights:

- 160 1. population tests have more power than accuracy tests in all our con-  
161 figurations.
- 162 2. The conservativeness decays as the sample grows (Figures 9a, 9b and  
163 10a)
- 164 3. For heavy tailed distributions (Figure 8b), the extra power of the loca-  
165 tion test vanishes.
- 166 4. The presence of correlations between coordinates reduces the signal to  
167 noise ratio (SNR), thus reduces power. More importantly, in the pres-  
168 ence of correlations the effect of regularization is amplified, increas-  
169 ing the power difference between regularized and non-regularized test  
170 statistics. Put differently- in low SNR regimes, regularization proves  
171 crucial (Figure 10b).
- 172 5. The z-scoring of the accuracies was introduced to deal with unbalanced  
173 foldings. If the z-scoring has any effect at all, it merely kills power.
- 174 6. Both accuracy and population tests are inappropriate for scale alter-  
175 natives (Figure 8a). This was to be expected and is reported mostly as  
176 a sanity check.
- 177 7. Balanced folding only affects the z-scored accuracy, in the opposite  
178 direction than we anticipated.
- 179 8. Increasing the SVM’s cost parameter, which reduces the number of  
180 support vectors entering the classifier, reduces power.

181 The major insight from simulations is that the use of accuracy tests for  
182 signal detection is underpowered compared to population tests. We now  
183 verify this finding on a neuroimaging dataset.

## 184 5 Neuroimaging Example

185 Figure 2 is an application of both a location and an accuracy test to the data  
186 of Pernet et al. [2015]. The authors of Pernet et al. [2015] collected fMRI



187 data while subjects were exposed to the sounds of human speech (vocal),  
 188 and other non-vocal sounds. Each subject was exposed to 20 sounds of each  
 189 type, totaling in  $n = 40$  trials in each scan. The study was rather large and  
 190 consisted of about 200 subjects. The data was kindly made available by the  
 191 authors at the OpenfMRI website<sup>2</sup>.

192 We perform group inference using within-subject permutations along the  
 193 analysis pipeline of Stelzer et al. [2013], which was also reported in Gilron  
 194 et al. [2016]. For completeness, the pipeline is described in Appendix A. To  
 195 demonstrate our point, we compare the *sd* population test with the *svm.cv.1*  
 196 accuracy test.

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

203 Having established that accuracy tests are typically underpowered for sig-  
 204 nal detection compared to population tests, we wish to identify the conditions  
 205 under which this will occur, and discuss practical implications.

## 206 6 Discussion

207 We have set out to understand which of the tests is more powerful: the  
 208 accuracy test or the population test. No amount of simulations can replace  
 209 the insight provided by a good closed-form analytic result. The finite sample  
 210 power of permutation tests is a formidable mathematical problem, so we  
 211 currently content ourselves with simulations. We have concluded that the  
 212 population tests are typically preferable. Their high dimensional versions,  
 213 such as Srivastava [2007] and Schäfer and Strimmer [2005], are particularly  
 214 well suited for neuroimaging problems such as MVPA. We attribute this  
 215 to several phenomena: (a) Discretization introduced in finite samples by  
 216 the accuracy test statistic. (b) Inefficient use of the data for the validation  
 217 holdout set. (c) Regularization crucial in high dimensional problems.

218 The presence of heavy tails shrinks the power advantage of the population  
 219 tests over accuracy tests. Our empirical example suggests that even if the  
 220 population test does not necessarily dominate the accuracy test in power,  
 221 empirically, it does have an advantage.

222 The degree of discretization is governed by the sample size. For this

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<sup>2</sup><https://openfmri.org/>



*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 population 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 population 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].

reason, an asymptotic analysis such as Ramdas et al. [2016] may uncover the holdout inefficiency, but will not uncover the discretization effect.

The practical advice for the practitioner, is that for the purpose of signal detection, there is typically a population test that is more powerful than an accuracy test. There is also a good chance that it would be easier to implement, and faster to run, since no cross validation will be involved.

## 6.1 Ease of implementation

A very important consideration 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 more prone to programming errors. This is because their unforgiveness to the type of inequalities used. Indeed, mistakenly replacing a weak inequality with a strong inequality in one's program

236 may considerably change the results. This is not the case for continuous test  
237 statistics.

## 238 6.2 Reservations

239 Some reservations to the generality of our findings are in order. Firstly,  
240 not all accuracy tests are concerned with signal detection. Consider brain  
241 decoding for machine interfaces, or clinical diagnosis, where the presence of  
242 a medical condition is predicted from imaging data [e.g. Olivetti et al., 2012,  
243 Wager et al., 2013]. In those examples, the purpose of the test is not to  
244 detect a difference between classes, but to actually test the performance of a  
245 particular classifier.

246 Secondly, it may be argued that accuracy tests permits the separation  
247 between classes in high dimensions, such as in *reproducing kernel Hilbert*  
248 *spaces* (RKHS) by using non-linear predictors. This is a false argument—  
249 accuracy test do not have any more flexibility than population tests. Indeed,  
250 it is possible to test for location in the same dimension the classifier is learned.  
251 Gretton et al. [2012] is an example where the test for location is performed  
252 in the RKHS of the data. It is also possible to test for the equality of two  
253 multivariate distributions [TODO: cite vogelstein]. On the other hand, based  
254 on our reported neuroimaging example, and others, we find that a population  
255 test in the original feature space is indeed a simple and powerful approach  
256 to signal detection.

## 257 6.3 A good accuracy test

258 For the cases a population test cannot replace an accuracy test, we collect  
259 some conclusions and best practices from our simulations. We give particular  
260 emphasis in this section to V-fold cross validation due to its popularity, but  
261 note that sampling the test set with replacement is actually preferable, as  
262 we discuss in Section 6.4.

263 **Sample size.** The conservativeness of accuracy tests decrease with sample  
264 size.

265 **Permute features.** Permuting features is easier than permuting labels.  
266 It allows to preserve balanced folds after a permutation without refolding.  
267 Although we did not find a power difference between balanced and  
268 unbalanced foldings.

269 **Use less folds.** For V-fold CV, power decreases as the number of folds  
270 increases. This is quite interesting since two phenomena compete as the  
271 number of folds increase: (a) the train set is larger so that better accuracies  
272 are achievable. (b) The test set is smaller so that the accuracy estimate is  
273 more variable. The decrease in power with increase fold number suggests  
274 that the latter dominates the former. Put differently: it is easier to detect a  
275 small stable departure from chance level, than a large but unstable one.

276 **Resubstitution accuracy in low dimension.** Resubstitution accuracy  
277 useful in low dimension. In high dimension, the power loss is considerable  
278 compared to a cross validated approach. We attribute this to the compound-  
279 ing of discretization and concentration effects: the difference between the  
280 sampling distribution of the resubstitution accuracy is simply indistinguish-  
281 able under the null and under the alternative. In low dimensional problems,  
282 the discretization is less impactful, and the computational burden of cross  
283 validation can be avoided by using the resubstitution accuracy. There is  
284 a fundamental difference between V-folding and resubstitution. The latter  
285 should not be thought of as the limit of the former.

286 **Regularize** Regularizing the accuracy test proves very useful in high di-  
287 mensional problems. Put differently: reducing variance by adding some bias  
288 is very useful to detect better-than-chance classification.

289 **Don't z-score.** There is no gain in z-scoring the accuracy scores. Our  
290 motivating rational was clearly flawed. [TODO: why?]

## 291 6.4 Smoothing accuracy estimates

292 It may be possible to alleviate the effect of discretization by appropriate  
293 cross-validation. The discreteness of the accuracy statistic is governed by  
294 the number of examples in the union (over all validation iterations) of test  
295 sets. For V-fold CV, for instance, this number is simply the sample size. This  
296 suggests that the accuracy can be “smoothed” by allowing the test sample to  
297 be drawn with replacement. The *bootstrap* may seem like a good candidate  
298 approach since it samples examples with replacement. It does so, however,  
299 for the train set, and not the test set. An algorithm that samples test sets  
300 with replacement is the *leave-one-out bootstrap estimator* (bLOO) and its  
301 derivation– the *0.632 bootstrap estimator* (b0.632) [Hastie et al., 2003, Sec  
302 7.11].

**Definition 3** (bLOO). The *leave-one-out bootstrap* estimate is the average accuracy of the holdout observations, over all bootstrap samples. Denoting by  $\mathcal{S}^b$ , a bootstrap sample  $b$ , sampled with replacement from  $\mathcal{S}$ . Also denote by  $C^{(i)}$  the index set of bootstrap samples,  $b$ , not containing observation  $i$ . The leave-one-out bootstrap estimate,  $\hat{\mathcal{E}}_{\mathcal{A}}^{bLOO}$ , is defined as:

$$\hat{\mathcal{E}}_{\mathcal{A}}^{bLOO} := \frac{1}{n} \sum_{i=1}^n \frac{1}{|C^{(i)}|} \sum_{b \in C^{(i)}} \mathcal{I}\{\mathcal{A}_{\mathcal{S}^b}(x_i) = y_i\}. \quad (6)$$

where  $|A|$  is the cardinality of set  $A$ . Equivalently [TODO: verify], denoting by  $S^{(b)}$  the indexes of observations,  $i$ , that are *not* in the bootstrap sample  $b$  and are not empty,

$$\hat{\mathcal{E}}_{\mathcal{A}}^{bLOO} = \frac{1}{B} \sum_{b=1}^B \frac{1}{|S^{(b)}|} \sum_{i \in S^{(b)}} \mathcal{I}\{\mathcal{A}_{\mathcal{S}^b}(x_i) = y_i\}. \quad (7)$$

**Definition 4** (b0.632). The b0.632 accuracy estimator,  $\hat{\mathcal{E}}_{\mathcal{A}}^{0.632}$ , is defined as

$$\hat{\mathcal{E}}_{\mathcal{A}}^{0.632} := 0.368 \hat{\mathcal{E}}_{\mathcal{A}}^{Resub} + 0.632 \hat{\mathcal{E}}_{\mathcal{A}}^{bLOO}. \quad (8)$$

Simulation results reported in Figure 3 with naming conventions in Table 2. It can be seen that selecting test sets with replacement does increase the power, when compared to V-fold cross validation, but still falls short from the power of population tests. It can also be seen that power increases with the number of bootstrap replications, itself reducing the level of discretization. The type of bootstrap, bLOO versus b0.632, does not change the power.

| Name       | Algorithm | Accuracy | B  | Z-scored | Parameters |
|------------|-----------|----------|----|----------|------------|
| lda.Boot.1 | LDA       | b0.632   | 10 | FALSE    | —          |
| lda.Boot.2 | LDA       | bLOO     | 10 | FALSE    | —          |
| svm.Boot.1 | SVM       | b0.632   | 10 | FALSE    | cost=1e1   |
| svm.Boot.2 | SVM       | bLOO     | 10 | FALSE    | cost=1e1   |
| svm.Boot.3 | SVM       | b0.632   | 50 | FALSE    | cost=1e1   |
| svm.Boot.4 | SVM       | bLOO     | 50 | FALSE    | cost=1e1   |

Table 2: The same as Table 1 for bootstrapped accuracy estimates. bLOO and b0.632 are defined in definitions 3 and 4 respectively.  $B$  denotes the number of Bootstrap samples.



*Figure 3: Bootstrap*— 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 tables 1 and 2. Effects vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). Simulation details in Appendix B.

## 311 6.5 High dimensional classifiers

312 Inspecting Figure 1a (for instance), it can be seen that Hotelling’s  $T^2$  test  
 313 has similar power to accuracy tests. It should thus be argued that the real  
 314 advantage of the population tests is due to their adaptation to high dimension  
 315 by regularization (*sd* and *Hotelling.shrink*), and not only to discretiza-  
 316 tion. To study this, we call upon several regularized classifiers, designed  
 317 for high dimensional problems. In the spirit of the regularized covariance of  
 318 *Hotelling.shrink*, we try an  $l_2$  regularized svm Friedman et al. [2010], and  
 319 shrinkage based LDA [Pang et al., 2009, Ramey et al., 2016]. In the spirit of  
 320 the diagonalized covariance of *sd*, we try a diagonalized LDA [Dudoit et al.,  
 321 2002], which can be thought of a method intersecting Fisher’s LDA and Naive  
 322 Bayes.

323 Simulation results reported in Figure 4 with naming conventions in Ta-  
 324 ble 3. It can be seen that regularizing a classifier in high dimension, just  
 325 like a parameter test, improves power. It can also be seen that (regularized)  
 326 parameter tests are still more powerful than (regularized) accuracy tests.

327 This was to be expected, since we already saw in (e.g. Figure 1a) that the  
 328 unregularized parameter test, *Hotelling*, is slightly more powerful than the  
 329 regularized accuracy test, *svm.CV.1* for instance.

330 We can compound regularization in this section with the bootstrapping  
 331 from Section 6.4, to improve finite sample power of the accuracy tests. This  
 332 is done in the *svm.highdim.2* test, which still falls short from the power of the  
 333 location tests, but is a much more powerful accuracy test than the original  
 334 non-regularized, V-fold validated, version of *svm.CV.1*.

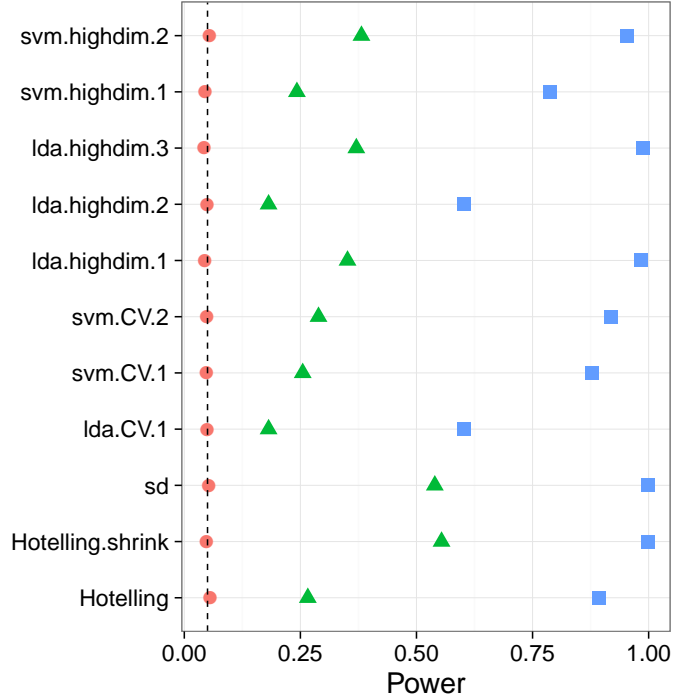
| Name          | Algorithm | Accuracy | Z-scored | Parameters      |
|---------------|-----------|----------|----------|-----------------|
| svm.highdim.1 | SVM       | V-fold   | FALSE    | cost=1e-1, V=4  |
| svm.highdim.2 | SVM       | b0.632   | FALSE    | cost=1e-1, B=50 |
| lda.highdim.1 | LDA       | V-fold   | FALSE    | V=4             |
| lda.highdim.2 | LDA       | V-fold   | FALSE    | V=4             |
| lda.highdim.3 | LDA       | V-fold   | FALSE    | V=4             |

Table 3: The same as Table 1 for regularized (high dimensional) predictors. *svm.highdim.1* is an  $l_2$  regularized SVM Friedman et al. [2010]. *svm.highdim.2* is the same with b0.632 instead of V-fold cross validation. *lda.highdim.1* is the Diagonal Linear Discriminant Analysis of Dudoit et al. [2002]. *lda.highdim.2* is the High-Dimensional Regularized Discriminant Analysis of Ramey et al. [2016]. *lda.highdim.3* is the Shrinkage-based Diagonal Linear Discriminant Analysis of Pang et al. [2009].

## 336 6.6 Related Literature

337 Ojala and Garriga [2010] study the power of two accuracy tests: one test-  
 338 ing the “no signal” null hypothesis, and the other testing the “independent  
 339 features” null hypothesis. They perform an asymptotic analysis, and a sim-  
 340 ulation study. They also apply various classifiers to various data sets. Their  
 341 emphasis is the effect of the underlying classifier on the power, and the po-  
 342 tential of the “independent features” test for feature selection. This is a very  
 343 different emphasis from our own.

344 Olivetti et al. [2012] and Olivetti et al. [2014] looked into the problem of  
 345 choosing a good accuracy test. They propose a new test they call an *indepen-*  
 346 *dence test*, and demonstrate by simulation that it has more power than other  
 347 accuracy tests, and can deal with non-balanced data sets. We did not include  
 348 this test in the battery we compared, but we note the following: (a) The in-



*Figure 4: HighDim Classifier*— 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 tables 1 and 3. Effects vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). Simulation details in Appendix B.

dependence test of Olivetti et al. [2012] relies on a discrete test statistic. It may thus be improved with the methods discussed in this section, before the application of Olivetti et al. [2012]’s independence test. (b) In contrast with the underlying motivation of Olivetti et al. [2012]’s independence test, we did not find that balancing the data folds is crucial for an accuracy test.

Golland et al. [2005] study accuracy tests using simulation, neuroimaging data, genetic data, and analytically. Their analytic results formalize our intuition from Section 1 on the effect of concentration of the accuracy statistic: The finite Vapnik–Chervonenkis (VC) dimension requirement [Golland and Fischl, 2003, Sec 4.3] prevents the permutation p-value from (asymptotically) concentrating near 1. Like ourselves, they also find that the power increases with the size of the test set (Figure 4, middle). This is seen in their Figure 4, where the size of the test-set,  $K$ , governs the discretization. Since they permute features, not labels, then all their permutation samples are balanced, and there is no issue of refolding.

Golland et al. [2005] simulate the power of accuracy tests by sampling



365 from a Gaussian mixture family of models, and not from a location family  
 366 as our own simulations. Under their model  $(x_i|y_i = 1) \sim p\mathcal{N}(\mu_1, I) +$   
 367  $(1 - p)\mathcal{N}(\mu_2, I)$  and  $(x_i|y_i = -1) \sim (1 - p)\mathcal{N}(\mu_1, I) + p\mathcal{N}(\mu_2, I)$ . Varying  $p$   
 368 interpolates between the null distribution ( $p = 0.5$ ) and a location shift model  
 369 ( $p = 0$ ). We now perform the same simulation as Golland et al. [2005], after  
 370 parameterizing  $p$  so that  $p = 0$  corresponds to the null model, and in the  
 371 same dimensionality as our previous simulations We find that also in this  
 372 mixture class of models a population test has more power than an accuracy  
 373 test (Figure 5).

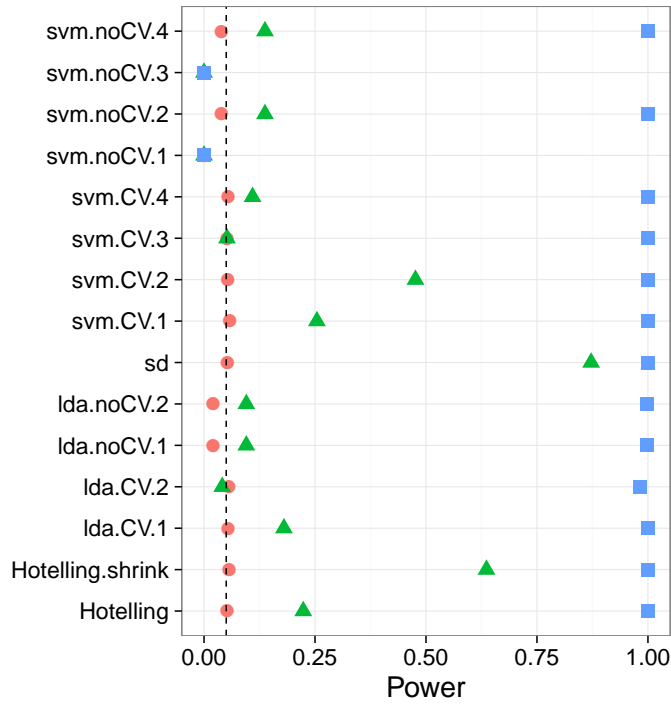


Figure 5: **Mixture**—  $\mathbf{x}_i = \chi_i \mu + \eta_i$ ;  $\chi_i = \{-1, 1\}$  and  $Prob(\chi_i = 1) = (1/2 - p)^{y_i^*} (1/2 + p)^{1-y_i^*}$ .  $\mu$  is a  $p$ -vector with  $3/\sqrt{p}$  in all coordinates. The effect,  $p$ , is color and shape coded and varies over 0 (red circle), 1/4 (green triangle) and 1/2 (blue square).

## 374 6.7 Epilogue

375 Given all the above, we find the popularity of accuracy tests quite puzzling.  
 376 We believe this is due to a reversal of the inference cascade. Researchers first  
 377 fit a classifier, and then ask if the classes are any different. Were they to  
 378 start by asking if classes are any different, and only then try to classify, then

379 population tests would naturally arise as the preferred method. As put by  
380 Ramdas et al. [2016]:

381       The recent popularity of machine learning has resulted in the ex-  
382       tensive teaching and use of prediction in theoretical and applied  
383       communities and the relative lack of awareness or popularity of  
384       the topic of Neyman-Pearson style hypothesis testing in the com-  
385       puter science and related “data science” communities.

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

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

## 390 **7 Acknowledgments**

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<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.
- S. Dudoit, J. Fridlyand, and T. P. Speed. Comparison of Discrimination Methods for the Classification of Tumors Using Gene Expression Data. *Journal of the American Statistical Association*, 97(457):77–87, Mar. 2002. ISSN 0162-1459. doi: 10.1198/016214502753479248.
- J. Friedman, T. Hastie, and R. Tibshirani. Regularization Paths for Generalized Linear Models via Coordinate Descent. *Journal of Statistical Software*, 33(1):1–22, 2010.
- 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.

- 425 T. Hastie, R. Tibshirani, and J. Friedman. *The Elements of Statistical Learn-*  
426 *ing*. Springer, July 2003. ISBN 0-387-95284-5.
- 427 J. Hemerik and J. Goeman. Exact testing with random permutations.  
428 *arXiv:1411.7565 [math, stat]*, Nov. 2014.
- 429 H. Hotelling. The Generalization of Student’s Ratio. *The Annals of Math-*  
430 *ematical Statistics*, 2(3):360–378, Aug. 1931. ISSN 0003-4851, 2168-8990.  
431 doi: 10.1214/aoms/1177732979.
- 432 W. Jiang, S. Varma, and R. Simon. Calculating confidence intervals for  
433 prediction error in microarray classification using resampling. *Statistical*  
434 *Applications in Genetics and Molecular Biology*, 7(1), 2008.
- 435 L. Juan and H. Iba. Prediction of tumor outcome based on gene expression  
436 data. *Wuhan University Journal of Natural Sciences*, 9(2):177–182, Mar.  
437 2004. ISSN 1007-1202, 1993-4998. doi: 10.1007/BF02830598.
- 438 N. Kriegeskorte, R. Goebel, and P. Bandettini. Information-based functional  
439 brain mapping. *Proceedings of the National Academy of Sciences of the*  
440 *United States of America*, 103(10):3863–3868, July 2006. ISSN 0027-8424,  
441 1091-6490. doi: 10.1073/pnas.0600244103.
- 442 E. L. Lehmann. Parametric versus nonparametrics: two alternative method-  
443 ologies. *Journal of Nonparametric Statistics*, 21(4):397–405, 2009. ISSN  
444 1048-5252. doi: 10.1080/10485250902842727.
- 445 G. J. McLachlan. The bias of the apparent error rate in discriminant analysis.  
446 *Biometrika*, 63(2):239–244, Jan. 1976. ISSN 0006-3444, 1464-3510. doi:  
447 10.1093/biomet/63.2.239.
- 448 D. Meyer, E. Dimitriadou, K. Hornik, A. Weingessel, and F. Leisch. *e1071:*  
449 *Misc Functions of the Department of Statistics, Probability Theory Group*  
450 *(Formerly: E1071), TU Wien*. 2015. R package version 1.6-7.
- 451 S. Mukherjee, P. Tamayo, S. Rogers, R. Rifkin, A. Engle, C. Campbell,  
452 T. R. Golub, and J. P. Mesirov. Estimating dataset size requirements  
453 for classifying DNA microarray data. *Journal of Computational Biology:*  
454 *A Journal of Computational Molecular Cell Biology*, 10(2):119–142, 2003.  
455 ISSN 1066-5277. doi: 10.1089/106652703321825928.
- 456 M. Ojala and G. C. Garriga. Permutation Tests for Studying Classifier Perfor-  
457 mance. *Journal of Machine Learning Research*, 11(Jun):1833–1863, 2010.  
458 ISSN 1533-7928.

- 459 E. Olivetti, S. Greiner, and P. Avesani. Induction in Neuroscience with  
460 Classification: Issues and Solutions. In G. Langs, I. Rish, M. Grosse-  
461 Wentrup, and B. Murphy, editors, *Machine Learning and Interpretation*  
462 *in Neuroimaging*, number 7263 in Lecture Notes in Computer Science,  
463 pages 42–50. Springer Berlin Heidelberg, 2012. ISBN 978-3-642-34712-2  
464 978-3-642-34713-9. doi: 10.1007/978-3-642-34713-9\_6.
- 465 E. Olivetti, S. Greiner, and P. Avesani. Statistical independence for the  
466 evaluation of classifier-based diagnosis. *Brain Informatics*, 2(1):13–19, Dec.  
467 2014. ISSN 2198-4018, 2198-4026. doi: 10.1007/s40708-014-0007-6.
- 468 H. Pang, T. Tong, and H. Zhao. Shrinkage-based Diagonal Discriminant  
469 Analysis and Its Applications in High-Dimensional Data. *Biometrics*, 65  
470 (4):1021–1029, Dec. 2009. ISSN 1541-0420. doi: 10.1111/j.1541-0420.2009.  
471 01200.x.
- 472 F. Pereira, T. Mitchell, and M. Botvinick. Machine learning classifiers and  
473 fMRI: A tutorial overview. *NeuroImage*, 45(1, Supplement 1):S199–S209,  
474 Mar. 2009. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2008.11.007.
- 475 C. R. Pernet, P. McAleer, M. Latinus, K. J. Gorgolewski, I. Charest, P. E. G.  
476 Bestelmeyer, R. H. Watson, D. Fleming, F. Crabbe, M. Valdes-Sosa, and  
477 P. Belin. The human voice areas: Spatial organization and inter-individual  
478 variability in temporal and extra-temporal cortices. *NeuroImage*, 119:164–  
479 174, Oct. 2015. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2015.06.050.
- 480 M. D. Radmacher, L. M. McShane, and R. Simon. A Paradigm for  
481 Class Prediction Using Gene Expression Profiles. *Journal of Computa-*  
482 *tional Biology*, 9(3):505–511, June 2002. ISSN 1066-5277. doi: 10.1089/  
483 106652702760138592.
- 484 A. Ramdas, A. Singh, and L. Wasserman. Classification Accuracy as a Proxy  
485 for Two Sample Testing. *arXiv:1602.02210 [cs, math, stat]*, Feb. 2016.
- 486 J. A. Ramey, C. K. Stein, P. D. Young, and D. M. Young. High-Dimensional  
487 Regularized Discriminant Analysis. *arXiv preprint arXiv:1602.01182*,  
488 2016.
- 489 J. Schäfer and K. Strimmer. A Shrinkage Approach to Large-Scale Covariance  
490 Matrix Estimation and Implications for Functional Genomics. *Statistical*  
491 *Applications in Genetics and Molecular Biology*, 4(1), Jan. 2005. ISSN  
492 1544-6115. doi: 10.2202/1544-6115.1175.

- 493 D. K. Slonim, P. Tamayo, J. P. Mesirov, T. R. Golub, and E. S. Lander. Class  
494 Prediction and Discovery Using Gene Expression Data. In *Proceedings of*  
495 *the Fourth Annual International Conference on Computational Molecular*  
496 *Biology*, RECOMB '00, pages 263–272, New York, NY, USA, 2000. ACM.  
497 ISBN 978-1-58113-186-4. doi: 10.1145/332306.332564.
- 498 M. S. Srivastava. Multivariate Theory for Analyzing High Dimensional Data.  
499 *Journal of the Japan Statistical Society*, 37(1):53–86, 2007. doi: 10.14490/  
500 jjss.37.53.
- 501 M. S. Srivastava, S. Katayama, and Y. Kano. A two sample test in high  
502 dimensional data. *Journal of Multivariate Analysis*, 114:349–358, Feb.  
503 2013. ISSN 0047-259X. doi: 10.1016/j.jmva.2012.08.014.
- 504 J. Stelzer, Y. Chen, and R. Turner. Statistical inference and multiple test-  
505 ing correction in classification-based multi-voxel pattern analysis (MVPA):  
506 Random permutations and cluster size control. *NeuroImage*, 65:69–82, Jan.  
507 2013. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2012.09.063.
- 508 A. W. van der Vaart. *Asymptotic Statistics*. Cambridge University Press,  
509 Cambridge, UK ; New York, NY, USA, Oct. 1998. ISBN 978-0-521-49603-  
510 2.
- 511 G. Varoquaux, P. R. Raamana, D. Engemann, A. Hoyos-Idrobo, Y. Schwartz,  
512 and B. Thirion. Assessing and tuning brain decoders: cross-validation,  
513 caveats, and guidelines. working paper or preprint, June 2016.
- 514 T. D. Wager, L. Y. Atlas, M. A. Lindquist, M. Roy, C.-W. Woo, and E. Kross.  
515 An fMRI-Based Neurologic Signature of Physical Pain. *New England Jour-*  
516 *nal of Medicine*, 368(15):1388–1397, Apr. 2013. ISSN 0028-4793. doi:  
517 10.1056/NEJMoa1204471.

## 518 A Analysis pipeline

519 Here is the analysis pipeline of Stelzer et al. [2013] we for the auditory data in  
 520 Gilron et al. [2016]. Denoting by  $i = 1, \dots, I$  the subject index,  $v = 1, \dots, V$   
 521 the voxel index, and  $s = 1, \dots, S$  the permutation index. Since regions<sup>4</sup> are  
 522 centered around a unique voxel, the voxel index  $v$  also serves as a unique  
 523 region index. Algorithm 1 computes a region-wise test statistic, which is  
 524 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

## 527 B Simulation Details

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

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

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



## C Simulation Results

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



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



Figure 8: Simulation details in Appendix B except the changes in the sub-captions.



Figure 9: Simulation details in Appendix B except the changes in the sub-captions.

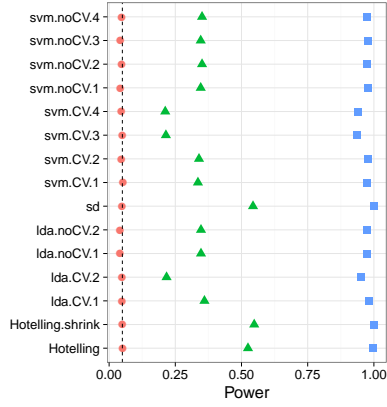


(a) Low-Dimension— False positive rates for  $n = 40$ .



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

Figure 10: Simulation details in Appendix B except the changes in the sub-captions.



(a) High-Dimension, local alternative—  
 $n = 400$ ,  
 $\mu \in \frac{1}{\sqrt{10}} \times \{0, 1/4, 1/2\}$ .



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