

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 citations¹ of Kriegeskorte
 41 et al. [2006] suggest.

42 The comparison between population 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 (population) 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

¹GoogleScholar. 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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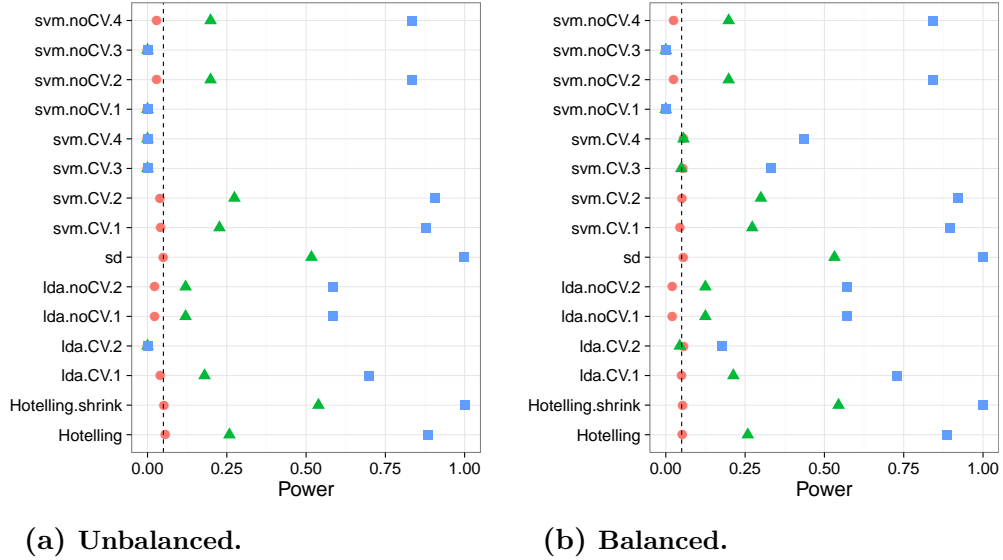
3 Controlling the False Positive Rate

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 pop-
165 ulation test vanishes.
- 166 4. Regularization is most beneficial to power in low signal to noise (SNR)
167 regimes. Low SNR may be the result of a high-dimensional problem,
168 or due to correlations. Indeed, the presence of positive correlations
169 amplifies the contribution of regularization to power ((Figure 10b)).
- 170 5. The z-scoring of the accuracies was introduced to deal with unbalanced
171 foldings. If the z-scoring has any effect at all, it merely kills power.
- 172 6. Both accuracy and population tests are inappropriate for scale alter-
173 natives (Figure 8a). This was to be expected and is reported mostly as
174 a sanity check.
- 175 7. Balanced folding only affects the z-scored accuracy, in the opposite
176 direction than we anticipated.
- 177 8. Increasing the SVM’s cost parameter, which reduces the number of
178 support vectors entering the classifier, reduces power.

179 The major insight from simulations is that the use of accuracy tests for
180 signal detection is underpowered compared to population tests. We have not
181 established, however, that the dominance of the population tests is not due to
182 their regularization. Indeed, the unregularized *Hotelling* test, is only slightly
183 superior to the accuracy tests. We return to this matter in Section 6.5. We
184 now verify our finding on a neuroimaging dataset.

185 5 Neuroimaging Example

186 Figure 2 is an application of both a population and an accuracy test to the
187 data of Pernet et al. [2015]. The authors of Pernet et al. [2015] collected fMRI
188 data while subjects were exposed to the sounds of human speech (vocal), and
189 other non-vocal sounds. Each subject was exposed to 20 sounds of each type,
190 totaling in $n = 40$ trials. The study was rather large and consisted of about
191 200 subjects. The data was kindly made available by the authors at the
192 OpenfMRI website².

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

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

204 6 Discussion

205 We have set out to understand which of the tests is more powerful: the ac-
206 curacy test or the population test. No amount of simulations can replace the
207 insight provided by a closed-form analytic result. The finite sample power
208 of permutation tests is a formidable mathematical problem, so we currently
209 content ourselves with simulations. We have concluded that the population
210 tests are typically preferable. Their high dimensional versions, such as Sri-
211 vastava [2007] and Schäfer and Strimmer [2005], are particularly well suited
212 for neuroimaging problems such as MVPA. We attribute this to several ef-
213 fects:

- 214 (a) The discrete nature of the accuracy test in finite samples.
- 215 (b) Inefficient use of the data when validating with a holdout set.
- 216 (c) The lack of regularization in high SNR regimes (high dimension or cor-
217 relations).

218
219 The degree of discretization is governed by the sample size. For this
220 reason, an asymptotic analysis such as Ramdas et al. [2016] may uncover

²<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].

the holdout inefficiency, but will not uncover the discretization effect. An asymptotic analysis of a finite complexity model would also fail to reveal the effect of the concentration of the resubstitution accuracy near 1. This effect would render the resubstitution estimates a legitimate asymptotic test, and a terrible finite sample test.

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

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.

234 6.1 Ease of implementation

235 A very important consideration is the ease of implementation. The need for
236 cross validation of the accuracy test greatly increases its computational com-
237 plexity. Moreover, anyone who has actually implemented tests with discrete
238 statistics, will attest they are more prone to programming errors. This is
239 because their unforgiveness to the type of inequalities used. Indeed, mistak-
240 enly replacing a weak inequality with a strong inequality in one’s program
241 may considerably change the results. This is not the case for continuous test
242 statistics.

243 6.2 Reservations

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

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

262 6.3 A good accuracy test

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

268 **Sample size.** The conservativeness of accuracy tests decrease with sample
269 size.

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

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

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

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

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

296 6.4 Smoothing accuracy estimates

297 It may be possible to alleviate the effect of discretization by appropriate
298 cross-validation. The discreteness of the accuracy statistic is governed by
299 the number of examples in the union (over all validation iterations) of test
300 sets. For V-fold CV, for instance, this number is simply the sample size. This

301 suggests that the accuracy can be “smoothed” by allowing the test sample to
 302 be drawn with replacement. The *bootstrap* may seem like a good candidate
 303 approach since it samples examples with replacement. It does so, however,
 304 for the train set, and not the test set. An algorithm that samples test sets
 305 with replacement is the *leave-one-out bootstrap estimator* (bLOO) and its
 306 derivation– the *0.632 bootstrap estimator* (b0.632) [Hastie et al., 2003, Sec
 307 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

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

308 Simulation results reported in Figure 3 with naming conventions in Ta-
 309 ble 2. It can be seen that selecting test sets with replacement does increase
 310 the power, when compared to V-fold cross validation, but still falls short
 311 from the power of population tests. It can also be seen that power increases
 312 with the number of bootstrap replications, itself reducing the level of dis-
 313 cretization. The type of bootstrap, bLOO versus b0.632, does not change
 314 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.

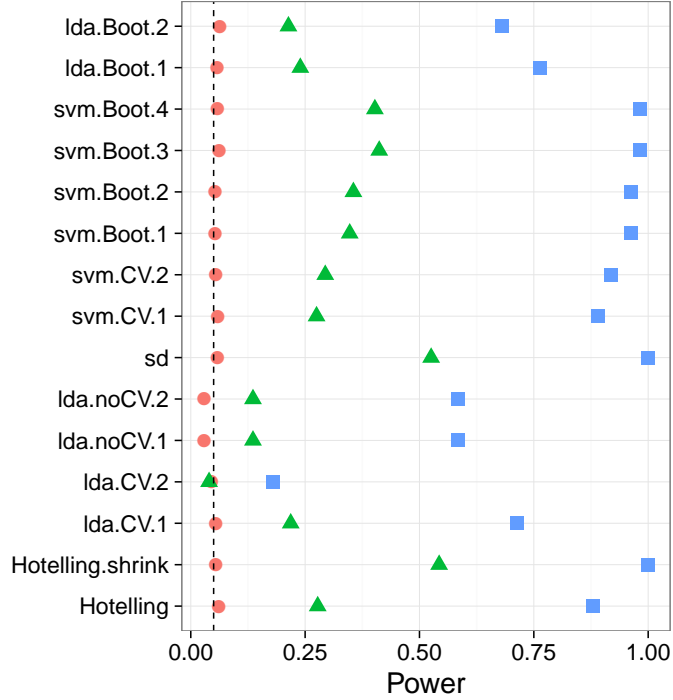


Figure 3: **Bootstrap**— The power of a permutation test with various test statistics. The power on the x axis. Effect are color and shape coded. The various statistics on the y axis. Their details are given in tables 1 and 2. Effects vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). Simulation details in Appendix B.

316 6.5 High dimensional classifiers

317 Inspecting Figure 1a (for instance), it can be seen that Hotelling’s T^2 test
318 has similar power to accuracy tests. It should thus be argued that the real
319 advantage of the population tests is due to their adaptation to high dimension
320 by regularization (*sd* and *Hotelling.shrink*), and not only to discretization.
321 To study this, we call upon several regularized classifiers, designed
322 for high dimensional problems. In the spirit of the regularized covariance of
323 *Hotelling.shrink*, we try an l_2 regularized svm Friedman et al. [2010], and
324 shrinkage based LDA [Pang et al., 2009, Ramey et al., 2016]. In the spirit of
325 the diagonalized covariance of *sd*, we try a diagonalized LDA [Dudoit et al.,
326 2002], which can be thought of a method intersecting Fisher’s LDA and Naive
327 Bayes.

328 Simulation results reported in Figure 4 with naming conventions in Table 3.
329 It can be seen that regularizing a classifier in high dimension, just
330 like a parameter test, improves power. It can also be seen that (regularized)
331 parameter tests are still more powerful than (regularized) accuracy tests.
332 This was to be expected, since we already saw in (e.g. Figure 1a) that the
333 unregularized parameter test, *Hotelling*, is slightly more powerful than the
334 regularized accuracy test, *svm.CV.1* for instance.

335 We can compound regularization in this section with the bootstrapping
336 from Section 6.4, to improve finite sample power of the accuracy tests. This
337 is done in the *svm.highdim.2* test, which still falls short from the power of
338 the population tests, but is a much more powerful accuracy test than the
339 original 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].

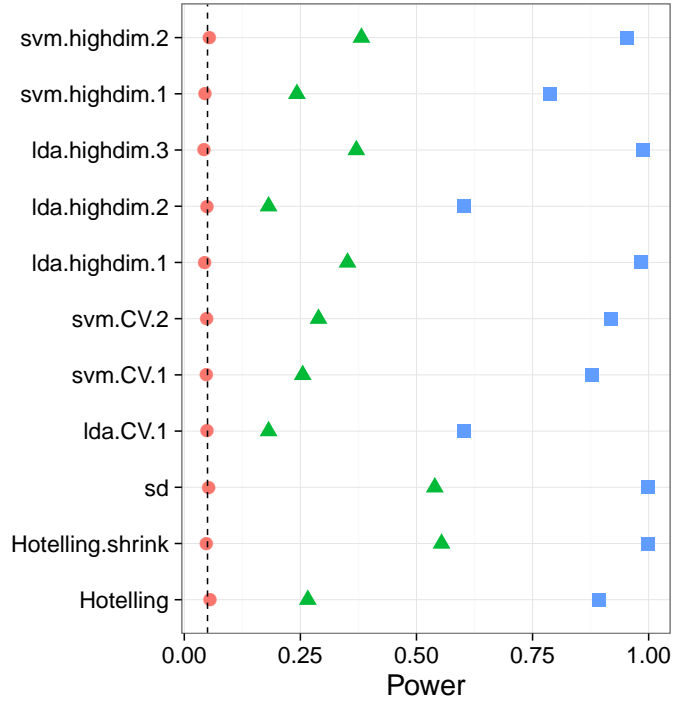


Figure 4: **HighDim Classifier**— The power of a permutation test with various test statistics. The power on the x axis. Effect are color and shape coded. The various statistics on the y axis. Their details are given in tables 1 and 3. Effects vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). Simulation details in Appendix B.

6.6 Related Literature

Ojala and Garriga [2010] study the power of two accuracy tests: one testing the “no signal” null hypothesis, and the other testing the “independent features” null hypothesis. They perform an asymptotic analysis, and a simulation study. They also apply various classifiers to various data sets. Their emphasis is the effect of the underlying classifier on the power, and the potential of the “independent features” test for feature selection. This is a very different emphasis from our own.

Olivetti et al. [2012] and Olivetti et al. [2014] looked into the problem of choosing a good accuracy test. They propose a new test they call an *independence test*, and demonstrate by simulation that it has more power than other accuracy tests, and can deal with non-balanced data sets. We did not include this test in the battery we compared, but we note the following: (a) The independence 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 from a Gaussian mixture family of models, and not from a location family as our own simulations. Under their model $(x_i|y_i = 1) \sim p\mathcal{N}(\mu_1, I) + (1 - p)\mathcal{N}(\mu_2, I)$ and $(x_i|y_i = -1) \sim (1 - p)\mathcal{N}(\mu_1, I) + p\mathcal{N}(\mu_2, I)$. Varying p interpolates between the null distribution ($p = 0.5$) and a location shift model ($p = 0$). We now perform the same simulation as Golland et al. [2005], after parameterizing p so that $p = 0$ corresponds to the null model, and in the same dimensionality as our previous simulations. We find that also in this mixture class of models a population test has more power than an accuracy test (Figure 5).

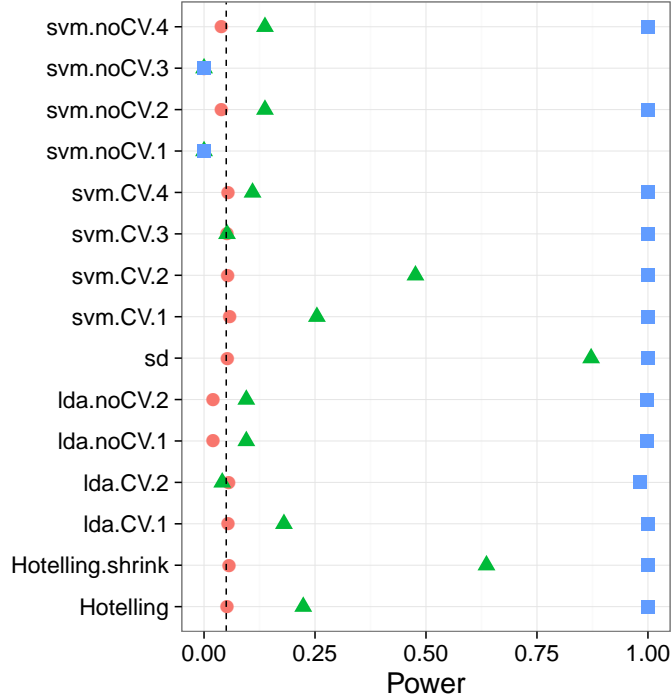


Figure 5: **Mixture**— $\mathbf{x}_i = \chi_i \mu + \eta_i$; $\chi_i = \{-1, 1\}$ and $Prob(\chi_i = 1) = (1/2 - p)^{y_i^*} (1/2 + p)^{1-y_i^*}$. μ is a p -vector with $3/\sqrt{p}$ in all coordinates. The effect, p , is color and shape coded and varies over 0 (red circle), $1/4$ (green triangle) and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

6.7 Epilogue

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

The recent popularity of machine learning has resulted in the extensive teaching and use of prediction in theoretical and applied communities and the relative lack of awareness or popularity of the topic of Neyman-Pearson style hypothesis testing in the computer science and related “data science” communities.

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

³<http://stats.stackexchange.com/questions/17408/how-to-assess-statistical-significance-of-the-accuracy-of-a-classifier>.

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

395 **7 Acknowledgments**

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.

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

- 464 E. Olivetti, S. Greiner, and P. Avesani. Induction in Neuroscience with
465 Classification: Issues and Solutions. In G. Langs, I. Rish, M. Grosse-
466 Wentrup, and B. Murphy, editors, *Machine Learning and Interpretation*
467 *in Neuroimaging*, number 7263 in Lecture Notes in Computer Science,
468 pages 42–50. Springer Berlin Heidelberg, 2012. ISBN 978-3-642-34712-2
469 978-3-642-34713-9. doi: 10.1007/978-3-642-34713-9_6.
- 470 E. Olivetti, S. Greiner, and P. Avesani. Statistical independence for the
471 evaluation of classifier-based diagnosis. *Brain Informatics*, 2(1):13–19, Dec.
472 2014. ISSN 2198-4018, 2198-4026. doi: 10.1007/s40708-014-0007-6.
- 473 H. Pang, T. Tong, and H. Zhao. Shrinkage-based Diagonal Discriminant
474 Analysis and Its Applications in High-Dimensional Data. *Biometrics*, 65
475 (4):1021–1029, Dec. 2009. ISSN 1541-0420. doi: 10.1111/j.1541-0420.2009.
476 01200.x.
- 477 F. Pereira, T. Mitchell, and M. Botvinick. Machine learning classifiers and
478 fMRI: A tutorial overview. *NeuroImage*, 45(1, Supplement 1):S199–S209,
479 Mar. 2009. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2008.11.007.
- 480 C. R. Pernet, P. McAleer, M. Latinus, K. J. Gorgolewski, I. Charest, P. E. G.
481 Bestelmeyer, R. H. Watson, D. Fleming, F. Crabbe, M. Valdes-Sosa, and
482 P. Belin. The human voice areas: Spatial organization and inter-individual
483 variability in temporal and extra-temporal cortices. *NeuroImage*, 119:164–
484 174, Oct. 2015. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2015.06.050.
- 485 M. D. Radmacher, L. M. McShane, and R. Simon. A Paradigm for
486 Class Prediction Using Gene Expression Profiles. *Journal of Computa-*
487 *tional Biology*, 9(3):505–511, June 2002. ISSN 1066-5277. doi: 10.1089/
488 106652702760138592.
- 489 A. Ramdas, A. Singh, and L. Wasserman. Classification Accuracy as a Proxy
490 for Two Sample Testing. *arXiv:1602.02210 [cs, math, stat]*, Feb. 2016.
- 491 J. A. Ramey, C. K. Stein, P. D. Young, and D. M. Young. High-Dimensional
492 Regularized Discriminant Analysis. *arXiv preprint arXiv:1602.01182*,
493 2016.
- 494 J. Schäfer and K. Strimmer. A Shrinkage Approach to Large-Scale Covariance
495 Matrix Estimation and Implications for Functional Genomics. *Statistical*
496 *Applications in Genetics and Molecular Biology*, 4(1), Jan. 2005. ISSN
497 1544-6115. doi: 10.2202/1544-6115.1175.

- 498 D. K. Slonim, P. Tamayo, J. P. Mesirov, T. R. Golub, and E. S. Lander. Class
499 Prediction and Discovery Using Gene Expression Data. In *Proceedings of*
500 *the Fourth Annual International Conference on Computational Molecular*
501 *Biology*, RECOMB '00, pages 263–272, New York, NY, USA, 2000. ACM.
502 ISBN 978-1-58113-186-4. doi: 10.1145/332306.332564.
- 503 M. S. Srivastava. Multivariate Theory for Analyzing High Dimensional Data.
504 *Journal of the Japan Statistical Society*, 37(1):53–86, 2007. doi: 10.14490/
505 jjss.37.53.
- 506 M. S. Srivastava, S. Katayama, and Y. Kano. A two sample test in high
507 dimensional data. *Journal of Multivariate Analysis*, 114:349–358, Feb.
508 2013. ISSN 0047-259X. doi: 10.1016/j.jmva.2012.08.014.
- 509 J. Stelzer, Y. Chen, and R. Turner. Statistical inference and multiple test-
510 ing correction in classification-based multi-voxel pattern analysis (MVPA):
511 Random permutations and cluster size control. *NeuroImage*, 65:69–82, Jan.
512 2013. ISSN 1053-8119. doi: 10.1016/j.neuroimage.2012.09.063.
- 513 A. W. van der Vaart. *Asymptotic Statistics*. Cambridge University Press,
514 Cambridge, UK ; New York, NY, USA, Oct. 1998. ISBN 978-0-521-49603-
515 2.
- 516 G. Varoquaux, P. R. Raamana, D. Engemann, A. Hoyos-Idrobo, Y. Schwartz,
517 and B. Thirion. Assessing and tuning brain decoders: cross-validation,
518 caveats, and guidelines. working paper or preprint, June 2016.
- 519 T. D. Wager, L. Y. Atlas, M. A. Lindquist, M. Roy, C.-W. Woo, and E. Kross.
520 An fMRI-Based Neurologic Signature of Physical Pain. *New England Jour-*
521 *nal of Medicine*, 368(15):1388–1397, Apr. 2013. ISSN 0028-4793. doi:
522 10.1056/NEJMoa1204471.

523 A Analysis pipeline

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

Algorithm 1: Compute a group parametric map.

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

```

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

Algorithm 2: Compute a permutation p-value map.

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

```

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

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

532 B Simulation Details

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

536 Each simulation is based on 4,000 replications. In each replication, we
537 generate n i.i.d. samples from a shift model $\mathbf{x}_i = \mu \mathbf{y}_i^* + \eta_i$. Where $y_i^* = \{0, 1\}$
538 is the class of subject i in dummy coding. Recalling that $y_i = \{-1, 1\}$ is the
539 class in effect coding, then clearly $y_i = 2y_i^* - 1$. The noise is distributed as
540 $\eta_i \sim \mathcal{N}_p(0, \Sigma)$. The sample size $n = 40$. The dimension of the data is $p = 23$.
541 The covariance $\Sigma = I$. Effects, i.e. shifts μ , are equal coordinate p -vectors
542 with coordinates that vary over $\mu \in \{0, 1/4, 1/2\}$.

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

C Simulation Results

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

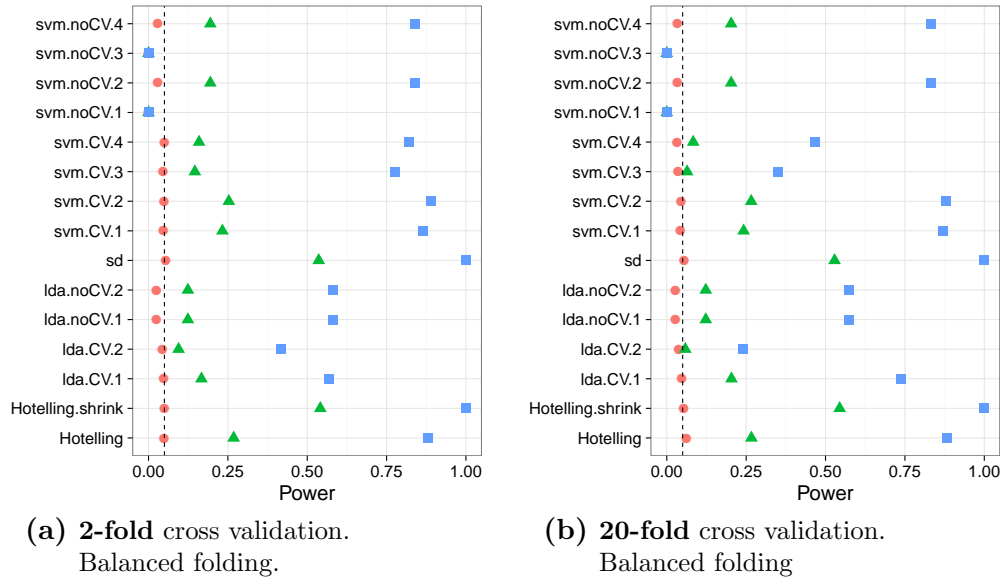


Figure 7: Simulation details in Appendix B except the changes in the sub-captions.

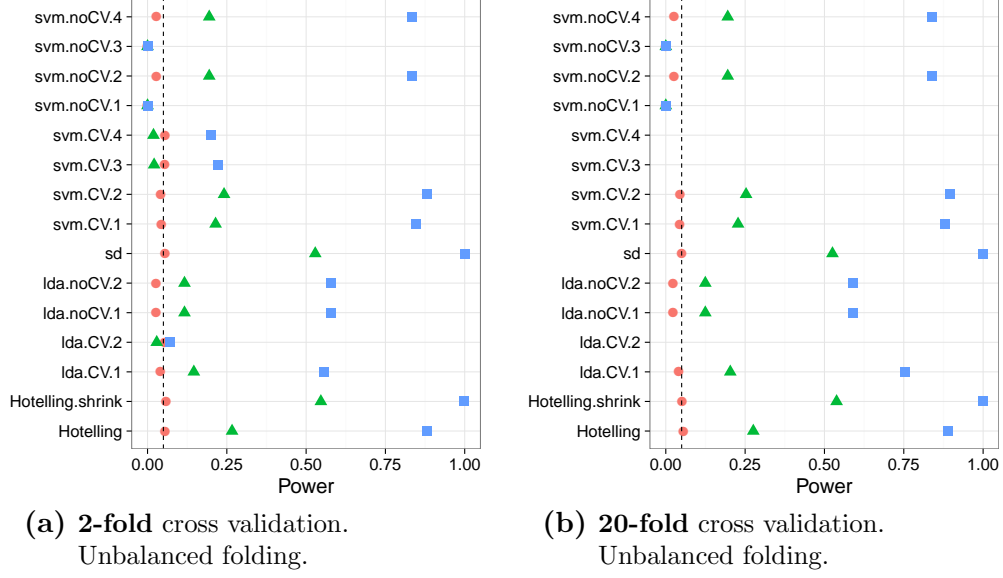


Figure 8: Simulation details in Appendix B except the changes in the sub-captions.

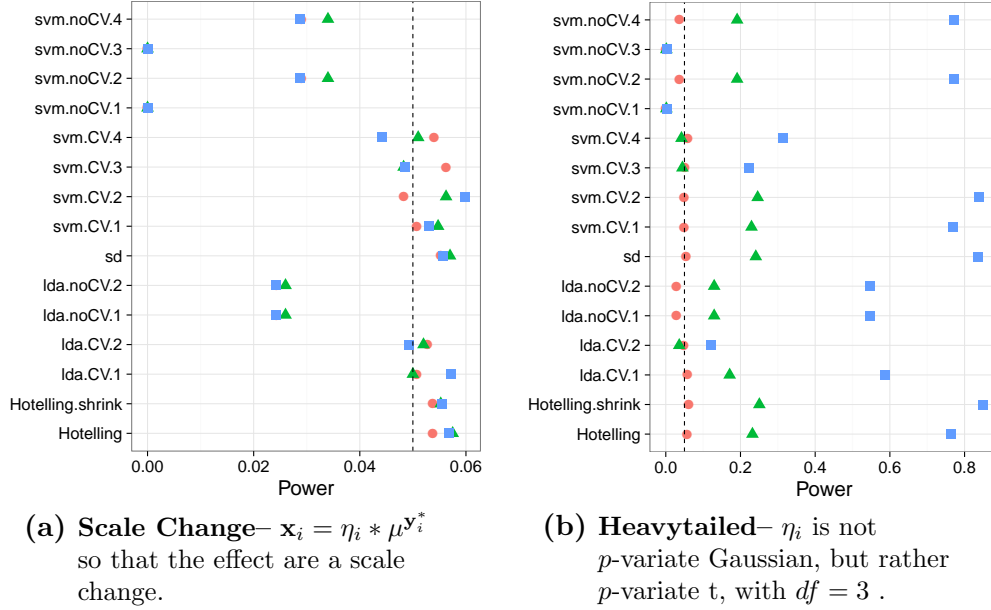
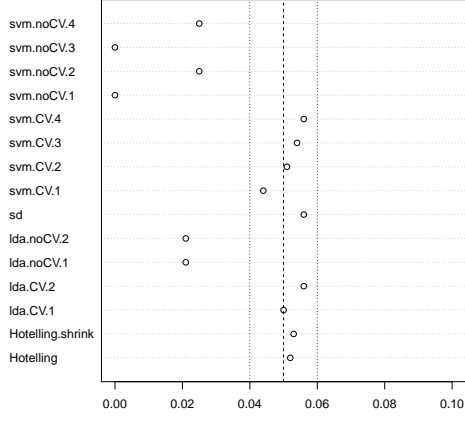
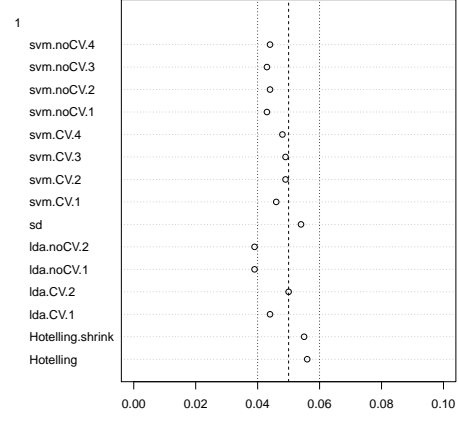


Figure 9: Simulation details in Appendix B except the changes in the sub-captions.

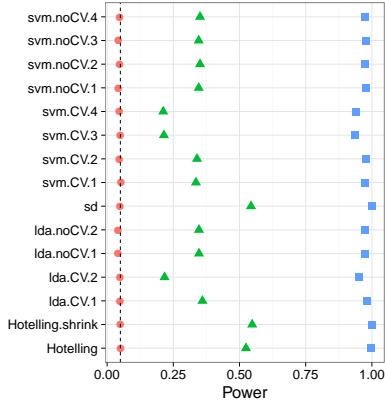


(a) Low-Dimension— False positive rates for $n = 40$.

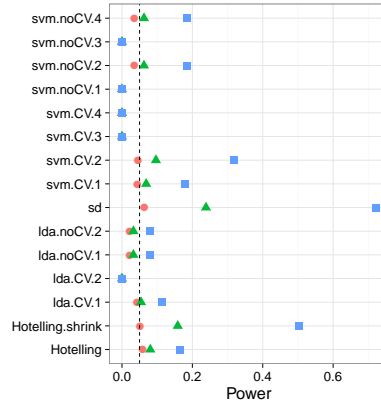


(b) High-Dimension— False positive rates for $n = 400$.

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