

# 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 the genetics literature, but to a lesser extent [Radmacher et al., 2002, Jiang et al., 2008].

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

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

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

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

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

The comparison between location and accuracy tests was precisely the goal of Ramdas et al. [2016], who compared the  $T^2$  location test to the accuracy of *Fisher’s linear discriminant analysis* classifier (LDA). By comparing the rates of convergence of the powers to 1, Ramdas et al. [2016] concluded that accuracy and location tests are rate equivalent. Judging by convergence rates alone, not much is (asymptotically) lost by using an accuracy test. Asymptotic relative efficiency measures (ARE) are typically used by statisticians to compare between test statistics with similar rates [van der Vaart, 1998].

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

Before discarding accuracy tests, we recall that Ramdas et al. [2016] analyzed a half-sample holdout. The authors thus conjecture that a leave-one-out approach, which makes more efficient use of the data, may have better performance. On the other hand, the analysis in Ramdas et al. [2016] is asymptotic. This eschews the discrete nature of the accuracy statistic, which will be shown to have a crucial impact. Since typical sample sizes in neuroscience

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

are not large, we seek to study which test is to be preferred in finite samples? Our conclusion will be quite simple: *location tests almost always have more power than accuracy tests.*

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

The discretization effect is aggravated if the test statistic is highly concentrated. For an intuition consider the usage of a the *training* accuracy as a test statistic. This is the *resubstitution classification* in Ramdas et al. [2016], and simply means that the accuracy is not cross validated. If the data is high dimensional, the train accuracy will be very high due to over fitting. In an extreme case, the train accuracy will be 1 for the observed data, but also for any permutaiton. The concentration of the train accuracy near 1, and its discreteness, render this test completely useless, with a power of 0.

To compare the power of accuracy tests and location tests in finite samples, we perform a simulation study of a battery of test statistics. The main findings are reported in Section 4, and the intuition for our findings is provided in Section 6, but first, the problem’s setup.

## 2 Problem setup

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

Given  $n$  pairs of  $(x_i, y_i)$ , typically assumed i.i.d., a location test amounts to testing whether  $x|y = 1$  has the the same distribution as  $x|y = -1$ . I.e., we test if the multivariate voxel activation pattern has the same distribution when given a vocal stimulus, as when given a non-vocal stimulus. An accuracy test amounts to learning a predictive model  $\hat{f}(x)$  from some assumed model class  $\hat{f} \in \mathcal{F}$ . The prediction accuracy, denoted  $T_{\hat{f}}^{acc}$ , is defined as the probability of a given classifier  $\hat{f}$  of making a correct prediction  $T_{\hat{f}}^{acc} := Prob(\hat{f}(x) = y)$  when given a randomly drawn data point,  $(x, y)$ .

101 A statistically significant “better than chance” estimate of  $T_{\hat{f}}^{acc}$  is evidence  
 102 that the classes are distinct.

## 103 2.1 Candidate Tests

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

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

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

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

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

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

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

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

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

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

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

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

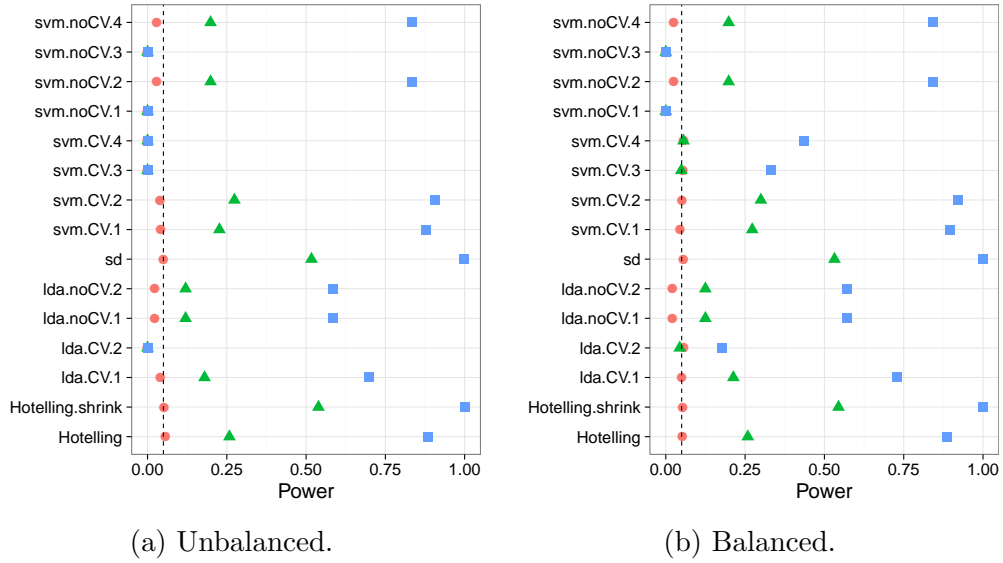
Table 1: This table enumerates the various test statistics we will be studying. Three are location tests: Hotelling, Hotelling.shrink, and sd. *Hotelling* is the classical two-group  $T^2$  statistic. *Hotelling.shrink* is a high dimensional version with the regularized covariance in Schäfer and Strimmer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

### 3 Controlling the False Positive Rate

Figure 1 demonstrates that all of the tests considered conserve the desired 0.05 false positive rate, up to varying levels of conservatism. This can be seen from the fact that the probability of rejection is no larger than 0.05 in the absence of any effect, encoded by a red circle. This is true, in particular if: (a) the folds are balanced or not, (b) the tuning parameters of some test

177 statistic are varied, (d) the number of folds is varied. We also observe that the  
 178 most conservative tests are the accuracy tests that are not cross validated.  
 179 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. They are assumed to be equal in all the 23 dimensions, and vary over 0 (red circle), 0.25 (green triangle), and 0.5 (blue square). The various statistics on the  $y$  axis. Their details are given in Table 1. Simulation code available at [TODO].



## 180 4 Power

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

- 185 1. Location tests have more power than accuracy tests in all our configurations.  
 186
- 187 2. The conservativeness decays as the sample grows (Figure 7), supporting  
 188 the statement that discretization is responsible for power loss.
- 189 3. The power may increase or decrease with the number of folds (Figure 3). [TODO:effect of n.folds.]  
 190

- 191 4. ... The z-scoring of the accuracies was introduced to deal with unbal-  
 192 anced foldings. If the z-scoring has any effect at all, it merely kills  
 193 power. There is really no reason to use it.
- 194 5. ... [TODO: effect of balancing].
- 195 6. ... [TODO: heavy tails].
- 196 7. ... [TODO: signal in scale].
- 197 8. ... [TODO: correlation between voxels].

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

## 201 5 Neuroimaging Example

202 Figure 2 is an application of both a location and an accuracy test to the data  
 203 of Pernet et al. [2015]. The authors of Pernet et al. [2015] collected fMRI  
 204 data while subjects were exposed to the sounds of human speech (vocal),  
 205 and other non-vocal sounds. Each subject was exposed to 20 sounds of each  
 206 type, totalling in  $n = 40$  trials in each scan. The study was rather large and  
 207 consisted of about 200 subjects. The data was kindly made available by the  
 208 authors at the OpenfMRI website<sup>2</sup>.

209 We perform group inference using within-subject permutations using the  
 210 pipeline of Stelzer et al. [2013], which was also reported in Gilron et al. [2016].  
 211 For completeness, the pipeline is described in Appendix A. To demonstrate  
 212 our point, we compare the *sd* location test with the *svm.cv.1* accuracy test  
 213 (see Table 1 for the definition of these statistics).

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

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

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

## 6 Discussion

We have set out to understand which of the tests is more powerful: the accuracy test or the location test. Using simulations, we have concluded that the location tests are preferable. We attribute this to several phenomena:

- (a) Discretization introduced in finite samples by the accuracy test statistic.
- (b) Inefficient use of the data for the validation set.

The sensitivity of the power to the number of folds suggests that most of the power is lost due to the discretization and not to the holdout.

The degree of discretization is governed by the sample size. For this reason, an asymptotic analysis such as Ramdas et al. [2016] may uncover the holdout inefficiency, but will not uncover the discretization effect.

The linear classifier assumption, (c), is immaterial since for every non-linear classifier, one may design a non-linear location test. See ? for an example of a location test in RKHS space. [TODO: relate to large sample

simulation] [TODO: discuss ARE, and holdout versus leave one out effect].  
[TODO: non-linear classification and testing].

Olivetti et al. [2012] and Olivetti et al. [2014] also looked into a similar problem as we do, namely, what is the preferred 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. This means that in the cases that the accuracy test is called upon for discriminating populations, it will probably be under-powered compared to location tests. (b) The problem of the accuracy test with unbalanced data-sets, which motivates Olivetti et al. [2012]’s independence test, can also be remedied by replacing the accuracy statistic with its z-score, as suggested in Section 2.1.

At this point some reservations to the generality of our findings are in order. Firstly, not all accuracy tests are concerned with signal detection. Indeed, it is possible that the purpose of the test is not to detect a difference between classes, but to actually test if a particular classifier is better than chance. This would be the case in decoding applications, like brain-machine interfaces, where the localization of a signal is not enough. Clinical diagnosis is another application, where the presence of a medical condition is “predicted” from imaging data. [e.g. Olivetti et al., 2012, Wager et al., 2013]

Secondly, not all signals are manifested in a shift of the null distribution. Put differently, the preferred alternative to an accuracy test is not always a location test. Indeed, one may consider signal, i.e. effects, as a change in scale, such as the *spiked covariance* model. In this case, other-than-Hotelling type tests are appropriate [TODO: cite change in covariance alternative]. Tests have been proposed even when the nature of the difference between populations is left unspecified [e.g. ?]. The fact that in our neuroimaging example (Section 5) some brain regions were detected with the accuracy test, and not the location test, is consistent with this observation. On the other hand, the far greater power of the location test, certainly in our example, does serve as empirical evidence that changes in location are a prevalent phenomenon. [TODO: signal in scale? heavy tails?]

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

278     Given all the above, we find the popularity of accuracy tests quite puz-  
 279     zling. We believe this is due to a reversal of the inference cascade. Re-  
 280     searchers first fit a classifier, and then ask if the classes are any different.  
 281     Were they to start by asking if classes are any different, and only then try  
 282     to classify, then location tests would naturally arise as the preferred method.  
 283     As put by Ramdas et al. [2016]:

284         The recent popularity of machine learning has resulted in the ex-  
 285         tensive teaching and use of prediction in theoretical and applied  
 286         communities and the relative lack of awareness or popularity of  
 287         the topic of Neyman-Pearson style hypothesis testing in the com-  
 288         puter science and related “data science” communities.

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## 368 A Analysis pipeline

369 Here is the analysis pipeline of Stelzer et al. [2013] we for the auditory data in  
 370 Gilron et al. [2016]. Denoting by  $i = 1, \dots, I$  the subject index,  $v = 1, \dots, V$   
 371 the voxel index, and  $s = 1, \dots, S$  the permutation index. Since regions<sup>3</sup> are  
 372 centred around a unique voxel, the voxel index  $v$  also serves as a unique  
 373 region index. Algorithm 1 computes a region-wise test statistic, which is  
 374 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>3</sup>*searchlight* or *sphere* in the MVPA parlance

377 **B Simulations**

Figure 3: [TODO].

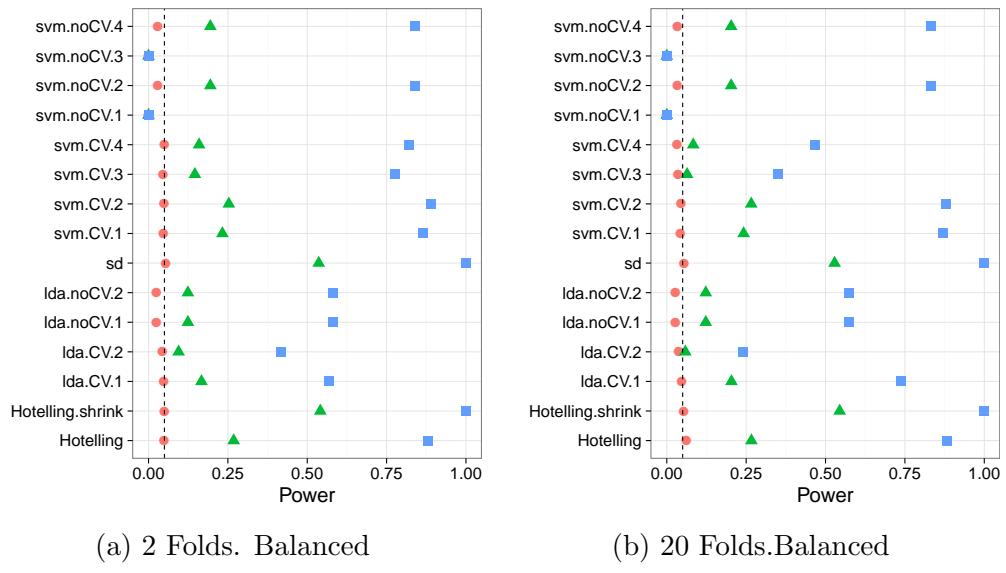


Figure 4: [TODO].

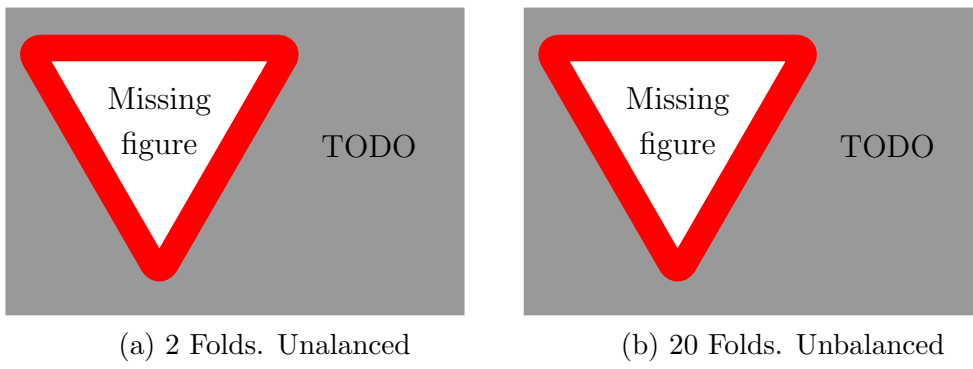


Figure 5: [TODO].

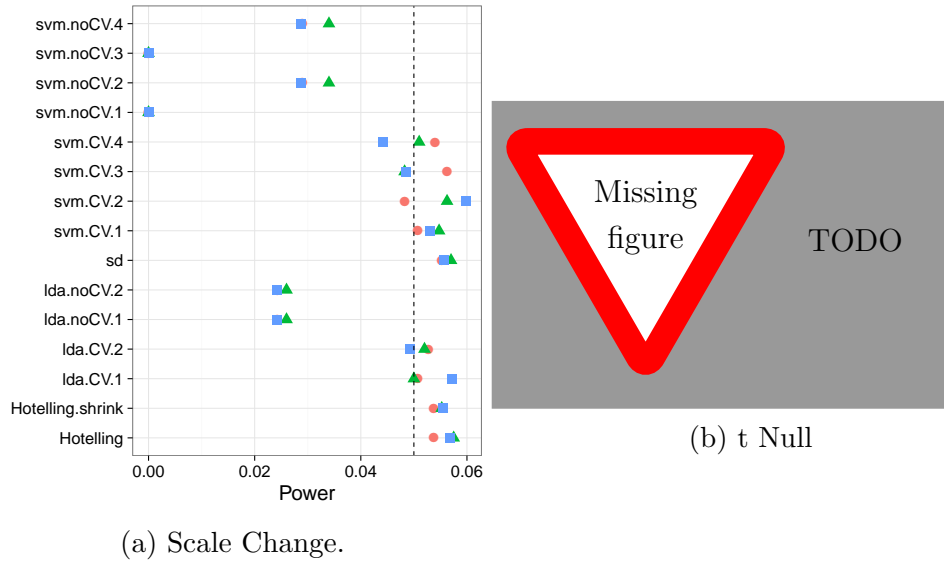


Figure 6: [TODO].

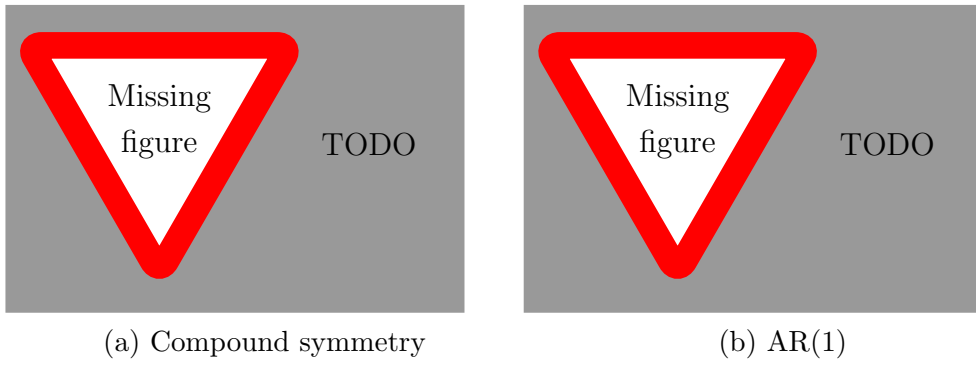




Figure 7: [TODO].

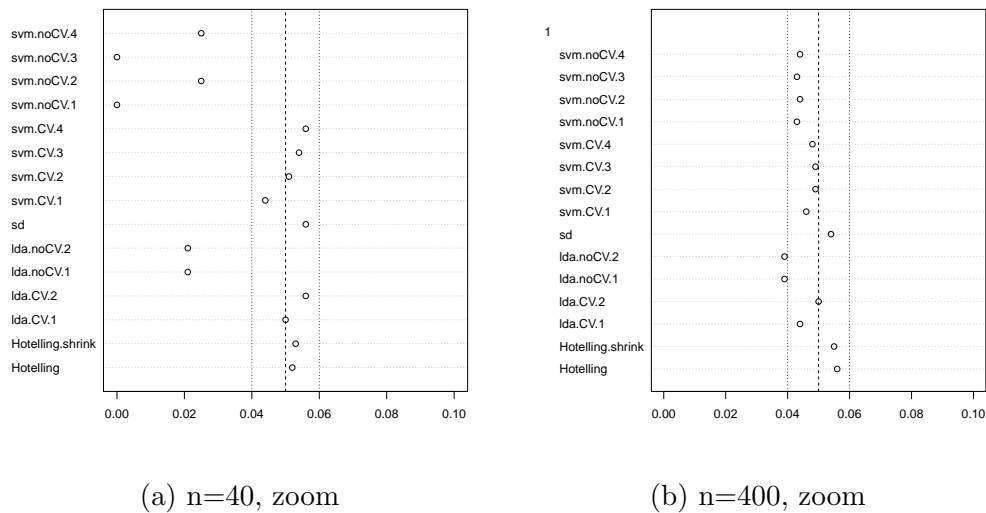


Figure 8: [TODO].

