

Better-than-chance classification for signal detection

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Abstract

[TODO]

1 Introduction

A common workflow in genetics or 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 genetics literature include Jiang et al. [2008], Radmacher et al. [2002] [TODO: elaborate]. Examples in the neuroscientific literature include [Golland and Fischl, 2003, Kriegeskorte et al., 2006, Pereira et al., 2009, Varoquaux et al., 2016]. The number of citations¹ of these papers attest to the popularity of the above workflow: 956 for Kriegeskorte et al. [2006], and 274 for Radmacher et al. [2002], as examples.

To fix ideas, we will adhere to a neuroscientific example: In Gilron et al. [2016], the authors seek to detect brain regions which encode differences between vocal and non-vocal stimuli. According to the MVPA analysis 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].

¹Based on GoogleScholar. Accesses on 26.7.2016.

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

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

31 A practitioner may then call upon a two-group location test such as Hotelling’s
 32 T^2 [Fujikoshi et al., 2011]. Alternatively, if the size of the brain region is too
 33 large compared to the number of observations, so that the spatial covariance
 34 cannot be fully estimated, then a high dimensional version of Hotelling’s test
 35 can be called upon, such as in Srivastava [2013] or Schäfer et al. [2005]. In
 36 contrast to *accuracy tests*, we call these *location tests*, a.k.a. *class comparison*
 37 in Simon et al. [2003].

38 At this point, it becomes unclear which is the preferred test. The compar-
 39 ison between location and accuracy tests was precisely the topic of Ramdas
 40 et al. [2016], who compared the Hotelling location test to the accuracy of
 41 *Fisher’s linear discriminant analysis* classifier (LDA) [Hastie et al., 2003].
 42 Using an asymptotic analysis, Ramdas et al. [2016] concluded that accuracy
 43 and location tests are equivalent with respect to their order of convergence
 44 to a consistent test, while they differ in constants. Judging by rate of conver-
 45 gence alone, this result may suggest that not much is (asymptotically) lost by
 46 using an accuracy test. On the other hand, asymptotic relative efficiency mea-
 47 sures (ARE) such as *Pitman’s*, *Bahadur’s*, *Lehman-Sheffe’s*, always assume
 48 equivalent convergence rates [van der Vaart, 1998].

49 Using the results of Ramdas et al. [2016], we derive that when signal
 50 is manifested in a location shift, the ARE between Hotelling’s T^2 (loca-
 51 tion) test and Fisher’s LDA (accuracy) test is $\sqrt{2\pi} \approx 2.5$. This means that
 52 Fisher’s LDA requires 2.5 more samples to achieve the same (asymptotic)
 53 power than the T^2 test. This means that Fisher’s LDA is remarkably ineffi-
 54 cient. For comparison, the t-test is only 1.04 more (asymptotically) efficient
 55 than Wilcoxon’s rank-sum test [Lehmann, 2009].

56 The relative efficiency, governing the power of the tests, may prove crucial
 57 when dealing with the finite sample sizes in neuroscience and genetics, and
 58 thus the focus of this study. We thus seek to study which test is to be
 59 preferred in finite samples? Our conclusion will be quite simple: *location*
 60 *tests almost always have more power than accuracy tests*.

61 The main argument for our statement rests upon the observation that
 62 with typical sample sizes, the accuracy test statistic is highly discrete. Dis-

63 crete test statistics are known to be conservative [?], since they cannot ex-
 64 haust the permissible false positive rate. For accuracy tests, the degree of
 65 discretization is governed by the number of samples. In our running neu-
 66 roscience example [Gilron et al., 2016], the classification is performed based
 67 on 40 trials, so that the test statistic may assume only 40 possible values.
 68 This number of examples is not unusual if considering this is the number of
 69 subject in a genetic study, or the number of trial-repeats in an fMRI brain
 70 scan.

71 The discretization effect is aggravated if the test statistic is highly concen-
 72 trated. For an intuition consider the usage of the *train* accuracy test statistic
 73 (i.e., not cross validated). In Section 4 we then address our main question-
 74 which test has more power? Based on the finding that the location test is
 75 typically more powerful, we try to offer an intuition for this phenomenon in
 76 the Discussion section.

77 2 Problem setup

78 Adhering to our neuroscientific example, we now formalize terminology and
 79 notation. Let $y \in \mathcal{Y}$ be a class encoding. In our vocal/non-vocal example
 80 we have $\mathcal{Y} = \{-1, 1\}$. Let $x \in \mathcal{X}$ be a p dimensional feature vector. In our
 81 vocal/non-vocal example p is the number of voxels in a brain region. We
 82 thus have $\mathcal{X} = \mathbb{R}^{27}$.

83 Given n pairs of (x_i, y_i) , typically assumed i.i.d., a location test amounts
 84 to testing whether $x|y = 1$ has the the same distribution as $x|y = -1$ (or
 85 at least the same location). I.e., the multivariate voxel activation pattern
 86 has the same distribution when given a vocal stimulus, as when given a non-
 87 vocal stimulus. An accuracy test amounts to learning a predictive model $\hat{f}(x)$
 88 from some assumed model class $\hat{f} \in \mathcal{F}$. The prediction accuracy, denoted
 89 $T_{\hat{f}}^{acc}$, is defined as the probability of a given classifier \hat{f} of making a correct
 90 prediction $T_{\hat{f}}^{acc} := Prob(\hat{f}(x) = y)$ when given a new, randomly drawn data
 91 point, (x, y) . A statistically significant “better than chance” estimate of $T_{\hat{f}}^{acc}$
 92 is evidence that the classes are distinct.

93 2.1 Candidate Tests

94 The design of a permutation test using the prediction accuracy, requires the
 95 following design choices:

- 96 1. How to estimate accuracy?
- 97 2. Is the statistic cross validated or not?

- 98 3. For a K-fold cross validated test statistic: should the data be refolded
99 in each permutation?
- 100 4. Permute labels of features?
- 101 5. For a K-fold cross validated test statistic: should the data folding bal-
102 anced? (a.k.a. stratified).
- 103 6. How many folds?

104 We will now address these questions while bearing in mind that unlike the
105 typical supervised learning setup, we are not interested in an unbiased esti-
106 mate of the prediction error, but rather in the mere detection of a difference
107 between two groups, leading to a better-than-chance accuracy.

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

120 **Cross validate or not?** Were we interested in an unbiased estimator of
121 the prediction error, there is no question that some independent validation
122 is in order. Since we are merely interested in detecting a difference between
123 classes, a biased error estimate is not an issue provided that bias is consistent
124 over all permutations. The underlying intuition is that if the exact same
125 computation is performed over all permutations, then a permutation test
126 will be “fair”, i.e., will not inflate the false positive rate. We will thus be
127 considering both cross validated accuracies, and *train* accuracies as our test
128 statistics.

129 **Refolding?** The standard practice in neuroimaging is to refold the data
130 after each permutation [Pereira et al., 2009]. This is imperative if permuting
131 labels while aiming at balanced data folds. This is not, however, imperative

132 in general. For simplicity, we will adhere to the standard practice of refolding
133 the data within each permutation.

134 **Permute labels of features?** While seemingly identical, the compound-
135 ing of permutations with data foldings renders these two approaches distinct.
136 As an example, consider balanced (stratified) K-fold cross validation where
137 the initial data folding is balanced. After a label permutation, the original
138 folds will probably not be balanced. If the *features* are permuted, then the
139 labels conserve their original fold assignments, and the original folds are bal-
140 anced after each permutation. Since we only report results while refolding the
141 data in each permutation, then the only difference between permuting labels
142 and permuting features seems to be a computational one. We thus adhere
143 to the more common, albeit less efficient practice, of permuting labels.

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

152 **How many folds?** Different authors suggest different rules for the num-
153 ber of folds. We will be varying the number of folds. This will affect the
154 concentration of permutation distribution of the estimated accuracy, which
155 will have a crucial effect on the conservativeness of the accuracy test. Our
156 intuition suggests that since more folds imply a less concentrated estimate,
157 then leave-one-out should be the less conservative, and 2-fold should be the
158 most conservative.

159 There are indeed many design choices when performing a permutation test
160 using a cross validated statistic. The subset of tests we will be comparing is
161 collected for convenience in Table 1.

162 3 Controlling the False Positive Rate

163 We start by verifying that the battery of tests in Table 1 control the false
164 positive rate at the desired 0.05 level, with varying conservativeness levels.
165 Figure 1 demonstrates that this is indeed the case. All our candidate tests

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 et al. [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 ($|T_{\hat{f}}^{acc} - \hat{p}_{max}| / \sqrt{\hat{p}_{max}(1 - \hat{p}_{max})}$, 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.

control the type I error, with varying degrees of conservativeness. In particular: (a) if the folds are balanced or not, (b) if the tuning parameters of some test statistic are varied, (d) if the number of folds is varied.

4 Power

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 comparing the power of location tests to accuracy tests. On the other hand, the results of our previous sections suggest that the conservativeness of some of the considered tests can be considerable, rendering them underpowered.

[TODO: discuss power of various tests after finishing simulations]

We see by now that the use of accuracy tests for signal detection is un-

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].



derpowered compared to location tests. Simulations alone cannot, however, support such a universal statement. We will thus verify on a neuroimaging dataset, and discuss the causes for this phenomenon with implications on the scope of our statement.

5 Neuroimaging Example

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

We perform permutation inference using the pipeline of Stelzer et al. [2013], which was also used in Gilron et al. [2016]. For completeness, the pipeline is described in Appendix A. To demonstrate our point, we compare

²<https://openfmri.org/>

192 the *sd* location test with the *svm.cv.1* accuracy test (see Table 1 for the
 193 definition of these statistics).

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

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

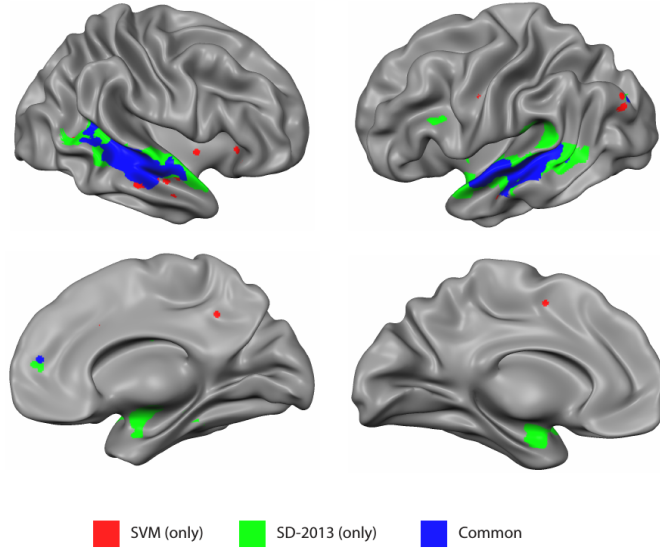


Figure 2: Brain regions encoding information discriminating between vocal and non-vocal stimuli. Map reports the centres of 27-voxel sized spherical regions, as discovered by an accuracy test (*svm.cv.1*), and a location test (*sd*). *svm.cv.1* was computed using 5-fold cross validation, and a cost parameter 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].

203 6 Discussion

204 We have set out to understand which of the tests is more powerful: the
 205 accuracy test or the location test. Using simulations, we have concluded
 206 that the location tests are preferable. We attribute this to the discretization
 207 introduced in finite samples by the accuracy test statistic. This also explains
 208 why an asymptotic analysis, such as Ramdas et al. [2016], did not find a
 209 qualitative difference. [TODO: relate to large sample simulation].

210 Olivetti et al. [2012] and Olivetti et al. [2014] also looked into a similar
 211 problem as we do, namely, what is the preferred accuracy test? They propose
 212 a new test they call an *independence test*, and demonstrate by simulation that
 213 it has more power than other accuracy tests, and can deal with non-balanced
 214 data sets. We did not include this test in the battery we compared, but we
 215 note the following: (a) The independence test of Olivetti et al. [2012] relies
 216 on a discrete test statistic. This means that in the cases that the accuracy
 217 test is called upon for discriminating populations, it will probably be under-
 218 powered compared to location tests. (b) The problem of the accuracy test
 219 with unbalanced data-sets, which motivates Olivetti et al. [2012]’s indepen-
 220 dence test, can also be remedied by replacing the accuracy statistic with its
 221 z-score, as suggested in Section 2.1.

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

230 Secondly, not all signals are manifested in a shift of the null distribution.
 231 Put differently, the preferred alternative to an accuracy test is not always a
 232 location test. Indeed, one may consider signal, i.e. effects, as a change in
 233 scale, such as the *spiked covariance* model. In this case, other-than-Hotelling
 234 type tests are appropriate [TODO: cite change in covariance alternative].
 235 Tests have been proposed even when the nature of the difference between
 236 populations is left unspecified [e.g. Gretton et al., 2012]. The fact that in our
 237 neuroimaging example (Section 5) some brain regions were detected with the
 238 accuracy test, and not the location test, is consistent with this observation.
 239 On the other hand, the far greater power of the location test, certainly in our
 240 example, does serve as empirical evidence that changes in location are a
 241 prevalent phenomenon. [TODO: signal in scale? heavy tails?]

242 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.

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 location 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.

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338 A Analysis pipeline

339 Here is the analysis pipeline of Stelzer et al. [2013] we for the auditory data in
 340 Gilron et al. [2016]. Denoting by $i = 1, \dots, I$ the subject index, $v = 1, \dots, V$
 341 the voxel index, and $s = 1, \dots, S$ the permutation index. Since regions³ are
 342 centred around a unique voxel, the voxel index v also serves as a unique
 343 region index. Algorithm 1 computes a region-wise test statistic, which is
 344 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
```

³*searchlight* or *sphere* in the MVPA parlance

B More Simulations

Figure 3: [TODO].

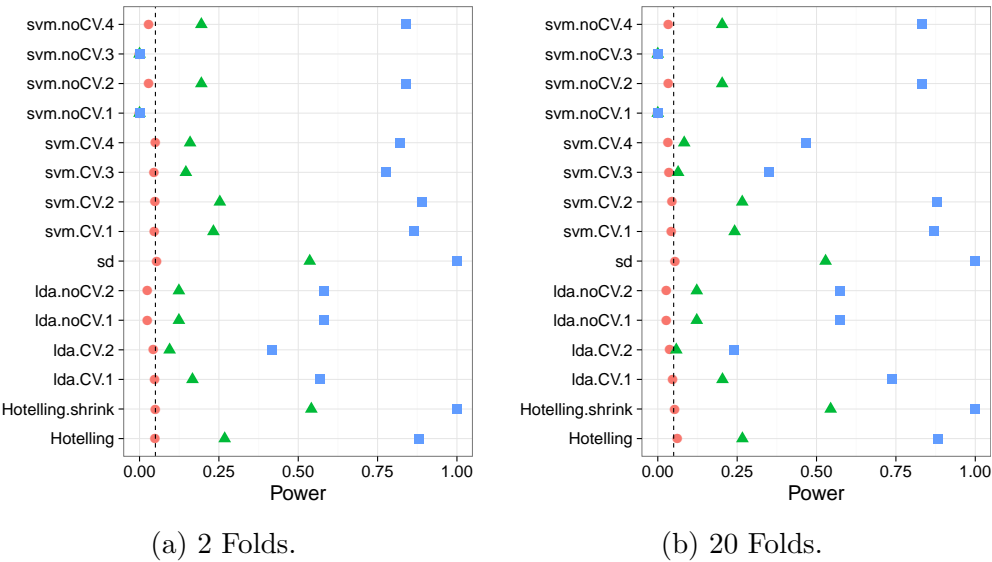


Figure 4: [TODO].

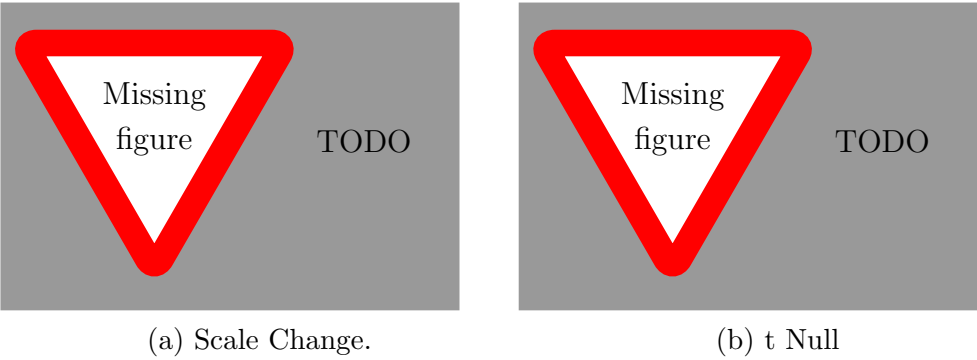
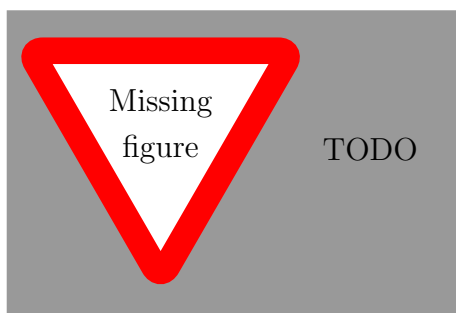


Figure 5: [TODO].

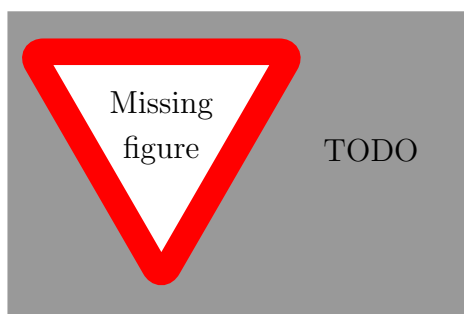


(a) Compound symmetry

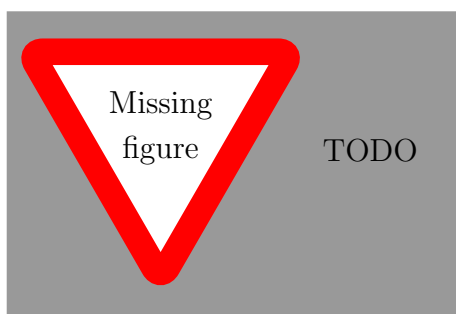


(b) AR(1)

Figure 6: [TODO].



(a) $n=400$



(b) ?