Modeling visual working memory with the MemToolbox

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Abstract

The MemToolbox is a collection of MATLAB functions for modeling visual working memory. In support of its goal to provide a full suite of data analysis tools, the toolbox includes implementations of popular models of visual working memory, real and simulated data sets, Bayesian and maximum likelihood estimation procedures for fitting models to data, visualizations of data and fit, validation routines, model comparison metrics, and experiment scripts. The MemToolbox is released under a BSD license and is freely available at memtoolbox.org.

Keywords: visual working memory, mixture models, model comparison

Introduction

Working memory is a storage system that actively holds information in mind and allows for its manipulation, providing a workspace for thought (Baddeley, 1986). Its strikingly limited capacity has inspired a slew of research aimed at characterizing those limits in terms of the spatiotemporal properties of the stimulus and the age, intelligence, sleepiness, and mental health of the individual.

A handful of experimental paradigms predominate. These include the delayed match-to-sample task used in studies of animal cognition (Blough, 1959) and the span tasks used in studies of verbal working memory (Daneman & Carpenter, 1980). Research on visual working memory relies primarily on two tasks: partial report and change detection (Fig. 1). In a partial report task, the participant is shown a set of letters, shapes, or colorful dots, and then after a brief delay is asked to report the properties of one or a subset of the items (Sperling, 1960; Wilken & Ma, 2004; Zhang & Luck, 2008).

In a change detection task, the participant is shown a pair of displays, one after the other, and is asked a question that requires comparing them, like whether they match (Luck & Vogel, 1997; Phillips, 1974; Pashler, 1988).

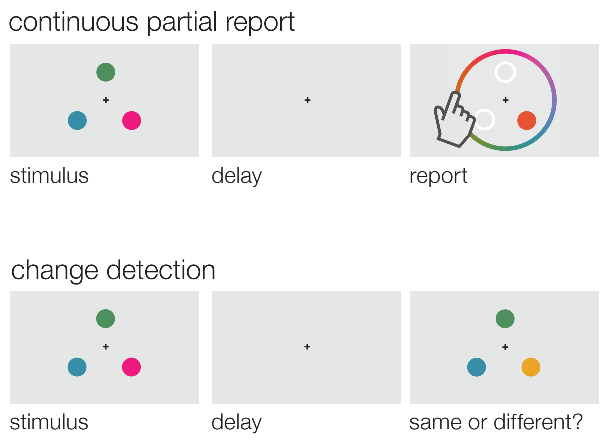

FIGURE 1: (a) A continuous partial report task. The observer sees the stimulus display, and then after a delay is asked to report the exact color of a single item. (b) A change detection task. The observer sees the stimulus display, then after a delay is asked to report whether the test display matches.

Formal models have been proposed that link performance in change detection and partial report tasks to the architecture and capacity of the working memory system. These include the item-limit model (Pashler, 1988), the slot model (Luck & Vogel, 1997; Cowan, 2001), the slots+averaging model (Figure 2; Zhang & Luck, 2008), the slots+resources model (Awh et al., 2007), the continuous resource model (Wilken & Ma, 2004), the resources+swaps model (Bays et al., 2009), the ensemble statistics+items model (Brady & Alvarez, 2011), and the variable-precision model (van den Berg et al., 2012). Each model specifies the structure of visual memory and the decision process used to perform the task.

These models have been used to make claims about the architecture and capacity of memory. For example, using an item-limit model to fit data from a change detection task, Luck & Vogel (1997) showed that the same number of features as conjunctions of features can be stored in working memory, and from this inferred that its storage format is integrated objects, not individual features. Using a continuous resource model to fit data from a partial report task, Bays et al. (2009) found that many errors in memory are due to spatial misattribution, and from this inferred that this spatial misattribution, not a fixed item-limit, is what determines the capacity of working memory.

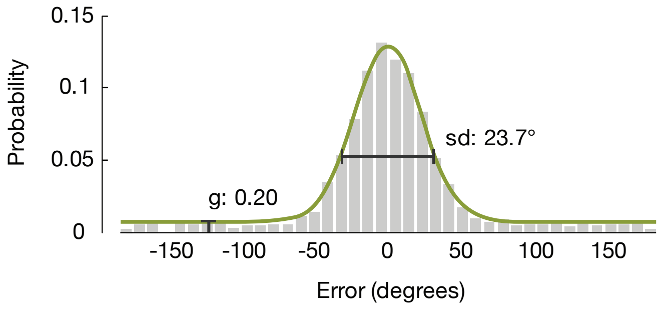

FIGURE 2: An example of a model's fit to continuous partial report data. Most responses fall within a relatively small range around the target item, but some response are far off. The data are fit using the mixture model of Zhang & Luck (2008), which attributes the gap to differences in the state of memory for the target item: with probability g the observer remembers nothing about the item and guesses randomly; with probability $1-g$ the observer has a noisy representation of the item, leading to responses centered at the true value and with a standard deviation sd that reflects the quality of the observer's memory.

The MemToolbox

We created the MemToolbox, a collection of MATLAB functions for modeling visual working memory. Though the toolbox provides everything needed to perform the analyses commonly used in studies of visual working memory, including model implementations, maximum likelihood routines, and data validation checks, it defaults to a Bayesian workflow that encourages a deeper look into the data and the models' fits. In the following sections, we highlight the toolbox's core functionality and review the improvements it offers to the standard workflow. We begin by reviewing the standard workflow and its implementation in the toolbox.

The standard workflow

The experimenter first picks a model. Then, to fit the model to experimental data using probabilistic methods, a likelihood function is defined that describes the model's predictions for each possible setting of its parameters. Formally, given a model M with free parameters θ, the model's likelihood function specifies a probability distribution $P(D|\theta)$ over possible datasets D. With the likelihood function in hand, an estimator is used to pick the parameter settings that provide the best fit to the data. A popular choice is the maximum likelihood estimator, which selects the parameter values that maximize the model's likelihood function for a given set of data (Dempster et al., 1977; Lagarias et al., 1998). Typically, this procedure is performed separately for each participant and experimental condition, resulting in estimates that are then compared using traditional statistical tests (e.g., Zhang & Luck, 2008).

The MemToolbox uses two MATLAB structures ("structs") to organize the information needed to analyze data using the standard workflow: one that describes the data to be fit, and another that describes the model and its likelihood function. The required contents of the data and model structures depends on the experimental paradigm. For example, in a continuous report paradigm, the data struct must contain a field called `errors` that indicates, for each trial, how far an observers' response was from the true value. In a 2AFC or change detection paradigm, this data struct must contain fields called `changeSize`, indicating the size of the difference between study and test; and `afcCorrect`, indicating whether observers got the trial correct. This data struct can optionally contain other information about each trial, for example, `distractors`, which gives the value of the other items in the display; or `n`, which indicates the number of stimuli present on the trial. Fitting a set of data with a model is then as simple as calling the built-in `MLE()` function. For example:

```
>> model = StandardMixtureModel();
>> data.errors = [-89,29,-2,6,-16,65,43,-12,10,0,178,-42];
>> fit = MLE(data, model)
```

This will return the maximum likelihood parameters for this observer's data, allowing for standard analysis techniques to be used.

Thus, with very little effort the MemToolbox can be used to simplify (and speed-up) existing workflows by allowing for straightforward fitting of nearly all of the standard models used in the visual working memory literature. In support of this goal, the toolbox includes what we refer to as the `StandardMixtureModel` (that of Zhang & Luck, 2008), the `SwapModel` of Bays et al. (2009), several variations of a `VariablePrecisionModel`, and many more.

The Bayesian workflow

Rather than simply returning the maximum likelihood estimate, the toolbox defaults to a Bayesian workflow that constructs a full probability distribution over parameter values. This probability distribution gives the reasonableness of each possible parameter setting after considering the observed data in light of prior beliefs. In doing so, it strongly encourages a thorough examination of model fit. The Bayesian workflow is implemented in `MemFit`, the toolbox's primary fitting function.

```
>> fit = MemFit(data, model)
```

Bayesian inference provides a rational rule for updating prior beliefs ("the prior") based on experimental data. The prior, $P(\theta)$, conveys which parameter values are thought to be reasonable, and specifying it can be as straightforward as setting upper and lower bounds (for example, bounding the guess rate between 0 and 1). For the purposes of exploratory data analysis, it is common to use a noninformative or weakly informative prior that spreads the probability thinly over a swath of plausible parameter values. Following this tradition, the toolbox uses the Jeffreys prior, a class of noninformative priors that is invariant under reparameterization of the model (Jeffreys, 1946; Jaynes, 1968). With sufficient data, these noninformative priors have almost no influence on the final inferences, serving only to limit the range of parameters to those that are meaningful. Once prior beliefs are specified, they are then updated (according to Bayes' rule) to take into account the experimental data. Bayes' rule stipulates that after observing data D, the posterior beliefs about the parameters ("the posterior") are given by

$$P(\theta|D) \propto P(D|\theta) \cdot P(\theta),$$

which combines the likelihood of the data given the parameters with the prior probability of the parameters.

Estimating the full posterior distribution is harder than finding the maximum likelihood estimate. For some models it is possible to derive closed-form expressions for the posterior distribution, but for most models this is intractable and so sampling-based algorithms are used to approximate it. One such algorithm, the Metropolis-Hastings variant of Markov Chain Monte Carlo (MCMC), is applicable to a wide range of models and is thus the one used by the toolbox (Metropolis et al., 1953; Hastings, 1970). The algorithm chooses an initial set of model parameters, and then, over several thousands iterations, proposes small moves to these parameter values, accepting or rejecting them based on how probable the new parameter values are in both the prior and the likelihood function. In this way, it constructs a random walk that visits parameter settings with frequency proportional to their probability under the posterior. This allows the estimation of the full posterior of the model in a reasonable amount of time, and is theoretically equivalent to the more straightforward (but much slower) technique of evaluating the model's likelihood and prior at every possible setting of the parameters (implemented in the `GridSearch` function).

With the posterior distribution in hand, there are a number of ways to analyze and visualize the results. First, the maximum of the posterior distribution (the *maximum a posteriori* or MAP estimate) can be used as a point-estimate that is analogous to the maximum likelihood estimate, differing only in the MAP's consideration of the prior. However, visualizing the full posterior distribution also provides information about how well the data constrain the parameter values and whether there are trade-offs between parameters (Fig. 3).

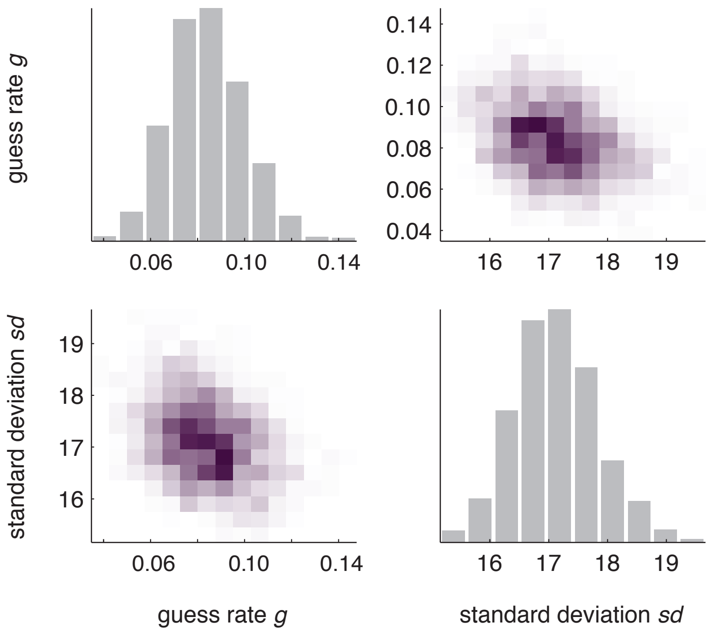

FIGURE 3: An example full posterior of the standard mixture model of Zhang & Luck (2008), where g is the guess rate and sd is the standard deviation of observers' report for remembered items.

Figure 3 shows a posterior distribution for data analyzed with the standard mixture model of Zhang & Luck (2008). The plots on the main diagonal are histograms of values for each parameter, the so-called "marginals" of the posterior distribution; the plots on the off-diagonoals reveal correlations between parameters. Note that in the standard mixture model, there is a slight negative correlation between the standard deviation parameter and the guess rate parameter: data can be seen as having either a slightly higher guess rate and lower standard deviation, or a slightly lower guess rate and higher standard deviation (as in Brady et al., 2011). Because of this correlation, neither parameter can be estimated independently as tightly as they can be together — the "hill" in the posterior is tilted, such that the range of reasonable parameters is wider if your cross it horizontally (in g) or vertically (in sd), than if you cross it diagonally. Examining the full posterior reveals this tradeoff, which remains hidden when using maximum likelihood fits.

Posterior predictive checks

Another technique applied by the MemToolbox is the automatic use of posterior predictive checks. Sometimes a whole class of models performs poorly, such that there are no parameter settings that will produce a good fit. In this case, maximum likelihood and maximum a posteriori estimates are misleading: they dutifully pick out the best, even if the best is quite bad. A good practice is to check the quality of the fit, examining which aspects of the data it captures, and which aspects of the data it fails to capture (Gelman et al., 1996, 2004). This can be accomplished through a posterior predictive check, which simulates new data from the posterior fit of the model, and then compares the histograms of the actual and simulated data (Fig. 4). Posterior predictive checks are a default function of `MemFit`.

A model that can accurately fit the data in a posterior predictive check does not necessarily provide a good fit. For example, the model may fit the averaged data but fail to fit observers' data from individual displays, perhaps because of reports of incorrect items (Bays et al., 2009) or because of the use of grouping or ensemble statistics (Brady & Tenenbaum, 2010). In addition, a good fit does not necessarily indicate a good model: an extremely flexible model that can mimic any data always provides a good fit, but this provides no evidence in favor of that model (Roberts & Pashler, 2000). However, models that systematically deviate in a posterior predictive check nearly always need improvement.

Hierarchical modeling

Typically, the question of interest in working memory research is not about a single observer, but a population: Do those who napped have higher working memory capacities? Is guess rate greater at set size 6 than at set size 3? When aggregating results from multiple subjects to answer such ques-

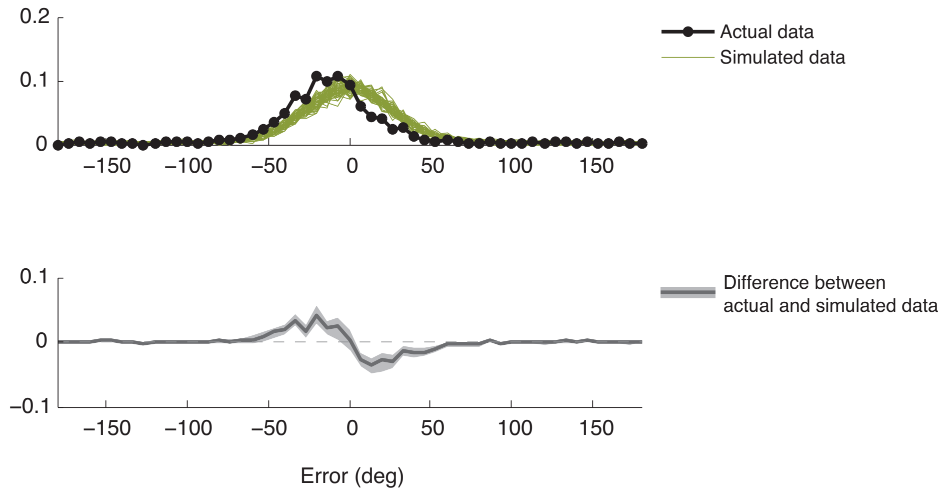

FIGURE 4: (a) Simulated data from the posterior of the model (green), with the actual data overlaid (black). The mismatch between the two is symptomatic of a poor fit. (b) The difference between the simulated and real data, bounded by 95% credible intervals. If at any spot the credible interval does not include zero, it is an indication that the model does not accurately fit the data.

tions, the standard technique is to separately fit a model to the data from each subject (using, for example, maximum likelihood estimation), and then to combine parameter estimates across subjects by taking their average or median and to analyze their variance by using t-tests or ANOVAs. This approach to analyzing data from multiple observers allows generalization to the population as a whole, since subject variance is taken into account by treating parameters as random effects (Daw, 2011). One flaw with this approach is that it entirely discards information about the reliability of each subject's parameter estimates. This is particularly problematic when there are differences in how well the data constrain the parameters of each subject (e.g., because of differences in the number of completed trials), or when there are significant trade-offs between parameters (as in the g and sd parameters of the standard model), in which case analyzing them separately can be problematic (Brady et al., 2011).

A better technique, although one that is more computationally intensive, is to fit a single hierarchical model of all the subjects together (e.g., Morey, 2011). This treats each of the subjects' parameters as samples from a normally-distributed population and uses the data to infer the population mean and SD of each parameter. This automatically gives more weight to subjects whose data give more reliable parameters estimates and causes "shrinkage" of each subject's parameter estimates towards the population mean, sensibly avoiding extreme estimates caused by noisy data. For example, using maximum likelihood estimates, subjects with high guess rates are sometimes estimated to have guess rates of near zero but standard deviations of 3000 degrees (resulting in a nearly flat normal distribution). This problem is avoided by fitting subjects in a hierarchical model.

Hierarchical modeling is the toolbox's default and can be performed by passing multiple data sets, one per subject, to the `MemFit` function:

```
>> data1 = MemDataset(1);
>> data2 = MemDataset(2);
>> model = StandardMixtureModel();
>> fit = MemFit({data1,data2}, model)
```

Using the standard non-hierarchical technique for fitting multiple subjects is also supported, using the `FitMultipleSubjects_Independent` function:

```
>> data1 = MemDataset(1);
>> data2 = MemDataset(2);
>> model = StandardMixtureModel();
>> fit = FitMultipleSubjects_Independent({data1,data2}, model)
```

which returns the maximum likelihood parameters for each subject and the mean and standard error for each parameter.

Model comparison

Often there is a question about which model best describes the data. Answering it requires considering both the resemblance between the model and data and also the flexibility of the model. Flexible models can fit many data sets, and so a good fit provides only weak evidence of a good match between model and data. In contrast, finding the same fit between an inflexible model and the data provides stronger evidence of a good match. To account for this, many approaches penalize more flexible models; these include the Akaike Information Criterion with correction for finite data (AIC_c ; Akaike, 1974; Burnham & Anderson, 2004), the Bayesian Information Criterion (BIC; Schwarz, 1978), the Deviance Information Criterion (DIC; Spiegelhalter et al., 2002), and the Bayes factor (Kass & Raftery, 1995). In addition, it is possible to perform cross-validation (fitting and testing on separate data) to eliminate the advantage of a more flexible model. Implementations of each of these model comparison techniques are included in the toolbox and can be accessed by passing multiple models to the `MemFit` function:

```
>> model1 = StandardMixtureModel();
>> model2 = SwapModel();
>> modelComparison = MemFit(data, {model1, model2})
```

This will output model comparison metrics as well as give descriptions of the metrics.

Despite the array of tools provided by the MemToolbox, we do not wish to give the impression that model selection can be automated. Choosing between competing models is no easier or more straightforward than choosing between competing theories (Pitt & Myung, 2002). Selection criteria like AIC$_C$ are simply tools for understanding model fits. Thus, in general, we recommend doing model comparison by choosing a metric that is the least generous to your preferred model. In particular, AIC$_C$ penalizes complex models the least, since it penalizes models only for having more parameters; BIC penalizes complex models more heavily, particularly at large sample sizes; and both DIC and Bayes Factors penalize complex models in a way dependent on their functional form, e.g., in terms of their actual flexibility rather than simply number of parameters (taking into account things like correlations between parameters). Of note is that this means both DIC and Bayes factors have the disadvantage of a major dependence on the prior, since the only way to know how flexible a model is without simply counting parameters is to quantify what data it could have predicted a priori.

In addition to choosing an appropriate model comparison metric, we recommend computing the metric for each subject independently and looking at consistency across subjects to make inferences about the best fitting models. Thus, if you believe the best model is the simpler model, you may wish to compute AIC$_C$ values for each subject, and then compare the AIC$_C$ values for the simpler model against those of the more complex model. On the other hand, if you wish to claim the more complex model is a better fit, it makes a stronger argument if you do so by comparing BIC values or Bayes Factors, which more heavily penalize complex models. Importantly, by fitting independently for each subject, you can take into account subject variance, and are thus able to generalize to the population as a whole (for example, by using an ANOVA over model likelihoods). By contrast, computing a single AIC$_C$ or BIC value across all subjects does not allow generalization to the population, as it ignores subject variance (one subject that is fit much better by a particular model can drive the entire AIC$_C$ or BIC value). This kind of *fixed effects* analysis can thus seriously overstate the true significance of results (Stephan et al., 2010). As in the case of estimating parameters, this technique of estimating model likelihoods for each subject and then performing an ANOVA or t-test over these parameters is only an approximation to the fully Bayesian hierarchical model that considers the evidence simultaneously from each subject (Stephan et al., 2009); however, in the case of model comparison we believe the simpler technique is sufficient for most visual working memory experiments.

To facilitate this kind of analysis, the MemToolbox performs model comparison on individual subject data and `MemFit` calculates many of the relevant model comparison metrics, so that you may choose the appropriate comparison for your theoretical claim.

Availability

The MemToolbox is available on the web at **memtoolbox.org**. To install the toolbox, place it somewhere sensible and then run the included Setup.m script, which will add it to MATLAB's default path. The distribution includes a tutorial that reviews all of the toolbox's functionality, demos, and source code. It is released under a BSD license, allowing free use for research or teaching.

Conclusion

We created the MemToolbox for modeling visual working memory. The toolbox provides everything needed to perform the analyses routinely used in visual working memory, including model implementations, maximum likelihood routines, and data validation checks. In addition, it provides tools that offer a deeper look into the data and the fit of the model to the data. This introduction gave a high-level overview of its approach and core features. To learn to use the toolbox, we recommend the tutorial, available in the supplementary materials or at **memtoolbox.org**.

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