Neuron
NeuroView

# Data Visualization in the Neurosciences: Overcoming the Curse of Dimensionality

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**In publications, presentations, and popular media, scientific results are predominantly communicated through graphs. But are these figures clear and honest or misleading? We examine current practices in data visualization and discuss improvements, advocating design choices which reveal data rather than hide it.**

Visualizations are vital tools for neuroscientists of every discipline, affording the ability to reveal relationships in large data sets and communicate information to a broad audience. But with the great power of graphs, one might say, comes great responsibility. Graphs can be fundamentally misleading about underlying data, and design choices can skew viewers' perceptions, leading them toward incorrect conclusions (Jones, 2006). For example, recent studies suggest that results rendered on aesthetically pleasing brain images are perceived as more persuasive and credible than identical information presented in other formats (Keehner et al., 2011; McCabe and Castel, 2008). Beyond the attractiveness of displays, readers may also be misled by the frequent errors that plague scientific figures (Cleveland, 1984) or a lack of sufficient information. In the words of statistician and graphic design expert Howard Wainer, effective data visualization must "remind us that the data being displayed do contain some uncertainty" and "characterize the size of that uncertainty as it pertains to the inferences we have in mind" (Wainer, 1996). It is our impression that such descriptions (along with more basic elements) are often lacking from published figures. In this NeuroView, we perform a survey of figures from leading neuroscience journals with an eye toward clarity and the portrayal of uncertainty. Based on survey results, we discuss methods to improve graphics (particularly for large data sets in which visualization poses a challenge) and propose a set of figure guidelines in the form of a checklist (Table 1). We hope these recommendations, compiled from a number of excellent resources on data visualization (Lane and Sándor, 2009; Tufte, 2001; Wainer, 1996), may be used by both internal and external reviewers to help evaluate figures for clarity and completeness.

## Surveying the Field

We sampled 288 articles published in 2010 from six neuroscience journals (*Frontiers in Systems Neuroscience*, *Human Brain Mapping*, *Journal of Neuroscience*, *Nature Neuroscience*, *NeuroImage*, and *Neuron*) and examined the 1,451 figures therein. We surveyed four basic features that were applicable to nearly all graphs and addressed Wainer's points above. The survey asked the following questions: (1) Is the dependent variable or quantity of interest labeled? (2) Is the scale of the dependent variable indicated? (3) Where applicable, is a measure of uncertainty displayed? (4) Is the type of uncertainty (e.g., standard error bars or confidence intervals) defined in the figure or accompanying legend? Examples of these graphical features are shown in Figure 1A for two-dimensional (2D) and 3D data sets.

Survey results, shown in Figure 1B, overwhelmingly suggest that graphical displays become less informative as the dimensions and complexity of data sets increase. Compared to graphs of 2D data, 3D displays provide poorer descriptions of the outcome of interest and rarely provide an indication of uncertainty. Only 43% of 3D graphics label the dependent variable (meaning that if you were asked, "What is being plotted here?" you would be able to answer less than half of the time) and only 20% portray the uncertainty of reported effects. Even for 2D data, the proportion of graphs displaying uncertainty is lower when explanatory variables are continuous (and typically take on many values) than when they are categorical (and typically represent a few conditions; Figure 1C). Of 2D figures that do indicate uncertainty, nearly 30% fail to define the type of uncertainty or variability being portrayed. Given the plurality of interpretations connoted by an error bar (e.g., a standard deviation [SD] of the sample, a standard error of the mean [SEM], a range, a parametric confidence interval [CI] of the mean, a bootstrap CI, a Bayesian probability interval, a prediction interval, etc.), it is unclear how including it without a proper label would offer readers any further understanding of the data; in contrast, the poor labeling or omission of error bars has been shown to encourage misinterpretation (Cumming and Finch, 2005; Vaux, 2004; Wainer, 1996).

A breakdown of results by journal (see supplementary analysis at http://mialab.mrn.org/datavis) further highlights the issue of data dimensionality in visualization: journals with lower proportions of

**Table 1. When Evaluating a Figure for Clarity and Completeness, Consider the Following Questions**

| Questions | Examples/Suggestions |
|---|---|
| **Design/Organization** | |
| Is the display consistent with the model or hypothesis being tested? | • If data have been residualized or transformed for statistical analysis they should also be transformed in the graph.<br>• If data are paired between conditions, the graph should reveal the pairwise differences rather than differences at the group level. |
| Are there "empty dimensions" in the display that could be removed? | • A 3D pie chart for 2D categorical data<br>• Extraneous colors that do not encode meaningful information |
| Does the display provide an honest and transparent portrayal of the data? | • Hiding, smoothing, or modifying data has been avoided<br>• Actual data points are emphasized over idealized models |
| **Axes** | |
| Are axes scales defined as linear, log, or radial? | |
| Does each axis label describe the variable and its units? | • For quantities with units: "Time to peak (ms)"<br>• For arbitrary units (a.u.): "BOLD signal intensity (a.u.)"<br>• For unitless quantities: "Spearman rank correlation" |
| Are axes limits appropriate for the data? | • The graphic should not be bounded at zero if the data can take on both positive and negative values. |
| Is the aspect ratio appropriate for the data? | • When x and y axes contrast the same variable under different conditions the graphic should be square. |
| **Color mapping** | |
| Is a color bar provided? | |
| Is the color map sensible for the data type? | • Use  when data is bipolar, and map zero to green<br>• Use  when data is unipolar, and map zero to black<br>• Use  when data is circular, and map $-\pi$, $+\pi$ to red |
| Does the color bar axis indicate the quantity, units, and scale? | |
| **Uncertainty** | |
| Does the display indicate the uncertainty of estimated parameters? | |
| Is the type of error surface appropriate for the data? | • Standard deviations or prediction intervals are useful to describe variability in the population.<br>• Standard errors or confidence intervals are useful to make inferences about parameters estimated from a sample.<br>• Parametric confidence intervals should only be used if data meet the assumptions of the underlying model. |
| Are the units of uncertainty defined? | • "Error bands indicate non-parametric 95% confidence intervals of the median" |
| **Color** | |
| Are contrasting colors consistent with a natural interpretation? | • Red for increases, blue for decreases |
| Can features be discriminated when printed in grayscale? | • Group A ---●---<br>Group B —○— |
| Has red/green contrast been avoided to accommodate common forms of colorblindness? | |
| **Annotation** | |
| *Information necessary to understand the display should be shown on the figure itself. Details & definitions may be relegated to the legend.* | |
| Are all symbols defined, preferably by directly labeling objects? | |
| Is the directionality of a contrast between conditions obvious? | • "Patients − Controls" |
| Is the number of samples or independent experiments indicated? | • "Each point represents the mean over 23 subjects" |
| Are statistical procedures and criteria for significance described? | • For a single test: "A repeated-measures ANOVA showed a significant effect of treatment ($F[2, 10] = 12.53$, $p = 0.002$)"<br>• For several tests: "Asterisks denote correlations different from zero ($p < 0.01$, two-tailed t tests, Bonferroni corrected for 10 tests)." |
| Are uncommon abbreviations avoided or clearly defined? | |
| Are abbreviations consistent with those used in the text? | |

2D and 3D graphical features are those that primarily publish neuroimaging and systems-level findings, in which results are often distilled from very large data sets using a hierarchy of models. That the so-called ''curse of dimensionality'' extends to the realm of data visualization is not surprising. Dependent variables are more difficult to label when they represent abstract parameter estimates rather than directly measured quantities; uncertainty is more challenging to render when data sets require error surfaces rather than error bars. However, these results are undesirable. As data sets become more complex, displays should become increasingly informative, elucidating relationships that would be inaccessible from tables or summary statistics. In the next section, we provide examples of creating more informative displays for

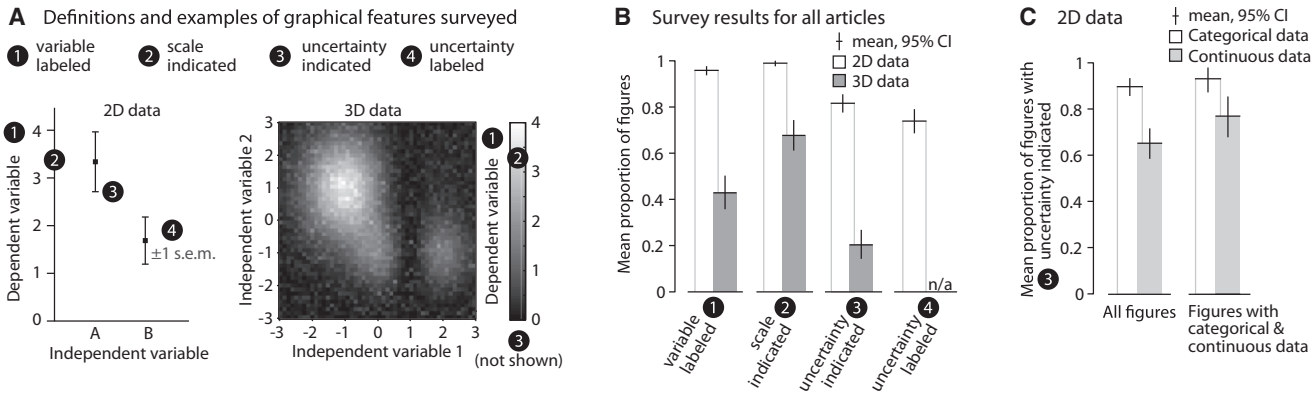


**Figure 1. Survey Results**

(A) Definitions and examples of graphical features for 2D (left) and 3D (right) data sets. (B) Mean proportion of 2D (white) and 3D (dark gray) figures displaying each feature. Error bars denote 95% nonparametric confidence intervals (10,000 resamples). (C) Mean proportion of 2D figures indicating uncertainty, separated by categorical (white) and continuous (light gray) data. Left panel considers all figures; right panel considers only figures with both categorical and continuous data.

simple and complex data sets by making design choices that reveal data, rather than hide it.

## Show More, Hide Less

Consider a simple experiment in which a researcher investigates the effect of different conditions on a single response variable. Having collected 50 samples of the response variable under each condition 1, 2, and 3, how should the researcher visualize the data to best inform themselves and their audience of the results? Figure 2 provides three possible designs. In panel A, a bar plot displays the sample mean and SEM under each condition. With no distributional information provided, the data density is quite low and the same information could be provided in a single sentence, e.g., "Mean response ± SEM for conditions 1, 2, and 3 were 4.9 ± 0.4, 5.0 ± 0.4, and 5.2 ± 0.4, respectively." Panel B offers some improvement, with box plots displaying the range and quartiles of each sample. This design reveals that response variables may take on both positive and negative values (hidden in panel A) and that condition 2 may be right skewed. Distributional differences are better understood in panel C when using violin plots to display kernel density estimates (smoothed histograms) of each data set (Hintze and Nelson, 1998). Violin plots make the skew in condition 2 more apparent and reveal that responses in condition 3 are bimodal (hidden in panels A and B). Although the additional distributional information in panel C does not change our initial inference that sample means are similar between conditions, we are certainly not likely to make the misinterpretation that condition has no effect on the response. Distributional differences also suggest that assumptions of the ANOVA (or other parametric models) may not be met and that the mean may not be the most interesting quantity to investigate.

This example is not meant to imply that bar plots should always be avoided in favor of more complex designs. Bar plots have numerous merits: they are easy to generate, straightforward to comprehend, and can efficiently contrast a large number of conditions in a small space. They are particularly effective for displaying frequencies or proportions (as in Figure 1), in which binary data samples are transformed into a height that intuitively reflects the fraction of "successes." Yet, bar plots are also commonly used in scenarios in which the distance from zero is not meaningful and in which distributional information would be of great benefit to readers. In roughly the same amount of space required by a bar plot, one can portray the full shape of distributions and overlay descriptive statistics, inferential statistics related to hypothesis testing, or even individual data points, creating a so-called "bean plot" (Kampstra, 2008). By increasing the amount of information available to the viewers, we allow them to assess the appropriateness of related statistical analyses and make their own inferences.

In Figure 3, we apply the guiding principle of "show more, hide less" to high-dimensional electroencephalographic (EEG) and functional magnetic resonance imaging (fMRI) data sets. We portray the results using a common design (panel A) and a modified design (panel B), in which each change is arrived at by following the guidelines in Table 1.

Figures 3Aa and 3Ba present data from an EEG visual flanker task. Subjects were asked to indicate the direction of a visual target which appeared shortly after the presentation of flanking distracters. For each participant, multichannel EEG time series were decomposed using independent component analysis, and a single component best matching the expected frontocentral topography for a performance monitoring process was selected for further analysis (Eichele et al., 2010). Here, we ask how the extracted event-related potential (ERP) differs according to the subject's response (i.e., correct or incorrect). Panel A provides a typical portrayal of results, in which mean ERPs are displayed for each condition. As Table 1 recommends, the axes are labeled, variable units are indicated, and experimental conditions are distinguished by line color with direct annotation on the plot. While this panel is clear, it is not complete: there is no portrayal of uncertainty. In panel B, we add 95% confidence bands around the average ERPs. The confidence bands are made slightly transparent to highlight overlap between conditions and to maintain the visual prominence of the means.

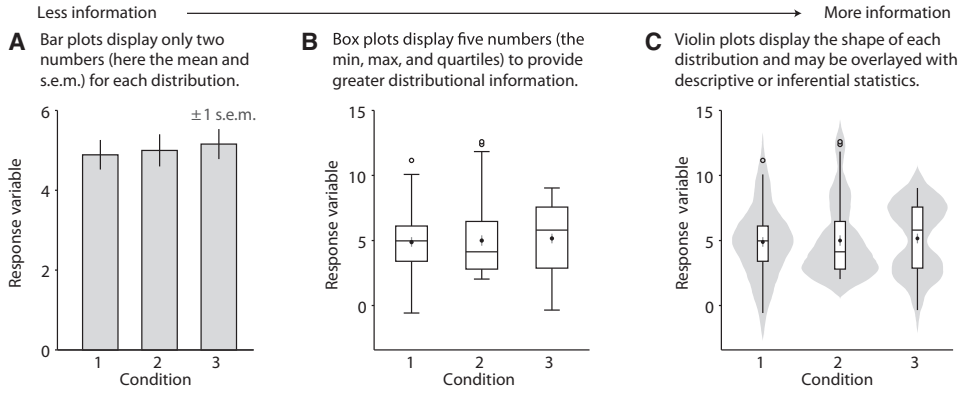


**Figure 2. Comparison of Graphical Designs**

The same synthetic data is summarized in a bar plot (A), box plot (B), and violin plot (C). Box plots in (B) and (C) also show the mean ± SEM and are drawn with a maximum whisker length of 1.5× the interquartile range. Data points (n = 50 for each condition) were sampled from a normal distribution (condition 1), a generalized $\chi^2$ distribution with 2 degrees of freedom (2), and an equal mixture of two normal distributions with different means (3).

Confidence intervals clarify that there is greater uncertainty in the error response than the correct response (because subjects make few errors) and that there is insufficient evidence to conclude a response difference after ~800 ms. In panel B, we also add verbal descriptions and additional annotation to the graphic (Lane and Sándor, 2009; Tufte, 2001). Labels indicate that the timeline is relative to the presentation of the target stimulus and specify our null and alternative hypotheses as well as the alpha level (type I error rate) chosen to determine statistical significance. Integrating descriptions into the figure (rather than the legend) discourages misinterpretation and permits readers to understand the display more quickly. Of course, annotation must be used judiciously and should not overwhelm or detract from the data visualization itself.

Figures 3Ab and 3Bb portray results from an auditory oddball event-related fMRI experiment. Participants responded to target tones presented within a series of standard tones and novel sounds. Blood oxygenation level-dependent (BOLD) time series at each brain voxel were regressed onto activation models for the target, novel, and standard stimuli (Kiehl et al., 2001). Here, we ask what brain regions might be involved in the novelty processing of auditory stimuli and compare beta parameters between novel and standard conditions. Panel A presents voxelwise differences between beta coefficients using a widely reproduced design: functional-imaging results are thresholded based on statistical significance and overlaid on a high-resolution structural image. Following Table 1, the variable of interest is labeled, the color map is sensible for the data and is mapped with symmetric endpoints, and annotation clearly indicates the directionality of the contrast (i.e., "Novel–Standard"). This design provides excellent spatial localization for functional effects but is not without problems. The display does not portray uncertainty and has a remarkably low data-ink ratio due to the prominent (nondata) structural image and sparsity of actual data (Habeck and Moeller, 2011). More crucially, the design encourages authors to hide results not passing a somewhat arbitrary statistical threshold. Given numerous correction methods and little consensus on the appropriate family-wise type I error rate (Lieberman and Cunningham, 2009), authors may arrive at a "convenient" threshold to reveal visually appealing and easily explained results. This design reduces a rich and complex data set to little more than a dichotomous representation (i.e., "significant or not?") that suffers from all the limitations of all-or-none hypothesis testing (Harlow et al., 1997).

Rather than threshold results, we suggest a dual-coding approach to represent uncertainty (Hengl, 2003). As shown in panel B, differences in beta estimates are mapped to color hue, and associated paired t statistics (providing a measure of uncertainty) are mapped to color transparency. Compared to panel A, no information is lost. Transparency is sufficient to determine structural boundaries and statistical significance is indicated with contours. However, substantial information is gained. The quality of the data is now apparent: large and consistent differences in betas are wholly localized to gray matter, while white matter and ventricular regions exhibit very small or very uncertain differences. In addition, isolated blobs of differential activation in panel A are now seen as the peaks of larger contiguous activations (often with bilateral homologs) that failed to meet significance criteria. The modified display also reveals regions in lateral parietal cortex, medial prefrontal cortex, and posterior cingulate cortex with reduced activation to novel stimuli compared to standard tones. These brain areas coincide with the so-called "default-mode network," a system preferentially active when subjects engage in internal rather than external processes (Buckner et al., 2008). We hope to impress upon the reader the wealth of findings that can be revealed simply by unhiding data. To encourage the use of this approach, we provide sample MATLAB scripts for hue and transparency coding on our website (http://mialab.mrn.org/datavis).

Along with increased annotation, panel B also displays the beta parameters for individual subjects, averaged over clusters of voxels passing significance (Figures 3Bb1 and 3Bb2). The 2D plots remove dependence on color mapping (which is more difficult for viewers to decode than position along an axis; Cleveland and McGill, 1985) and allow us to access the data in greater detail. Scatter plots indicate the beta estimates

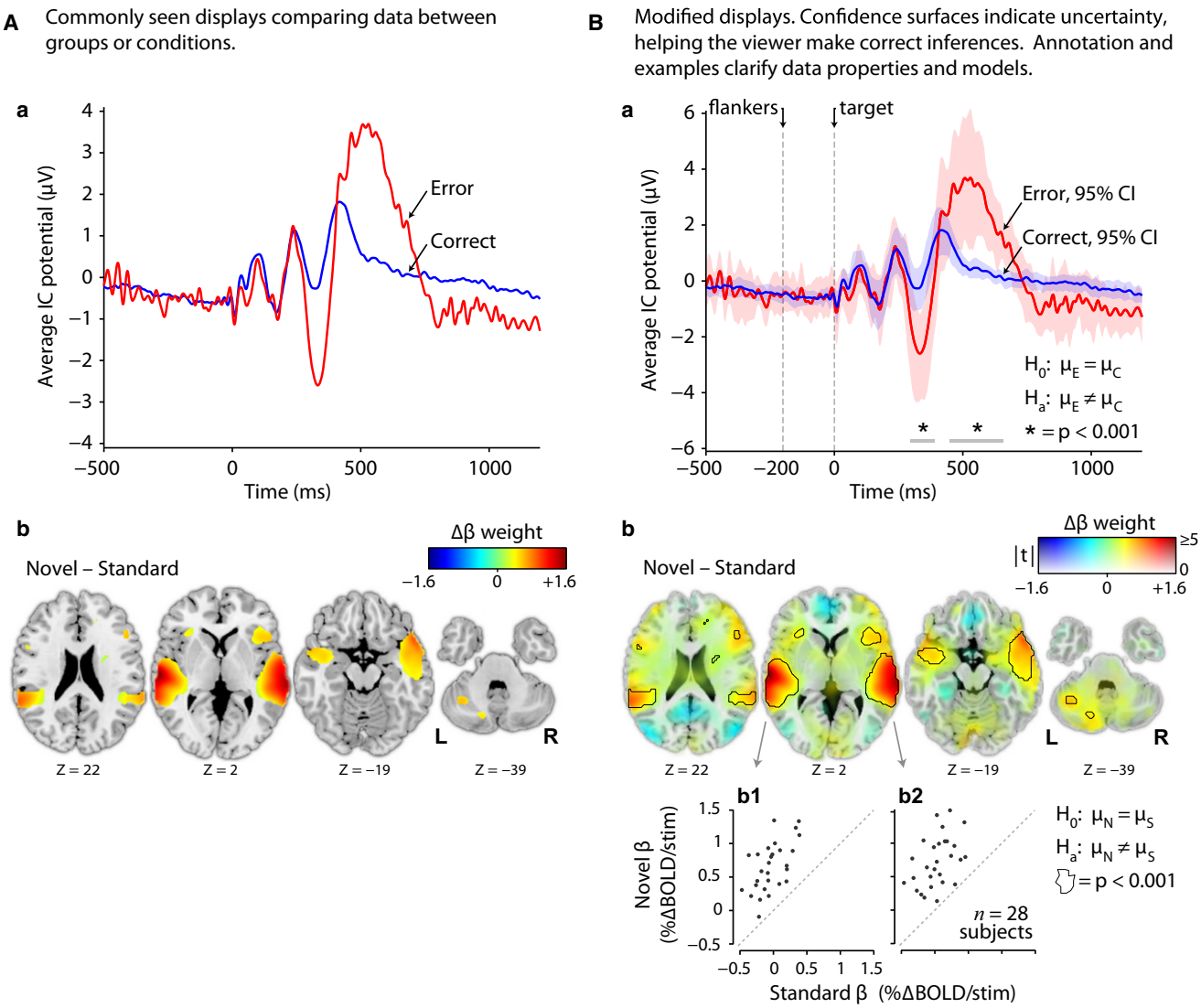


**Figure 3. Redesigning Figures**

Conventional (A) and modified (B) designs. Captions describe panel (B). (a) EEG flanker data. ERPs for error trials (red) and correct trials (blue) averaged over ten subjects. Error bands are 95% nonparametric CIs (1,000 bootstraps). Asterisks indicate significantly different ERPs at $p < 0.001$ (nonparametric randomization test, 10,000 randomizations, and implicit correction for multiple comparisons). (b) FMRI auditory oddball data. Axial slices show the difference between novel and standard beta weights averaged over 28 subjects. Beta difference is mapped to color hue; t statistic magnitude is mapped to transparency. Contours denote significantly different betas at $p < 0.001$ (two-tailed paired t tests corrected with false discovery rate). (b1 and b2) Scatter plots of standard versus novel betas for select regions. Beta weights are averaged over clusters of contiguous voxels passing significance (b1 = 2,426 voxels; b2 = 1,733 voxels). Dotted lines indicate y = x.

for each condition (rather than just the difference), reveal the degree of variability across subjects (and the absence of outliers), and validate our "paired" statistical approach, because beta values covary across conditions.

## Conclusion

A single figure may portray experimental data painstakingly collected over months or even years. Rather than use standard designs such as bar plots and thresholded maps that hide these data, we, as authors, peer reviewers, and editors, can establish new standards for visualizations that reveal data and inform readers.

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Supplementary survey analysis and MATLAB hue and transparency scripts for

# Data visualization in the neurosciences: overcoming the curse of dimensionality

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## 1 Survey details

Characteristics of surveyed figures are provided in Table S1. Survey questions were: 1) is the dependent variable or quantity of interest labeled? 2) Is the scale of the dependent variable indicated? 3) Where applicable, is a measure of uncertainty displayed? (We consider uncertainty or variability to be appropriate for descriptions of data distributions or parameter estimates, such as a population mean.) 4) Is the type of uncertainty (e.g., standard error bars or confidence intervals) defined in the figure or accompanying legend? While a definition of uncertainty may be provided elsewhere in the text, we believe it should be readily available to readers without having to scour the manuscript from beginning to end.

Examples of these graphical features are shown in Figure 1A for synthetic 2-dimensional (2D) and 3D datasets. For the 2D data (left), features 1 and 2 describing the dependent variable and its scale are found along the y-axis. Feature 3 is represented by error bars surrounding the parameter estimates, and feature 4 is found as the error bar label on the graph. For the 3D data (right), the outcome of interest is plotted as a function of two independent variables using a color map, which maps the values of the dependent variable to a continuous progression of color hue, or in this case, brightness. We define a color map as a display where the mapping between data values and color is *intentionally* performed by a researcher (in contrast to many photographic images and reconstructions where mapping is implicit). In the articles we sampled, color maps were by far the most common design used to display higher dimensional datasets. In the example, surveyed features 1 and 2 are indicated on the color-axis, or color bar. In this case, feature 3 is not shown, though generally uncertainty may be portrayed in a second color map (e.g., a map of standard errors), or integrated into a single map by plotting a test-statistic or using a dual-coding system as discussed in the main text. Because of the extra intention and notation required to display uncertainty surfaces, feature 4 does not apply to 3D axes. (Essentially, if it is clear that uncertainty is displayed, then it must have been labeled somewhere.)

For each article, binary ratings (yes or no) were assigned to all figures that displayed data in 2D or 3D graphs; schematics and other expository graphics were not evaluated. For multi-paneled figures, a single rating was assigned for each type of display (2D or 3D) based on the features present in the majority of panels. For results reported in Figures 1 and S1, proportions were determined first within each article then averaged over articles to remove the influence of the number of figures per article. Separation of survey

results by journal in Figure S1A shows that the prevalence of graphical features varies considerably, and that 2D and 3D graphical features covary slightly (Fig. S1B).

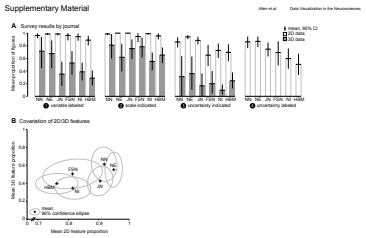



Figure S1: Survey results separated by journal. (A) Mean proportion of 2D (white) and 3D (dark gray) figures displaying each feature. Error bars denote 95% non-parametric confidence intervals (10,000 resamples). NN = *Nature Neuroscience*; NE = *Neuron*; JN = *Journal of Neuroscience*; FSN = *Frontiers in Systems Neuroscience*; NI = *Neuroimage*; HBM = *Human Brain Mapping*. (B) Scatter plot of the mean 2D feature proportion (averaged over features 1--4) versus the mean 3D feature proportion (averaged over features 1--3) for each journal. Crosses indicate mean data values; gray ellipses denote 95% confidence regions. See Table S1 for more information on the articles and figures surveyed.

Table S1: Frequencies and proportions of figures surveyed

| | Articles | Figures | Figures with 2D data | Figures with 3D data | Figures with 2D and 3D data | Figures with 2D categorical data | Figures with 2D continuous data | Figures with 2D categorical & continuous data |
|---|---|---|---|---|---|---|---|---|
| NN | 51 | 283 | 272 (0.96 $\pm$ 0.12) | 42 (0.13 $\pm$ 0.27) | 31 (0.10 $\pm$ 0.22) | 184 (0.61 $\pm$ 0.36) | 103 (0.35 $\pm$ 0.33) | 45 (0.14 $\pm$ 0.19) |
| NE | 50 | 344 | 332 (0.96 $\pm$ 0.13) | 44 (0.14 $\pm$ 0.27) | 32 (0.10 $\pm$ 0.23) | 236 (0.69 $\pm$ 0.33) | 141 (0.42 $\pm$ 0.32) | 75 (0.22 $\pm$ 0.25) |
| JN | 50 | 278 | 252 (0.89 $\pm$ 0.20) | 61 (0.25 $\pm$ 0.34) | 35 (0.14 $\pm$ 0.27) | 144 (0.51 $\pm$ 0.38) | 86 (0.33 $\pm$ 0.37) | 29 (0.11 $\pm$ 0.23) |
| FSN | 38 | 156 | 100 (0.55 $\pm$ 0.43) | 64 (0.43 $\pm$ 0.42) | 11 (0.06 $\pm$ 0.13) | 40 (0.23 $\pm$ 0.34) | 44 (0.24 $\pm$ 0.30) | 7 (0.03 $\pm$ 0.11) |
| NI | 49 | 190 | 141 (0.71 $\pm$ 0.33) | 88 (0.50 $\pm$ 0.36) | 39 (0.20 $\pm$ 0.31) | 45 (0.28 $\pm$ 0.32) | 59 (0.26 $\pm$ 0.30) | 7 (0.04 $\pm$ 0.14) |
| HBM | 50 | 200 | 121 (0.59 $\pm$ 0.35) | 122 (0.66 $\pm$ 0.31) | 43 (0.25 $\pm$ 0.28) | 57 (0.31 $\pm$ 0.33) | 31 (0.11 $\pm$ 0.25) | 3 (0.01 $\pm$ 0.06) |
| all | 288 | 1451 | 1218 (0.79 $\pm$ 0.32) | 421 (0.35 $\pm$ 0.38) | 191 (0.14 $\pm$ 0.26) | 706 (0.45 $\pm$ 0.38) | 464 (0.29 $\pm$ 0.33) | 166 (0.09 $\pm$ 0.19) |

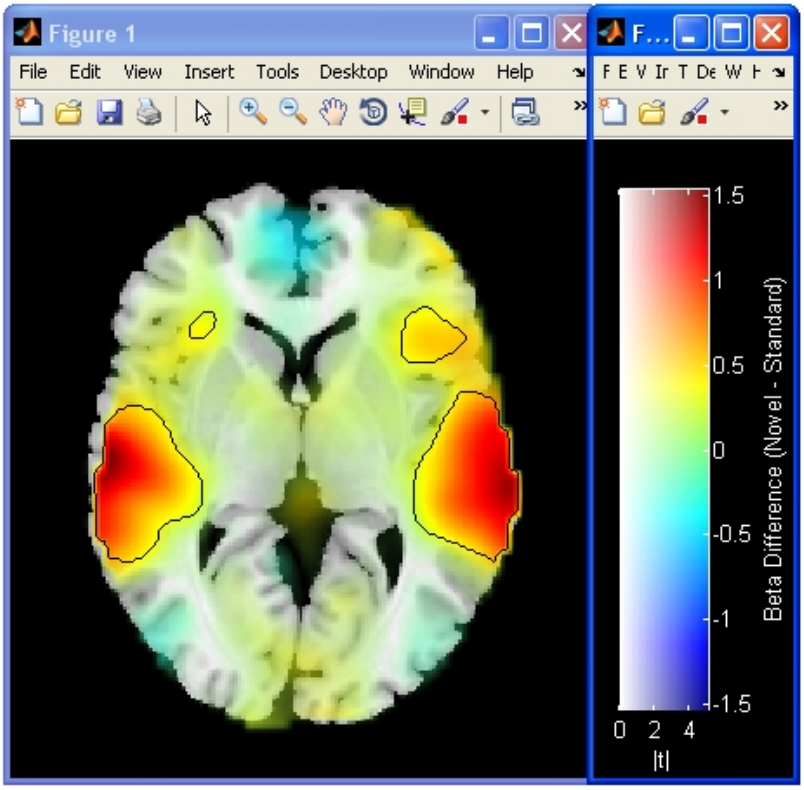
Data presented as number of occurences (mean proportion over articles $\pm$ s.d.). NN = *Nature Neuroscience*; NE = *Neuron*; JN = *Journal of Neuroscience*; FSN = *Frontiers in Systems Neuroscience*; NI = *Neuroimage*; HBM = *Human Brain Mapping*.

# 2 Creating dual coded images

Here we provide sample MATLAB scripts to encourage the generation of rich displays that portray uncertainty. We use example data from an fMRI auditory oddball (AOD) experiment to demonstrate dual color-mapping. Quantitative effects are mapped to color hue and effect uncertainty is mapped to color transparency. To run the code and see an example of dual coding, simply un-zip `sample_code.zip` in its own folder and run `dualcodeImage.m` from the command line:

```
>> cd sample_code
>> dualcodeImage
```

You should see something this:



## 2.1 dualcodeImage.m

The steps to produce this image are detailed in `dualcodeImage`.

```
%--------------------------------------------------------------------------
% Sample Matlab code for creating images with hue and alpha color-mapping.
%
%  Notes for using this code:
%  You must have OpenGL available on your system to use transparency (alpha).
%  When rendering transparency MATLAB automatically uses OpenGL if it is
%  available. If it is not available, transparency will not display.
%  See the figure property RendererMode for more information.
%
% EA Allen August 30, 2011
% eallen@mrn.org
%--------------------------------------------------------------------------

%% 1. Load the AOD_data.mat file with sample data from the fMRI AOD experiment
%--------------------------------------------------------------------------
load AOD_data.mat
% For a single axial slice (Z = 2 mm) of data, you should have:
% Bmap_N_S: 'Difference between Novel and Standard betas averaged over 28 subjects'
% Tmap_N_S: 'T-statistics for the paired t-test comparing Novel and Standard betas'
% Pmap_N_S: 'Binary map indicating significance at P<0.001 (fdr corrected)'
% Underlay: 'Structural image ch2bet from MRIcron, warped to functional data'
%--------------------------------------------------------------------------

%% 2. Set some defaults that will affect the appearance of the image
%--------------------------------------------------------------------------
% Set the Min/Max values for hue coding
absmax = max(abs(Bmap_N_S(:)));
H_range = [-absmax absmax]; % The colormap is symmetric around zero

% Set the Min/Max T-values for alpha coding
A_range = [0 5];
% Voxels with t-stats of 0 will be completely transparent;
% voxels with t-stat magnitudes greater or equal than 5 will be opaque.

% Set the labels for the colorbar
hue_label = 'Beta Difference (Novel - Standard)';
alpha_label = '|t|';

% Choose a colormap for the underlay
CM_under = gray(256);

% Choose a colormap for the overlay
CM_over = jet(256);
%--------------------------------------------------------------------------

%% 3. Do the actual plotting
%--------------------------------------------------------------------------
% Make a figure and set of axes
F = figure('Color', 'k', 'Units', 'Normalized', 'Position', [0.3, 0.4, 0.2, 0.35]);
axes('Position', [0 0 1 1]);
```

```
51
52 % Transform the underlay and beta map to RGB values, based on specified colormaps
53 % See function convert_to_RGB() for more information
54 U_RGB = convert_to_RGB(Underlay, CM_under);
55 O_RGB = convert_to_RGB(Bmap_N_S, CM_over, H_range);
56
57 % Plot the underlay
58 layer1 = image(U_RGB); axis image
59 hold on;
60 % Now, add the Beta difference map as an overlay
61 layer2 = image(O_RGB); axis image
62
63 % Use the T-statistics to create an alpha map (which must be in [0,1])
64 alphamap = abs(Tmap_N_S);
65 alphamap(alphamap > A_range(2)) = A_range(2);
66 alphamap(alphamap < A_range(1)) = 0;
67 alphamap = alphamap/A_range(2);
68
69 % Adjust the alpha values of the overlay
70 set(layer2, 'alphaData', alphamap);
71
72 % Add some (black) contours to annotate nominal significance
73 hold on;
74 [C, CH] = contour(Pmap_N_S, 1, 'k');
75 %--------------------------------------------------------------------------
76
77 %% 4. Create a 2D colorbar for the dual-coded overlay
78 %--------------------------------------------------------------------------
79 G = figure('color', 'k', 'Units', 'Normalized', 'Position', [0.5, 0.4, 0.06, 0.35]);
80 x = linspace(A_range(1), A_range(2), 256);
81 % x represents the range in alpha (abs(t-stats))
82 y = linspace(H_range(1), H_range(2), size(CM_over,1));
83 % y represents the range in hue (beta weight difference)
84 [X,Y] = meshgrid(x,y); % Transform into a 2D matrix
85 imagesc(x,y,Y); axis xy; % Plot the colorbar
86 set(gca, 'Xcolor', 'w', 'Ycolor', 'w')
87 colormap(CM_over);
88 alpha(X);
89 alpha('scaled');
90 xlabel(alpha_label)
91 set(gca, 'YAxisLocation', 'right')
92 ylabel(hue_label)
93 %--------------------------------------------------------------------------
```

## 2.2 convert_to_RGB.m

The script above is dependent on convert_to_RGB, which is used to transform pixel values with arbitrary scaling into a truecolor RGB image.

```
function IMrgb = convert_to_RGB(IM, cm, cmLIM)
% convert_to_RGB - converts any image to truecolor RGB using a specified colormap
%
% USAGE: IMrgb = convert_to_RGB(IM, cm, cmLIM)
%
% INPUTS:
%    IM    = the image [m x n]
%    cm    = the colormap [p x 3] <optional; default = jet(256)>
%    cmLIM = the data limits [min max] to be used in the color-mapping
%            <optional; default = [min(IM) max(IM)]>
% OUTPUTS:
%    IMrgb = the truecolor RGB image [m x n x 3]
%
% Based on ind2rgb from the Image Processing Toolbox
% EA Allen August 30, 2011
% eallen@mrn.org
%--------------------------------------------------------------------------
if nargin < 2
    cm = jet(256);
end

if nargin < 3
    cmLIM = [min(IM(:)) max(IM(:))];
end

IM = IM-cmLIM(1);
IM = IM/(cmLIM(2)-cmLIM(1));
nIND = size(cm,1);
IM = round(IM*(nIND-1));

IM = double(IM)+1;
r = zeros(size(IM)); r(:) = cm(IM,1);
g = zeros(size(IM)); g(:) = cm(IM,2);
b = zeros(size(IM)); b(:) = cm(IM,3);

IMrgb = zeros([size(IM),3]);
% Fill in the r, g, and b channels
IMrgb(:,:,1) = r;
IMrgb(:,:,2) = g;
IMrgb(:,:,3) = b;
```