A new method for estimating population receptive field topography in visual cortex

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Abstract

We introduce a new method for measuring visual population receptive fields (pRFs) with functional magnetic resonance imaging (fMRI). The pRF structure is modeled as a set of weights that can be estimated by solving a linear model that predicts the Blood Oxygen Level-Dependent (BOLD) signal using the stimulus protocol and the canonical hemodynamic response function. This method does not make a priori assumptions about the specific pRF shape and is therefore a useful tool for uncovering the underlying pRF structure at different spatial locations in an unbiased way. We show that our method is more accurate than a previously described method (Dumoulin and Wandell, 2008) which directly fits a 2-dimensional isotropic Gaussian pRF model to the fMRI time-series. We demonstrate that direct-fit models do not fully capture the actual pRF shape, and can be prone to pRF center mislocalization when the pRF is located near the border of the stimulus space. A quantitative comparison demonstrates that our method outperforms the direct-fit methods in the pRF center modeling by achieving higher explained variance of the BOLD signal. This was true for direct-fit isotropic Gaussian, anisotropic Gaussian, and difference of isotropic Gaussians model. Importantly, our model is also capable of exploring a variety of pRF properties such as surround suppression, receptive field center elongation, orientation, location and size. Additionally, the proposed method is particularly attractive for monitoring pRF properties in the visual areas of subjects with lesions of the visual pathways, where it is difficult to anticipate what shape the reorganized pRF might take. Finally, the method proposed here is more efficient in computation time than direct-fit methods, which need to search for a set of parameters in an extremely large searching space. Instead, this method uses the pRF topography to constrain the space that needs to be searched for the subsequent modeling.

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from the fMRI time-series by solving a set of linear equations for each voxel. This approach is similar to linear reverse correlation methods applied in electrophysiology (Ringach, 2004; Simoncelli et al., 2004). By avoiding a-priori assumptions, our method enables us to visualize pRF features such as surround suppression, or the anisotropic shape of the pRF. Visual inspection of the pRF topography can then guide the development of more appropriate models for fitting the pRF weights. This is particularly important in regions where the pRF shape is unknown. Even in early visual cortex, exploring the pRF topography reveals that pRF centers would be best modeled by an anisotropic Gaussian, in contrast to prevailing methods (Dumoulin and Wandell, 2008; Harvey and Dumoulin, 2011; Ziederbaan et al., 2012). This approach yields an estimate of the orientation and elongation of the pRF center in addition to an estimate of its location and size.

In order to evaluate the method we proposed, we compared its performance to that of direct pRF model fitting methods. Our method of estimating the pRF center outperforms the direct-fit isotropic Gaussian (DIG) (Dumoulin and Wandell, 2008), the direct-fit anisotropic Gaussian (DAG), and the direct-fit difference of isotropic Gaussians (DDoIG) (Harvey and Dumoulin, 2011; Ziederbaan et al., 2012) models by i) explaining a larger part of the BOLD signal variance, and by ii) providing more accurate eccentricity maps. In addition, visualizing the pRF topography as proposed here can make the subsequent modeling more efficient in computation time by constraining the pRF shape prior to the modeling. In contrast, direct-fit methods need considerably longer computation time as they have to select the best set of parameters in a much larger searching space.

**Material and methods**

**Subjects**

fMRI data were acquired from 4 participants (2 females, ages 23–26). All participants had normal or corrected-to-normal visual acuity. Experiments were conducted with the informed written consent of each participant and were approved by the Ethical Committee of the Medical Faculty of the University of Tübingen.

**Stimulus**

While scanning, participants fixated a central spot (radius: 0.0375°, 2 pixels) while a moving bar aperture exposed a moving square-checkerboard pattern with 100% contrast travelling across the visual field. The checkerboard pattern aligned to the longitudinal axis of the bar aperture moved in orthogonal directions of the bar movement. The stimulus was presented only over the central part of the visual field within a circular disk with radius 11.25°. The bar was moved sequentially in 8 different directions according to the following sequence [0, 135, 270, 315, 180, 45, 90, 225°] (Fig. 1A), where angles are reported counter-clockwise from the horizontal (0°) direction of the right visual hemifield. The long axis of the bar was orthogonal to the drifting direction. In each direction, the bar drifted 24 steps with each moving step being 0.9375°. The bar width was 1.875°. The position of the bar was updated for every image volume acquisition. The visual stimuli were generated with an adaptation of an open toolbox (VISTADISP), and Psychtoolbox (Brainard, 1997) in MATLAB (The Mathworks, Inc.). The stimulus was presented only over the central part of the visual field. The checkerboard pattern aligned to the longitudinal axis of the bar. The bar was moved sequentially in 8 different directions according to the following sequence [0, 135, 270, 315, 180, 45, 90, 225°] (Fig. 1A), where angles are reported counter-clockwise from the horizontal (0°) direction of the right visual hemifield.

**Data acquisition and preprocessing**

All subjects participated in scanning sessions to obtain T1-weighted anatomical volume and functional volume data. MRI and functional imaging were performed using a 3T whole body scanner (Trio Tim, Siemens, Erlangen, Germany) with a 12-channel head coil. Two T1-weighted anatomical volumes (T1 MPRAGE scan) were acquired for each subject and averaged to increase signal to noise ratio [matrix size = 256 × 256, voxel size = 1 × 1 × 1 mm³, 176 partitions, flip angle = 9°, TR = 1900 ms, TE = 2.26 ms, TI = 500 ms]. The structural data were used for segmentation of anatomical data into white and gray matter (Teo et al., 1997). Functional BOLD image volumes were acquired using gradient echo sequences of 28 contiguous 3 mm-thick slices covering the entire brain [repetition time [TR] = 2,000 ms, echo time [TE] = 40 ms, matrix size = 64 × 64, voxel size = 3 × 3 × 3 mm³, flip angle = 90°].

We performed 5–9 identical scanning sessions. In each functional session, 195 image volumes were acquired, the first 3 of which were discarded to allow for signal stabilization. Motion artifacts within and between runs were corrected (Nestares and Heeger, 2000). The functional images were co-registered with the averaged anatomical image using a mutual information method (Maes et al., 1997). All these preprocessing steps were performed using VISTA software (http://white.stanford.edu/software/). After detrending fMRI data in each scan with a cut-off frequency of 1 cycle per scan, all functional images across scans were averaged to formulate a volume series of 192 images.

**Estimation of pRF topography based on linear system analysis**

To predict the fMRI signals, we used a linear model for the fMRI response (Birn et al., 2001; Boynton et al., 1996; Friston et al., 1995; Hansen et al., 2004; Worsley and Friston, 1995). As opposed to the pRF model which directly uses a Gaussian model with a single sigma (Dumoulin and Wandell, 2008) to fit the BOLD data, we first use the BOLD data to estimate a weight vector representing the detailed topography of the pRF. Then, in a second step, we select an appropriate model to fit the observed pRF structure. The “stimulus presentation space” corresponding to a circular disk in the visual field, is represented as M pixels with size of 0.0187 × 0.0187 degrees per pixel. The stimulus at time t is denoted as $s(t) \in \mathbb{R}^M$ and the pRF at voxel i is denoted as $p_i \in \mathbb{R}^M$. Under the linear model, the presentation of the effective stimulus to the pRF of voxel i causes the following response:

$$r(t) = p_i^T s(t) \quad (1)$$

After convolution with the canonical hemodynamic response function (HRF) $h(t)$, the prediction of the BOLD response $d_i(t)$ at voxel i and time t is obtained:

$$d_i(t) = h(t) \ast \left( p_i^T s(t) \right) \quad (2)$$

The convolution in Eq. (2) is reformulated into:

$$d_i = Kp_i = Hs_i \quad (3)$$

where $H$ is a matrix form for the convolution of $h(t)$ and $S = [s(1), \ldots, s(t), \ldots, s(N)]^T$, (N: the number of volume instances). In our study, a two-gamma function (Friston et al., 1998; Glover, 1999; Worsley et al., 2002) with the default parameters in the VISTA software was used as the canonical HRF as follows:

$$h(t) = \left( d_1 / \alpha_1 \right) \exp((-t-d_1) / \beta_1) - c(t/d_2)^{\alpha_2} \exp(-(t-d_2) / \beta_2) \quad (4)$$

where $d_1 = 5.4, \alpha_1 = 5.98, \beta_1 = 0.90, c = 0.35, d_2 = 10.8, \alpha_2 = 11.97,$ and $\beta_2 = 0.90$.

Then, when the observed signal vector $y_i$ at voxel i is given, the pRF $p_i$ can be estimated via a least-square fit:

$$J_i = ||y_i - d_i||^2 = ||y_i - Kp_i||^2 \quad (5)$$
However, as this problem is underdetermined (i.e., $N \ll M$), it is necessary to exploit a mathematical trick and implement reasonable constraints in order to solve this problem. The first solution is to use the Moore–Penrose pseudoinverse (Haykin, 1999):

$$p_i = \left(K^T K\right)^{-1} K^T y_i$$  \hspace{1cm} (6)

While this technique provided the solution of Eq. (6), it did not reveal a smooth or clear topography for the pRF. The reason for this derives from the fact that the linear problem is underdetermined and fMRI signals are usually contaminated with various artifacts and noise. The underdetermined problem can be solved by introducing additional constraints on the receptive field structure via a regularization technique such as the ridge regression (using L2-norm minimization) (Hastie et al., 2001; Hoerl, 1970; Jain, 1985), the lasso regression (using L1-norm minimization) (Hastie et al., 2001; Tibshirani, 1996, 2011), and the elastic-net regression (using combinations of L2-norm and L1-norm minimizations) (Zou and Hastie, 2005). Generally, the lasso regression and the elastic-net provide a sparser solution than the ridge regression, but they are computationally expensive as they are not differentiable.

An appropriate method was selected as follows: a reasonable assumption for the pRF shape is that it should be localized in the visual space (i.e., sparseness in the distribution of weights; sparseness in the distribution does not guarantee localization in space, yet localization in space implies sparseness in the distribution) and it should change smoothly in space due to the fact that the pRF reflects aggregate properties of large numbers of single units with different receptive fields. In our investigation, the ridge regression yielded pRF shapes that satisfy the assumption. The lasso regression provided a sparse solution but not a reasonable pRF topography (i.e., not localized and smooth). The elastic-net yields a similar pRF shape to the one obtained by ridge regression since it also includes the L2-norm minimization. In the pRF topography of a visually responsive voxel, 3 central patches are obtained by thresholding at $k = [0.3, 0.5, 0.7]$, which are denoted by the dashed red lines. Then, among these patches, the best model is selected by assessing the explained variance (EV) of each model. In this example voxel, the model with threshold, $k = 0.7$, is selected as the best model, $m$. The text contains a more detailed account of the modeling process with the mathematical formulae and the calculation of explained variance. However, to illustrate the process of selecting a model for the pRF central region, the following is an example of the modeling process:

- Center Thresholding
- Model Evaluation
- Model at voxel $i$: $m_i = m_{i,k=0.7}$

Fig. 1. Illustration of the stimulus presentation protocol and the modeling of the pRF central region. (A) Stimulus presentation sequence. Checkerboard patterns were presented through a bar aperture within the stimulus presentation space, which is a circular disk of radius 11.25°. The stimulus presentation space is marked with a blue dot circle (not shown during the actual experiments). The bar moved sequentially in 8 different directions as indicated by the arrows. (B) Histogram of voxels as a function of the explained variance (EV) of each voxel’s pRF topography, illustrating here for $\lambda_1 = 5$. At a region of interest from non-visually responsive voxels, the mean of explained variance (0.11) of pRF topographies was calculated and used as threshold to select visually responsive voxels. In the histogram, the area above the threshold (dashed red line) corresponds to visually responsive voxels. (C) Process followed in modeling of the pRF central region. The left upper, left bottom, and right panels show the pRF topography; thresholding at the cross-section (black arrow in the pRF topography) of the topography (only for illustration purposes), and model evaluation, respectively. In the pRF topography of a visually responsive voxel, 3 central patches are obtained by thresholding at $k = [0.3, 0.5, 0.7]$, which are denoted by the dashed red lines. Then, among these patches, the best model is selected by assessing the explained variance (EV) of each model. (D) Process followed in modeling of the pRF central region. The left upper, left bottom, and right panels show the pRF topography; thresholding at the cross-section (black arrow in the pRF topography) of the topography (only for illustration purposes), and model evaluation, respectively. In the pRF topography of a visually responsive voxel, 3 central patches are obtained by thresholding at $k = [0.3, 0.5, 0.7]$, which are denoted by the dashed red lines. Then, among these patches, the best model is selected by assessing the explained variance (EV) of each model. In this example voxel, the model with threshold, $k = 0.7$, is selected as the best model, $m$. The text contains a more detailed account of the modeling process with the mathematical formulae and the calculation of explained variance. Note that the appearance of bar patterns across the pRF center originates not from the pRF structure but from the use of the bar aperture. See the Results section for a more detailed explanation. (D) Fraction of voxels that achieve a certain level of explained variance, across different $\lambda_1$ choices, in one subject. These graphs show the distribution of only the visually responsive voxels. The data from the other subjects behaved very similarly (not shown). The fraction is defined as the ratio of the number of voxels for a certain $\lambda_1$ to the maximum number of voxels across $\lambda_1$ s that belong in the same EV bin (e.g., 0.1–0.3). At each EV bin, the fraction of voxels is plotted across $\lambda_1 = [0.1, 0.5, 1, 5, 7, 10, 13, 16, 20, 25, 30]$. 

$\text{J}_i = ||y_i - K^+ p_i ||^2 + \lambda_1 ||p_i ||^2$  \hspace{1cm} (7)

where $K^+ = \left[ K^{-1} K \right]$, $p_i = [p_1 \alpha]$ ($\alpha$ is a constant value introduced to account for the bias), and $\lambda_1$ is a free parameter to control the extent to
which the least-square function is regularized. The solution of Eq. (7) is given:

\[
p_i^+ = (K^T K + \lambda_I I)^{-1} K^T y_i
\]  
(8)

Where \(I = \begin{bmatrix} 1 & 1 & \cdots & 0 \\ 0 & 1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & 1 \end{bmatrix} \) and \(\lambda_I = \lambda^{M-M} \).

In our experiments, the screen resolution was 800 × 600 pixels, and a circular disk circumscribed within a central square area composed of 360,000 (600 × 600) pixels was used to present the stimulus. The stimulus size corresponding to the square was down-sampled to 101 × 101 to increase the computation efficiency (This value is the default setting in the VISTA software; implementations of our algorithm were carried out using VISTA software by replacing Dumoulin’s method (Dumoulin and Wandell, 2008)).

**Modeling the central region of the pRF**

Here, we define pRF center, pRF central region, and pRF center model. The pRF center is the point which exhibits the maximum positive peak in the receptive field and the pRF central region is the area that is positive, surrounding the center point. These notions parallel the classical receptive field terminology commonly used in physiology. The pRF center model denotes the model we apply to fit the pRF central region.

In our model, there are two free parameters: the regularization parameter, \(\lambda\), and the cut-off threshold to define the pRF central region, \(k\). For each value of \(\lambda\), topographies of pRFs were estimated for all gray matter voxels and visually responsive voxels were identified (Fig. 1B).

For this, a region of interest (ROI) of a sphere with a radius of 10 mm was created in a non-visually responsive area. Then, explained variance (EV) was computed as:

\[
EV(p_i) = 1 - \frac{\|y_i - K^+ p_i\|^2}{\|y_i\|^2}
\]  
(9)

The mean EV (\(\langle EV > \approx 0.1\)) in a non-visually responsive ROI (e.g., a sphere of diameter 10 mm from the lower medial prefrontal cortex) was used as a threshold to select voxels that visually respond. The mean explained variance in a visually non-responsive area corresponds to the portion of the explained variance that could be due to noise. This is a reasonable choice for setting the threshold for identifying voxels that visually respond, since we want to err on the side of caution, i.e., not exclude any visually responsive voxels from the initial pRF estimate. After estimating the full pRF topography (\(p_i\)), we define a strategy for extracting the pRF central region. Typically, the structure of the pRF has a dominant region while more distant visual field locations have much smaller, potentially suppressive, contributions. Fig. 1C illustrates the strategy we use to identify and model the central part of the pRF topography, which presents the dominant excitatory field (Fig. 1C). First, the components of the pRF vector \(p_i\) are normalized to lie between 0 and 1. Then, three regions of the pRF vector (corresponding to more or less restrictive estimates of the pRF central region) at each voxel are obtained by thresholding the topography at three values, \(k = \{0.3, 0.5, 0.7\}\). The pRF topography patch remaining after thresholding (i.e., each topography of the pRF central region) was fitted with a 2D-Gaussian model:

\[
\exp\left(-\frac{1}{2(\mathbf{g} - \mathbf{\mu})^T \sum_i^{-1} (\mathbf{g} - \mathbf{\mu})}\right)
\]  
(10)

whose center and dispersion are

\[
\mathbf{\mu} = [x_i y_i]^T
\]  
(11-1)

and

\[
\sum = \begin{bmatrix} \cos \theta & -\sin \theta \\ \sin \theta & \cos \theta \end{bmatrix} \begin{bmatrix} \sigma_x^2 \\ \sigma_y^2 \end{bmatrix}
\]  
(11-2)

To find the optimal parameters for each pRF central patch, we applied a nonlinear curve-fitting method at voxel \(i\) and threshold \(k\):

\[
\min_{\mathbf{a}, \mathbf{b}, \mu, \lambda} \|p_i - \mathbf{a} \exp\left(-\frac{1}{2(\mathbf{g} - \mathbf{\mu})^T \sum_i^{-1} (\mathbf{g} - \mathbf{\mu})}\right) + \mathbf{b}\|^2,
\]  
(12)

where \(p_i\) is the topography patch for the pRF central region at voxel \(i\) and threshold \(k\), and \(\mathbf{g} = \mathbf{g}_k\) the corresponding stimulus space, and \(a, b = \mathbf{a}\) and \(\mathbf{b}\) are a scale and a bias, respectively. This implementation was performed via the optimization toolbox of MATLAB. After determining the parameters of the 2D-Gaussian model, the EV of each model at each voxel was obtained:

\[
EV(m_k^i) = 1 - \frac{\|y_i - \mathbf{K} m_k + \beta_i\|^2}{\|y_i\|^2},
\]  
(13)

where \(m_k^i = \exp\left(-\frac{1}{2(\mathbf{g} - \mathbf{\mu})^T \sum_i^{-1} (\mathbf{g} - \mathbf{\mu})}\right)\) at voxel \(i\) and threshold \(k\), \(\beta_i\) and \(\beta_2\) are a scale factor and a bias, respectively. That is, each voxel has 3 different models according to the threshold, \(k\), defining the pRF central region. Among the three different models, the best one was selected with respect to the EV (Fig. 1C). Hereafter \(m_k^i\) indicates the model with the best threshold among the candidates.

To select the best \(\lambda\) across the range \(\lambda = [0.1–30]\), we considered the distribution of voxels with EVs ranging from 0.1 to 0.9 binned in intervals of size 0.2 (Fig. 1D). As \(\lambda\) increases, the fraction of voxels with lower and intermediate EV values (0.1-0.7) was quickly saturated (Fig. 1D), suggesting that it was insensitive to high values of \(\lambda\). However, at the EV bin (0.7–0.9), the number started decreasing after reaching a maximum (Fig. 1D). From this pattern, to maximize the mean EV in low EV bins while minimizing the loss of the EV in the high EV bins, we chose the lambda for which the mean fraction (thick black line in Fig. 1D) of voxels across all of the EV bins reached 0.95. Data from all other subjects showed similar results (not shown here). Hereafter, we used the selected lambda for all the following analyses.

**Estimates from the direct-fit models**

Direct-fit methods first model the pRF shape as a certain parametric model, and then find optimal parameters for the model to minimize the residual between the observed fMRI signal and the signal predicted from the model (Dumoulin and Wandell, 2008). This approach used a two-stage coarse-to-fine search to reduce the computation time. In the coarse search, sparsely sampled voxels were used to estimate parameters in the grid fitting after spatial smoothing. That is, the grid fitting had hundreds of thousands of sets of different parameters (e.g., 2-location and 1-dispersion parameters per voxel in the DIG model), which were assessed with respect to the explained variance to find the best parameter set at an individual voxel. Then, after interpolating the parameters of all gray voxels from the parameters of the sparsely sampled voxels, the fine search was applied in unsmoothed raw data to further optimize the parameter set.

The grid-search method in this approach requires a long computation time. Even though this approach permits the use of various models such as the anisotropic Gaussian model and the difference of Gaussians model, its applicability to testing models composed of more parameters is limited because the search space increases exponentially with the number of parameters.
Comparison between methods

We compared our method with the previously described method that directly fits isotropic Gaussian (DIG) models (Dumoulin and Wandell, 2008). Even though many recent studies only tested DIG models (Dumoulin and Wandell, 2008; Levin et al., 2010; Winawer et al., 2010), to be fair, we further compared our method with the directly fitting anisotropic Gaussian (DAG) method.

For a quantitative comparison, we used a cross-validation strategy by using a ‘leave-one-scan-out’ method. That is, for each turn, data from a single fMRI scan were left out for testing while data from all remaining scans were used to estimate the model. This process was repetitively performed for all scans. Since we collected a different number of scans in subjects, ‘x’-fold cross validation was performed, where ‘x’ indicates the number of scans in each subject. Each time, the comparison test was performed by measuring the amount of variance accounted for by the estimated model.

For the model estimation in the training data, we considered only patches covering the central region of the pRF model that were modeled as two-dimensional Gaussians because the main aim of our modeling here was to estimate the pRF central area. Note that this comparison used patches from the models rather than the extracted area from the topography since the direct fitting methods cannot provide the topography. The patch $m^{thr}_i$ which covered the central region of the pRF model was obtained by thresholding the normalized Gaussian models (i.e. a magnitude of 0-1) with a range of $thr = [0.1, 0.3, 0.5, 0.7]$ after building the models (i.e., $exp(-1/2(g - \mu)^T \sum^{-1}(g - \mu)$) in our and DAG approaches and $exp(-1/2\pi(g - \mu)^T(g - \mu))$ in the DIG approach (Dumoulin and Wandell, 2008) with the estimated parameters. We call this value the threshold for the pRF central region. The threshold value of 0 indicates a complete stimulus area. Then, we assessed how much variance the patch from each model explains in the testing data:

$$EV(m^{thr}_i) = 1 - \frac{\|y_i - (\beta_1 d^{thr}_i + \beta_2 S^{thr}_i)\|^2}{\|y_i\|^2}$$ (13)

Where $d^{thr}_i = HS^{thr}_i m^{thr}_i$, $S^{thr}_i$ is the stimulus area corresponding to $m^{thr}_i$ (central patch after thresholding the best model, $m_0$, at $thr$), and $\beta_1$ and $\beta_2$ are a scale factor and a bias, respectively.

This comparison was performed at the voxels where the EV of either the proposed model, or the DIG/DAG model was above 0.2 (small enough to include all early visual areas). The use of the union set means that voxel selection was not biased to either method. To avoid penalizing the direct-fit methods that completely miss pRF parameters in some voxels (leading to $EV = 0$ despite EV from the proposed >0.2) we excluded those voxels. On the contrary, we did not exclude any voxels estimated by our method; therefore this gives an advantage to the direct-fit methods in the comparison. More specifically, in the first stage of computation the direct-fit method performs pRF estimation only in the sampled voxels after spatial smoothing and the subsequent interpolation process derives the model parameters along all cortical voxels from the parameters of the sampled voxels. This interpolation process might sometimes provide completely different parameter values from the actual ones by estimating model parameters from sampled poor BOLD signals. Therefore, good signals could be excluded in the later optimization stage (see Appendix A for more details).

To avoid potential errors of pRF center estimation near the border of the stimulus space, the comparison was performed only on pRFs whose center resides within the stimulus space for both methods, and which have EV above 0.2. This is also a relative disadvantage for our method that provides more accurate estimates of the pRF centers near the border of stimulus space (see Results section).

In order to compare the models we evaluated their ability to estimate the pRF center over the central region of the receptive field as defined by the thresholded topography. This is a fair comparison, particularly since the DIG and DAG models intrinsically assume that the pRF consists only of a strong excitatory field without any surround inhibition, and therefore will be prone to errors arising from the existence of the surround. On the other hand, Zuiderbaan et al. (2012) used the direct-fit difference of isotropic Gaussians (DDoIG) to account for the surround inhibition as well as the excitatory center. Therefore, we also compared the proposed and DDoIG methods for the pRF center modeling as above.

Results

PRF topographies and comparison between pRF center models

We ensured that our model could estimate reasonable pRF structures based on the assumption of localization and smoothness in space (Fig. 2A), enforced by regularization (see Material and methods section). In the typical topography, we observe one strong positive peak and weaker bar patterns crossing the peak (Fig. 2A). The strong positive peak corresponds to the pRF center since it is located in the most responsive position. The appearance of bar patterns in the topography is associated with the fact that areas along directions of the bar movements across the pRF center are stimulated at the same time as the pRF central region. That is, while the pRF central region evokes a robust BOLD response eight times (from 8 bar sweeps), the non-central bar areas along each orientation that are simultaneously stimulated with the center induce a BOLD response twice (from 2 sweeps in each orientation) and thus crossing bar patterns appear appropriately weaker in the topography.

The central region of the pRF topography was modeled with an anisotropic Gaussian in our method. This model was qualitatively compared to direct-fit methods (Dumoulin and Wandell, 2008). As shown in Fig. 2B, the DIG method could not capture anisotropy in the pRF by definition (being isotropic), while direct-fit anisotropic models (DAG) can capture anisotropies better. However, even the introduction of anisotropy in the model, i.e. DAG, could not capture the pRF orientation as well as the proposed method (see voxel 141960 in Fig. 2B). Furthermore, either direct-fit method could not localize the pRF center as well as the proposed method (see voxels 129112 and 321775 in Fig. 2B). This is probably because the direct-fit methods minimize the residual between their prediction and the observed fMRI signal regardless of the actual location of the pRF center region (Fig. 2B).

For a quantitative comparison, we used cross-validation tests by employing a ‘leave-one-scan-out’ method (see Material and methods section). Specifically, after obtaining the mean explained variance (mEV) at each voxel from the testing data, the distributions of the mEV difference between the two methods were plotted at each voxel. EVs were obtained only taking into account the pRF center regions, which were determined using the thresholds [0.1–0.7] for each method. This comparison showed that the method we propose performs better as threshold increases, leading more voxel EVs to be positive and greater than EVs estimated with the DIG or DAG models (Fig. 3; EV-diff > 0.05 with $p > 0.5$ at $thr = 0.1$, and EV-diff > 0.05 with $p < 1e-10$ for $thr = 0.3, 0.5, 0.7$ for both DIG and DAG models; one-tailed t-test). This implies that the proposed method models the pRF center region better than direct-fit methods. As expected, the difference between the two methods is smaller at lower thresholds. This is because direct-fit methods optimize the parameters in the full stimulus space, while the topography-based method selects the local area of the pRF center prior to model optimization. Since the pRF center resides in the local stimulus space (narrowing its localization to within a few degrees of visual angle) compared to a range of ~11° (stimulus space radius) for the full stimulus space, optimizing the pRF parameters in the full stimulus space leads to a less accurate estimate, and lower EVs.

The direct-fit methods sometimes yield pRF models with centers at higher eccentricity than the radius of the stimulus presentation area (i.e., the pRF center can be located outside the stimulus presentation space; see Fig. 4). Since our method estimates the topography it can...
better optimize the model fit for voxels whose pRF center falls outside the stimulus space outperforming the direct-fit methods there. To ensure that this is not the only reason we outperformed the DIG and DAG methods, we performed the same analysis restricted to voxels for which the eccentricity of the pRF center from both models falls within the stimulus space. This comparison also shows that the method we propose performs better as threshold increases, leading to more voxel EVs to be positive and greater than EVs estimated with the DIG and DAG models. Supplementary Fig. 1; EV-diff > 0.01 with \( p > 0.5 \) at \( \text{thr} = 0.1 \), and EV-diff > 0.01 with \( p < 1 \times 10^{-10} \) for \( \text{thr} = 0.3, 0.5, 0.7 \) for both DIG and DAG models; one-tailed t-test.). These results show that the proposed method is more robust in estimation of pRF center parameters both within and outside the stimulus presentation space than direct-fit methods. Note that this is the case despite the fact that this comparison was chosen to be biased in favor of direct-fit methods: i.e. we excluded voxels that could not be reliably modeled with the direct-fit methods because of their proximity to the stimulus border.

Eccentricity and polar angle maps

We compared the eccentricity maps for the three methods. Differences between the maps were mainly observed at high eccentricities (Fig. 4A). The proposed method yielded more voxels than the DIG and DAG methods with centers at 8°–11.25° eccentricity, but fewer voxels.
Fig. 4. Comparison of eccentricity maps derived from the proposed method versus direct-fit models. (A) Eccentricity maps from one subject are illustrated. From the top to the bottom row, eccentricity maps are shown for the full eccentricity range, for 8–11.25°, and for >11.25° of eccentricity, respectively. The panels left to right show eccentricity maps from the DIG (direct-fit isotropic Gaussian), the DAG (direct-fit anisotropic Gaussian), and the proposed methods, respectively. (B) PRF topographies from the 3 locations shown in (A). In panel (A), the locations are indicated by *, **, and *** respectively. On the top of each panel, the pRF center eccentricity in degrees and the corresponding explained variance is shown. Normalized pRF weights are plotted in the range from 0 to 1.
with centers beyond the border of the stimulus presentation space, i.e. > 11.25° (Fig. 4A). In addition, the eccentricity maps derived from the direct-fit models exhibit discontinuities by showing some regions where distant eccentricities intermingle (areas outlined by the white dashed lines in Fig. 4A). This differs from the results of our method, which leads to relatively gradual changes in the eccentricity map. For example, in Fig. 4, the non-physiological distinct eccentricity “island” patterns (inside the dashed circles) seen with the direct-fit methods are far less prominent using the method we propose here. To illustrate the difference, we examined the pRF topography at the voxels marked with * and ** in Fig. 4A. In the first voxel (*), the DIG, the DAG, and the proposed method estimated the pRF center to lie at 12.4°, 13.1°, and 7.8° eccentricity with explained variances of 0.77, 0.79, and 0.79, respectively (Fig. 4B). In the second voxel (**), the corresponding numbers are 21.3°, 14.4°, and 7.3° with explained variances of 0.31, 0.53, and 0.53, respectively. For both voxels, the pRF topographies (Fig. 4B) clearly show that the pRF center is well within the stimulus space indicating that our method provides more accurate results in this range of eccentricities. This is even more striking for voxels whose pRF centers, as estimated by the direct-fit models, lie at eccentricities > 11.25°. Markedly fewer voxels are estimated to have centers that lie in this eccentricity range using our method compared to estimates derived from the direct-fit models (Fig. 4A). An example is the voxel marked with *** in Figs. 4A and B. Note again that its center is estimated erroneously to lie at 21.5° and 20.3° with the DIG and DAG methods, as compared to 8.6° with the method proposed here. Inspired by these examples, we examined the relation between the difference in eccentricity and the difference in explained variance of the pRF-center estimates derived from the proposed versus the direct-fit methods (see Supplementary Fig. 2). Supplementary Fig. 2 shows that pRF center estimates derived by direct fit methods that lie in high (non-physiologic) eccentricities do not typically lead to higher explained variance as compared to the proposed method. These results would originate from the fact that direct-fit methods minimize the residual between the actual BOLD signal and their prediction without first constraining the location of the pRF center. Therefore, noisy or suppressive surround regions distant from the true pRF center can contribute significantly to explained variance estimates and lead to erroneous or biased fitting of the pRF center. On the other hand, the proposed method first suppresses low SNR responses in the pRF topography via regularization (see Eq. (7)) and then fits a model to the high SNR peak of the pRF topography.

We then examined the distribution of the voxels’ eccentricity estimated by the 3 different methods (Fig. 5). A strong bias is observed at high eccentricities in the histogram of the two direct-fit methods, seen at ~22.5°. This is particularly evident in the DIG method, but does not appear at all in the proposed method. This bias is not physiological, given the known properties of population receptive field size as a function of eccentricity, particularly for early visual areas (Burkhalter and Van Essen, 1986; Felleman and Van Essen, 1987; Gattass et al., 1981, 1987; Newsome et al., 1986). Moreover, this result is inconsistent with the previous finding that the number of voxels gradually decreases with increase of eccentricity (Daniel and Whitteridge, 1961; Hubel and Wiesel, 1974). For the proposed method, another bias was observed at eccentricities near the border of the stimulus presentation space. This happens particularly when voxels with low explained variance (EV > 0.2) are included (Fig. 5). This bias manifests as a sharp drop in the histogram peak as pRF center eccentricity crosses the stimulus space border. This happens because the proposed method tends to map the center of pRFs that are truncated by the stimulus space border inside that border, even though sometimes they may be located outside the stimulus space (see Fig. 6C). The proposed method models pRFs with centers just outside the stimulus presentation space with a smaller error than direct-fit methods because it calculates the model based on the thresholded excitatory fields observed in the pRF topography. PRFs with centers far outside the border of the stimulus presentation space are unlikely to yield strong excitatory fields within the stimulus presentation space in the pRF topography. As the threshold for the explained variance increases both biases are degraded by removing inaccurate estimates arising from low SNR signals (Fig. 5 and Supplementary Fig. 3). Nonetheless, the direct-fit methods still result in many voxels whose pRF center resides far outside the stimulus space, e.g., greater than 5° distant to the stimulus space border, whereas the proposed method does not.

In addition, the proposed method identified more voxels with higher explained variance (e.g., 0.4) in all visually responsive voxels (Fig. 5), as well as in the visual field maps of areas V1-3 specifically (Supplementary Fig. 3). Since pRF centers lying at eccentricities 6°–8° are unlikely to be truncated by the border of the stimulus presentation aperture (11.25°), the superior performance of the proposed method in explaining variance results at least in part from the accurate capture of pRF center shapes.

We examined the relationship between eccentricity and explained variance (Supplementary Fig. 4). Given the relationship between pRF size and eccentricity (Burkhalter and Van Essen, 1986; Felleman and Van Essen, 1987; Gattass et al., 1981, 1987; Newsome et al., 1986), pRF centers lying far beyond the stimulus presentation area are expected to yield lower explained variances than those just outside the stimulus presentation area. Our methods of pRF center estimation obey this expectation. In contrast, direct-fit methods yield high explained variance even for voxels whose pRF centers lie far beyond the stimulus presentation space. This further suggests that pRF centers estimated by the direct-fit method to lie far beyond the stimulus space are unlikely to be correct.

In Figs. 6A, B, and C we illustrate the conditions under which different pRF estimation methods could potentially misbehave. When the pRF center is inside the stimulus space, an anisotropic Gaussian model can reliably identify the pRF properties (Fig. 6A) regardless of whether the true pRF is isotropic or anisotropic. If the true pRF center is outside the stimulus space and the pRF central region is isotropic, an isotropic model may, in principle, better estimate the true pRF center (Fig. 6B). Regardless of the pRF actual shape, however, the DIG and DAG methods tend to mis-localize the pRF center when it lies near the stimulus space border leading to the large, non-physiological bias seen at large eccentricities (Fig. 5). This is because these methods minimize the residual between the actual BOLD signal and its prediction without constraining the stimulus space over which the optimization is done. This bias is stronger in the DIG method in part because pRFs are not necessarily isotropic, and in part because errors in pRF localization from models assuming isotropy can be large and biased towards high eccentricities (pRF C2 in Fig. 6C).

For the proposed method, the pRF center modeling can be successfully performed only for the pRF center located within the stimulus space. On the other hand, when the pRF center is outside the stimulus space, the subsequent modeling process is prone to identify one location of the stimulus space border as the pRF center (pRF C1 in Fig. 6C). These qualifications notwithstanding, the method proposed here results in more accurate positioning of the pRF center than the directly-fitting models (Dumoulin and Wandell, 2008). This is because having access to the pRF topography allows us to constrain the central region of the pRF prior to fitting, and because even for pRF topographies that are in part outside the stimulus presentation space, the actual pRF centers are likely to lie close to the border of the stimulus presentation space as mentioned above. This is because the typical pRF size at corresponding eccentricities in early visual areas remains restricted below 5° (Burkhalter and Van Essen, 1986; Felleman and Van Essen, 1987; Gattass et al., 1981, 1987; Newsome et al., 1986). Regardless of what shape the pRF structure is outside the stimulus presentation space, direct-fit methods are subject to large errors in localizing the pRF center when it lies outside the stimulus presentation space (e.g., C2 of Fig. 6C). In contrast, even when it is unable to precisely identify the exact pRF center location, the proposed method can at least give us an approximate estimate of the pRF center location by extrapolating from the portion of the true pRF topography that lies within the stimulus presentation space.
On the contrary, comparing polar angle maps showed no discernible difference between the models (Fig. 7). As shown in Figs. 6 A and B, even when the pRF center is outside the stimulus space, similar polar angles are estimated with both methods if the dominant peak (i.e., a part of the pRF center) is at least observable near the border of stimulus space. In other words, the polar angle of the pRF center is dependent on the location of its peak, and thus estimates from both methods are likely to be similar (Figs. 6A and B). Even though the direct-fit models are not constrained by pre-calculating the pRF topography, all the methods provided polar angle estimates similar to those of the actual pRF centers (as determined by the topography).

pRF size estimates using different methods

We also examined whether the proposed method yielded different relationships between pRF size and eccentricity in comparison with the DIG and DAG methods (Fig. 8). For this analysis, the pRF size was defined as the single Gaussian dispersion parameter $\sigma$ for the DIG and $(\sigma_1 + \sigma_2)/2$ from Eq. (11-2) for the DAG and the proposed methods. The comparison was performed in the visual field maps V1-3 of the left hemisphere of all 4 subjects. For this comparison, we selected voxels with explained variance above 0.4 in the visual field maps of areas V1-3 and then plotted the relationship between pRF size and eccentricity for eccentricities 2° - 9°. For these eccentricities modeling of the pRF centers was reliable for all three methods given the bar aperture size, sweep step, and stimulus space extent that we have used (see Fig. 8 and also Figs. 4-5). This comparison showed that while all the 3 methods showed similar linear relationships between pRF size and eccentricity, the proposed method modeled pRFs across V1-3 more reliably than the DIG and DAG methods as it identified more voxels with EV > 0.4. These results support that the higher explained variance obtained with our method did not originate from arbitrary capturing of the pRF shape.

Presence of surround suppression in the pRF

The visualization of pRF topographies allowed us to observe evidence of surround suppression. To examine whether the proposed method can capture characteristics of surround suppression, we carefully examined the pRF topographies and the raw BOLD signals. Surround suppression...
manifests in the topography as a suppression or disappearance of the crossing bar patterns near the pRF central region (Fig. 9A). This suppression particularly occurs when negative BOLD responses (NBR) are observed (Fig. 9A). For instance, when the bar aperture moved from the left to the right, the bar pattern faded away before reaching the positive peak (left panel of Fig. 9A). Correspondingly, a negative dip was observed before the main positive BOLD response (see the first red circle in Fig. 9A). To illustrate how surround suppression is related to the NBR, a hypothetical pRF model with surround suppression was considered by using the difference of two Gaussians (DoG) (Fig. 9B). This choice was based on the assumption that NBRs can be explained by convolving the response from the surround of the pRF (e.g., \(-0.3G(6,0.5,4,0)\) in Fig. 9B) with the HRF under the linear assumption (Zuiderbaan et al., 2012). Using this hypothetical model, an estimate of the BOLD signal was generated by using the stimulus applied in our experiment and the canonical HRF. The proposed method was then applied to estimate the pRF topography (Fig. 9C). In this topography crossing bar patterns disappeared near the pRF central region (Fig. 9C) because of the surround inhibition introduced in the generating model (panel B). As expected, the DoG model yielded negative dips in the BOLD signal immediately before or after the main BOLD peaks caused by stimulation of the pRF central region (Fig. 9C). These results closely match the actual BOLD response and the actual pRF topography of the voxel shown in Fig. 9A. Then we modeled the pRF from the topography shown in Fig. 9C using one single Gaussian (i.e., ignoring surround suppression), and predicted the BOLD responses. The predicted BOLD signal (Fig. 9C, green curve) did not show strong negative dips (Fig. 9C). This exercise confirmed that the observed negative dips can be interpreted as an effect of surround suppression, which a single Gaussian model does not capture. The proposed method can therefore be used to model pRFs with center surround structure.

A question arises whether the improved performance of the method we propose could be due to the existence of the inhibitory surround. This might be because the proposed method uses a thresholding step to separate the pRF central region from the full pRF topography (that includes the surround) before fitting, which the DIG and the DAG methods could not do. In order to investigate whether this is the case, we also compared the proposed method to the direct-fit difference of isotropic Gaussians (DDoIG) model (Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012). The DDoIG model models the surround suppression as an additive negative isotropic Gaussian and can therefore take into account the symmetric aspects of surround suppression while modeling the pRF center. For this comparison, we used only isotropic Gaussians to build the pRF center and surround model in the direct-fit method, following the approach of (Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012). In fact, anisotropy in the pRF center has been revealed in our study through direct observation of the topographies; it has not been assumed in previous studies (Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012). Moreover, given the present computing power of PCs, it is impractical to introduce anisotropic Gaussians for the pRF center and surround in the direct-fit method as the computation time increases dramatically.

It is important to note that there are also other reasons not to model the surround in this study. Specifically, although the pRF topography from the proposed method reveals the presence of surround suppression for some voxels (Fig. 10), the surround suppression generated by our stimulation protocol was generally weak, making it thus difficult to 1) separate surround suppression from noise artifacts, and to 2) dissociate the late dip of the hemodynamic response function (i.e., the negative gamma function of Eq. (4) following an early strong excitation response) from the weak negative BOLD response of surround suppression. Furthermore, the extent of suppression might be asymmetric (like the center) along different directions than the pRF center and partially depends on the regularization parameter \(\lambda_1\) of Eq. (7). Furthermore, a recent study by (Goense et al., 2012) reported a larger nonlinearity in the negative BOLD response than in the positive one, which further hinders the estimation of the surround. Therefore, we examined whether the estimate of the pRF center derived from the DDoIG model (Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012), could outperform the estimate of the pRF center model derived from the proposed method.

The difference in explained variance between the proposed and the DDoIG method for pRF center modeling (Fig. 10) is smaller than the one between the proposed, and the DIG and DAG methods (Fig. 3). This suggests that inclusion of the surround suppression in the pRF modeling improves the estimate of the pRF center (Supplementary Fig. 5). However, as we demonstrate in Fig. 10, despite introduction of the surround suppression in the direct-fit method, the direct-fit method could not outperform the proposed method in modeling the pRF center. Specifically, our method resulted in equal or higher explained variances compared to the DDoIG method for all thresholds tested: EV-diff > 0.1 with \(p > 0.5\) at thr = 0 (whole stimulus space), and EV-diff > 0.1 with \(p < 0.05\) at thr = 0.3 and \(p < 1e-10\) at thr = 0.5, 0.7; one-tailed t-test.

In addition, the DDoIG methods still had the problem of erroneous mapping of the pRF centers into high eccentricities beyond the stimulus space (Supplementary Figs. 2–4). This implies that a) constraining the pRF central region and b) capturing the anisotropy of the pRF as indicated by the pRF topography is required to model the pRF center more accurately.

For the pRF size in relationship to eccentricity, the DDoIG method provided a similar result to the ones of the DIG, the DAG, and the proposed method (Supplementary Fig. 6).
Here, we propose a new method for estimating population receptive field (pRF) parameters, such as retinotopic location and spatial structure, in vivo by fMRI. Our method allows us to reconstruct and visualize the visual field topography of the pRF, and has several advantages over previously proposed methods (Dumoulin and Wandell, 2008; Engel et al., 1994; Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012). First, our approach enables us to observe the pRF shape before fitting, allowing us to choose an appropriate model that fits the structure of the data. Separate fits can be made for the pRF center region and the surround, facilitating the extraction of information about the latter. In addition, the proposed method is computationally more efficient than the direct fitting method. The direct fitting method (Dumoulin and Wandell, 2008; Harvey and Dumoulin, 2011; Zuiderbaan et al., 2012) requires searching over very large model-parameter spaces by assessing the
explained variance of a model with each candidate set of parameters and selecting the best one. This means that the computation time exponentially increases with the number of parameters limiting the application of this approach to a variety of models with few parameters. In contrast, the proposed method uses the pRF topography as a starting point, which already constrains the space of search for possible parameters (e.g., the peak location in the topography constrains the range of possible locations of the pRF center, while the spread of the pRF center in the topography constrains the standard deviation of the Gaussian model) making it possible to estimate a model with more parameters in less time. In addition, even though the direct-fitting method tries to reduce the computation time by sparsely-sampling voxels in the first stage of parameter estimation, this method still requires model evaluation in all sampled voxels to select visually responsive voxels, and is prone to missing some visually responsive voxels (see Appendix A). The proposed method is more efficient in computation time by selecting visually responsive voxels from the explained variance, which is obtained from the pRF topography via a matrix–vector multiplication.

The method we propose results in a pRF center model that explains a higher proportion of the variance both in lower eccentricities (Supplementary Fig. 1), i.e. away from the stimulus presentation border and in all eccentricities (Fig. 3). This is in part because we restrict the stimulus space to be modeled by thresholding the pRF topography prior to applying a model fit to its center. This makes the final modeling step less susceptible to noise contamination and surround suppression presence. In contrast, the DIG and DAG methods minimize the residual between the actual BOLD signal and the prediction of the pRF-center model over the full stimulus space, and is more susceptible to noise and the surround suppression.

Moreover the DIG (Dumoulin and Wandell, 2008; Levin et al., 2010; Winawer et al., 2010; Zuidervan et al., 2012), DAG, and DDoIG methods provide less reliable eccentric maps, especially near the border of the stimulus presentation space. Fig. 4 shows that for direct-fit methods the minimum residual can sometimes be obtained with model parameters distant to the true ones, providing less reliable eccentricity maps. By contrast, the receptive field estimation method we propose here reflects relatively more accurate eccentricity of the pRF centers, because it is based on calculating and thresholding the pRF topography prior to performing the final model fitting. This difference is particularly clear near the stimulus space border (see Figs. 4 and 5). The erroneous mis-localization of the pRF centers near the stimulus space border by the direct-fit methods leads to a strong non-physiological bias in the eccentricity map, which persists even after removing voxels with low explained variances (Fig. 5). This is manifested by the large number of pRF centers estimated to lie at very high eccentricities, i.e. > 5° beyond the stimulus space border (see Fig. 5 and Supplementary Fig. 3). This non-physiological mapping of pRF centers to distant eccentricities happens because the direct-fit methods minimize the residual over the whole stimulus space and are prone to mislocalization error as explained in Fig. 6C. The proposed method also sometimes mislocalizes pRF centers that lie near the stimulus space border. However, resulting errors are generally much smaller, i.e. on the order of the pRF radius, and error number drops rapidly for voxels with high explained variances (see Fig. 5). On the other hand, polar-angle maps were similar for the three methods, as pRF center locations computed with the two approaches mainly differ along the radial direction (see Figs. 6 and 7).

Our discussion here is limited to the estimation of the pRF center. It is generally difficult to measure surround suppression accurately because surround suppression is relatively weak and requires integration over a large area of the visual field. It is therefore susceptible to contamination by noise for the usual bar stimulation paradigms employed. Nonetheless, the proposed method is useful for inspecting whether the pRF of a voxel contains surround suppression by visualizing the pRF topography. We modeled receptive fields with surround suppression as a difference of Gaussian (Fig. 9) and then tested whether the model predicted characteristics of surround suppression observed in empirical data. The pRF topography and BOLD responses from the model matched those observed from empirical data closely by showing negative BOLD regions (NBRs) and the disappearance of bar patterns around the pRF centers in the topography (Fig. 9). A previous study showed that stimulation evokes neuronal depolarization of the central stimulated region and hyperpolarization of surrounding areas, and the NBR in the surround was associated with arteriolar vasoconstriction and neuronal inhibition there (Devor et al., 2007; Shmuel et al., 2006). These results point to the need for a more systematic study of the structure of pRF surrounds, but this will likely require new stimulation paradigms and lies beyond the scope of the current study.

We also compared the performance of our method against direct-fit difference of isotropic Gaussians (DDoIG). Even that model, which takes into account the surround suppression, did not outperform the proposed method for modeling the pRF center (Fig. 10). Importantly, adding the surround suppression did not solve the problem of erroneously mapping pRF centers into higher eccentricities, often extending far beyond the stimulus presentation space (see Supplementary Figs. 2–4). This may in part be because the DDoIG method uses concentric isotropic Gaussians to fit the center and the surround, which may lie to the mislocalization of the pRF center. Unfortunately, comparing a direct-fit anisotropic DoG model to the method we proposed was not feasible at this time, because in direct-fit methods computation time increases exponentially with the number of parameters.

Classical retinotopic mapping strategies, including the present study, estimate receptive fields by using generic flickering checkerboard stimuli modulated over a spatio-temporal frequency range known to activate well receptive field centers. The neural activity is then modeled by considering stimulated areas as on-fields and other areas as off-fields. This approach leaves unexplored how the structure of the pRF depends on the properties of the visual stimulus. This is an important direction to pursue in the future. Recent fMRI studies confirm that different pRF responses can arise from specific properties of the visual stimulus. For example, Sasaki and colleagues showed a radial bias in the orientation selectivity of voxels in human and primate visual cortex (Freeman et al., 2011; Sasaki et al., 2006). There is an ongoing debate whether it is this global radial bias versus orientation preference patterns irregularly distributed over multiple voxels that lead to the success of visual stimulus orientation decoding via the BOLD signal (Freeman et al., 2011; Harrison and Tong, 2009; Kamitani and Tong, 2005; Mannion et al., 2009; Sasaki et al., 2006).
information is embedded in multiple scales, it is possible that using different orientations as the bar background pattern might provoke different BOLD responses and presumably influence the derived properties of pRFs (e.g., different pRF shapes may result from gratings oriented perpendicularly vs. parallel to the bar sweep direction). These results reinforce the need to start using stimuli with specific properties in order to investigate more thoroughly the properties of pRFs in the visual cortex.

In summary, we demonstrated that our model successfully measures the structure of population receptive fields in vivo from the BOLD signal. By deriving the pRF topology as a first step our method is able to guide population receptive field modeling better than other existing methods. In addition, the proposed method is more efficient in terms of computation time. We have shown that the proposed method outperforms the direct-fit pRF estimation models. This improvement is particularly evident near the border of the stimulus presentation space, where direct methods lead to considerable pRF center mislocalization in the radial direction. Because the proposed method is subject to fewer biases than the more commonly applied direct Gaussian models, we anticipate that it will be particularly useful for monitoring how visual pRFs change with different types of visual stimulation, as a function of adaptation, or in different visual tasks. Because the proposed method is subject to fewer biases than the more commonly applied direct Gaussian models, we anticipate that it will be particularly useful for monitoring how visual pRFs change with different types of visual stimulation, as a function of adaptation, or in different visual tasks. Because the proposed method is subject to fewer biases than the more commonly applied direct Gaussian models, we anticipate that it will be particularly useful for monitoring how visual pRFs change with different types of visual stimulation, as a function of adaptation, or.

Conflicts of interest

There is no conflict of interest.

Appendix A. Direct-fit methods occasionally miss visually responsive voxels

The direct-fit method proposed by Dumoulin and Wandell (2008) adopts the following two-stage process: In the first stage, spatial smoothing of the fMRI data along the cortical surface is performed and then voxels are sparsely sampled for pRF estimation in order to save computation time. For the selected voxels, pRF model parameters are estimated by computing and optimizing the explained variance of the pRF model. Then, model parameters are reconstructed for all voxels by interpolating from the sampled voxels along the cortical sheet. Then, at the second stage, a finer optimization process is performed only for the raw BOLD signal time-series that have explained variance above a certain threshold.

When model parameters are interpolated from sampled voxels with low signal-to-noise ratio (SNR), voxels with high SNR that lie near a sampled voxel with low SNR can be potentially excluded in the second fine optimization. In contrast, the proposed method uses explained variances estimated from the topography and therefore does not miss voxels with good SNR. Fig. 11 shows such an example in which direct-fit methods miss a good signal, while the proposed method does not. Our performance comparison (Figs. 3 and 10, and Supplementary Fig. 1) was conservative in that we excluded all voxels which the direct-fit methods missed (i.e. about 5% of compared voxels for which direct-fit methods set the estimated variance below threshold, to zero) while the proposed method accepted (EV > 0.2).

Appendix B. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.neuroimage.2013.05.026.

References


