Appendix A

Linear algebra and numerical techniques

In this appendix, we introduce some elements of linear algebra and numerical techniques that are used elsewhere in the book. We start with some basic decompositions in matrix algebra, including the singular value decomposition (SVD), eigenvalue decompositions, and other matrix decompositions (factorizations). Next, we look at the problem of linear least squares, which can be solved using either the QR decomposition or normal equations. This is followed by non-linear least squares, which arise when the measurement equations are not linear in the unknowns or when robust error functions are used. Such problems require iteration to find a solution. Next, we look at direct solution (factorization) techniques for sparse problems, where the ordering of the variables can have a large influence on the computation and memory requirements. Finally, we discuss iterative techniques for solving large linear (or linearized) least squares problems. Good general references for much of this material include the work by Björck (1996), Golub and Van Loan (1996), Trefethen and Bau (1997), Meyer (2000), Nocedal and Wright (2006), and Björck and Dahlquist (2010).

A note on vector and matrix indexing. To be consistent with the rest of the book and with the general usage in the computer science and computer vision communities, I adopt a 0-based indexing scheme for vector and matrix element indexing. Please note that most mathematical textbooks and papers use 1-based indexing, so you need to be aware of the differences when you read this book.

Software implementations. Highly optimized and tested libraries corresponding to the algorithms described in this appendix are readily available and are listed in Appendix C.2.

A.1 Matrix decompositions

In order to better understand the structure of matrices and more stably perform operations such as inversion and system solving, a number of decompositions (or factorizations) can be used. In this section, we review singular value decomposition (SVD), eigenvalue decomposition, QR factorization, and Cholesky factorization.

A.1.1 Singular value decomposition

One of the most useful decompositions in matrix algebra is the *singular value decomposition* (SVD), which states that any real-valued $M \times N$ matrix $\boldsymbol{A}$ can be written as

$$\begin{aligned} \boldsymbol{A}_{M\times N} &= \boldsymbol{U}_{M\times P}\boldsymbol{\Sigma}_{P\times P}\boldsymbol{V}^T_{P\times N} \qquad (A.1) \\ &= \left[\begin{array}{c|c|c} \boldsymbol{u}_0 & \cdots & \boldsymbol{u}_{p-1} \end{array} \right] \left[\begin{array}{ccc} \sigma_0 & & \\ & \ddots & \\ & & \sigma_{p-1} \end{array} \right] \left[\begin{array}{c} \boldsymbol{v}_0^T \\ \hline \cdots \\ \hline \boldsymbol{v}_{p-1}^T \end{array} \right], \end{aligned}$$

where $P = \min(M, N)$. The matrices $\boldsymbol{U}$ and $\boldsymbol{V}$ are orthonormal, i.e., $\boldsymbol{U}^T\boldsymbol{U} = \boldsymbol{I}$ and $\boldsymbol{V}^T\boldsymbol{V} = \boldsymbol{I}$, and so are their column vectors,

$$\boldsymbol{u}_i \cdot \boldsymbol{u}_j = \boldsymbol{v}_i \cdot \boldsymbol{v}_j = \delta_{ij}. \qquad (A.2)$$

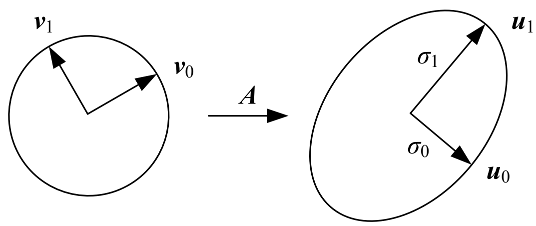


Figure A.1 The action of a matrix $\boldsymbol{A}$ can be visualized by thinking of the domain as being spanned by a set of orthonormal vectors $\boldsymbol{v}_j$, each of which is transformed to a new orthogonal vector $\boldsymbol{u}_j$ with a length σ_j. When $\boldsymbol{A}$ is interpreted as a covariance matrix and its eigenvalue decomposition is performed, each of the $\boldsymbol{u}_j$ axes denote a principal direction (component) and each σ_j denotes one standard deviation along that direction.

The singular values are all non-negative and can be ordered in decreasing order

$$\sigma_0 \geq \sigma_1 \geq \cdots \geq \sigma_{p-1} \geq 0. \tag{A.3}$$

A geometric intuition for the SVD of a matrix $\boldsymbol{A}$ can be obtained by re-writing $\boldsymbol{A} = \boldsymbol{U\Sigma V}^T$ in (A.2) as

$$\boldsymbol{AV} = \boldsymbol{U\Sigma} \quad \text{or} \quad \boldsymbol{A}\boldsymbol{v}_j = \sigma_j \boldsymbol{u}_j. \tag{A.4}$$

This formula says that the matrix $\boldsymbol{A}$ takes any basis vector $\boldsymbol{v}_j$ and maps it to a direction $\boldsymbol{u}_j$ with length σ_j, as shown in Figure A.1

If only the first r singular values are positive, the matrix $\boldsymbol{A}$ is of *rank* r and the index p in the SVD decomposition (A.2) can be replaced by r. (In other words, we can drop the last $p - r$ columns of $\boldsymbol{U}$ and $\boldsymbol{V}$.)

An important property of the singular value decomposition of a matrix (also true for the eigenvalue decomposition of a real symmetric non-negative definite matrix) is that if we truncate the expansion

$$\boldsymbol{A} = \sum_{j=0}^{t} \sigma_j \boldsymbol{u}_j \boldsymbol{v}_j^T, \tag{A.5}$$

we obtain the best possible least squares approximation to the original matrix $\boldsymbol{A}$. This is used both in eigenface-based face recognition systems (Section 14.2.1) and in the separable approximation of convolution kernels (3.21).

A.1.2 Eigenvalue decomposition

If the matrix $\boldsymbol{C}$ is symmetric ($m = n$),[1] it can be written as an eigenvalue decomposition,

$$\begin{aligned} \boldsymbol{C} &= \boldsymbol{U\Lambda U}^T = \left[\begin{array}{c|c|c} \boldsymbol{u}_0 & \cdots & \boldsymbol{u}_{n-1} \end{array} \right] \begin{bmatrix} \lambda_0 & & \\ & \ddots & \\ & & \lambda_{n-1} \end{bmatrix} \begin{bmatrix} \boldsymbol{u}_0^T \\ \hline \cdots \\ \hline \boldsymbol{u}_{n-1}^T \end{bmatrix} \\ &= \sum_{i=0}^{n-1} \lambda_i \boldsymbol{u}_i \boldsymbol{u}_i^T. \end{aligned} \tag{A.6}$$

[1] In this appendix, we denote symmetric matrices using $\boldsymbol{C}$ and general rectangular matrices using $\boldsymbol{A}$.

(The eigenvector matrix $\boldsymbol{U}$ is sometimes written as $\boldsymbol{\Phi}$ and the eigenvectors $\boldsymbol{u}$ as $\boldsymbol{\phi}$.) In this case, the eigenvalues

$$\lambda_0 \geq \lambda_1 \geq \cdots \geq \lambda_{n-1} \tag{A.7}$$

can be both positive and negative.[2]

A special case of the symmetric matrix $\boldsymbol{C}$ occurs when it is constructed as the sum of a number of outer products

$$\boldsymbol{C} = \sum_i \boldsymbol{a}_i \boldsymbol{a}_i^T = \boldsymbol{A}\boldsymbol{A}^T, \tag{A.8}$$

which often occurs when solving least squares problems (Appendix A.2), where the matrix $\boldsymbol{A}$ consists of all the $\boldsymbol{a}_i$ column vectors stacked side-by-side. In this case, we are guaranteed that all of the eigenvalues λ_i are non-negative. The associated matrix $\boldsymbol{C}$ is *positive semi-definite*

$$\boldsymbol{x}^T \boldsymbol{C} \boldsymbol{x} \geq 0, \quad \forall \boldsymbol{x}. \tag{A.9}$$

If the matrix $\boldsymbol{C}$ is of full rank, the eigenvalues are all positive and the matrix is called *symmetric positive definite* (SPD).

Symmetric positive semi-definite matrices also arise in the statistical analysis of data, since they represent the *covariance* of a set of $\{\boldsymbol{x}_i\}$ points around their mean $\bar{\boldsymbol{x}}$,

$$\boldsymbol{C} = \frac{1}{n} \sum_i (\boldsymbol{x}_i - \bar{\boldsymbol{x}})(\boldsymbol{x}_i - \bar{\boldsymbol{x}})^T. \tag{A.10}$$

In this case, performing the eigenvalue decomposition is known as *principal component analysis* (PCA), since it models the principal directions (and magnitudes) of variation of the point distribution around their mean, as shown in Section 5.1.1 (5.13–5.15), Section 14.2.1 (14.9), and Appendix B.1.1 (B.10). Figure A.1 shows how the principal components of the covariance matrix $\boldsymbol{C}$ denote the principal axes $\boldsymbol{u}_j$ of the uncertainty ellipsoid corresponding to this point distribution and how the $\sigma_j = \sqrt{\lambda_j}$ denote the standard deviations along each axis.

The eigenvalues and eigenvectors of $\boldsymbol{C}$ and the singular values and singular vectors of $\boldsymbol{A}$ are closely related. Given

$$\boldsymbol{A} = \boldsymbol{U}\boldsymbol{\Sigma}\boldsymbol{V}^T, \tag{A.11}$$

we get

$$\boldsymbol{C} = \boldsymbol{A}\boldsymbol{A}^T = \boldsymbol{U}\boldsymbol{\Sigma}\boldsymbol{V}^T\boldsymbol{V}\boldsymbol{\Sigma}\boldsymbol{U}^T = \boldsymbol{U}\boldsymbol{\Lambda}\boldsymbol{U}^T. \tag{A.12}$$

From this, we see that $\lambda_i = \sigma_i^2$ and that the left singular vectors of $\boldsymbol{A}$ are the eigenvectors of $\boldsymbol{C}$.

This relationship gives us an efficient method for computing the eigenvalue decomposition of large matrices that are rank deficient, such as the scatter matrices observed in computing eigenfaces (Section 14.2.1). Observe that the covariance matrix $\boldsymbol{C}$ in (14.9) is exactly the same as $\boldsymbol{C}$ in (A.8). Note also that the individual difference-from-mean images $\boldsymbol{a}_i = \boldsymbol{x}_i - \bar{\boldsymbol{x}}$ are long vectors of length P (the number of pixels in the image), while the total number of exemplars N (the number of faces in the training database) is much smaller. Instead of forming $\boldsymbol{C} = \boldsymbol{A}\boldsymbol{A}^T$, which is $P \times P$, we form the matrix

$$\hat{\boldsymbol{C}} = \boldsymbol{A}^T\boldsymbol{A}, \tag{A.13}$$

[2] Eigenvalue decompositions can be computed for non-symmetric matrices but the eigenvalues and eigenvectors can have complex entries in that case.

which is $N \times N$. (This involves taking the dot product between every pair of difference images $\boldsymbol{a}_i$ and $\boldsymbol{a}_j$.) The eigenvalues of $\hat{\boldsymbol{C}}$ are the squared singular values of $\boldsymbol{A}$, namely $\boldsymbol{\Sigma}^2$, and are hence also the eigenvalues of $\boldsymbol{C}$. The eigenvectors of $\hat{\boldsymbol{C}}$ are the right singular vectors $\boldsymbol{V}$ of $\boldsymbol{A}$, from which the desired eigenfaces $\boldsymbol{U}$, which are the left singular vectors of $\boldsymbol{A}$, can be computed as

$$\boldsymbol{U} = \boldsymbol{A}\boldsymbol{V}\boldsymbol{\Sigma}^{-1}. \tag{A.14}$$

This final step is essentially computing the eigenfaces as linear combinations of the difference images (Turk and Pentland 1991a). If you have access to a high-quality linear algebra package such as LAPACK, routines for efficiently computing a small number of the left singular vectors and singular values of rectangular matrices such as $\boldsymbol{A}$ are usually provided (Appendix C.2). However, if storing all of the images in memory is prohibitive, the construction of $\hat{\boldsymbol{C}}$ in (A.13) can be used instead.

How can eigenvalue and singular value decompositions actually be computed? Notice that an eigenvector is defined by the equation

$$\lambda_i \boldsymbol{u}_i = \boldsymbol{C}\boldsymbol{u}_i \quad \text{or} \quad (\lambda_i \boldsymbol{I} - \boldsymbol{C})\boldsymbol{u}_i = 0. \tag{A.15}$$

(This can be derived from (A.6) by post-multiplying both sides by $\boldsymbol{u}_i$.) Since the latter equation is *homogeneous*, i.e., it has a zero right-hand-side, it can only have a non-zero (non-trivial) solution for $\boldsymbol{u}_i$ if the system is rank deficient, i.e.,

$$|(\lambda \boldsymbol{I} - \boldsymbol{C})| = 0. \tag{A.16}$$

Evaluating this determinant yields a *characteristic* polynomial equation in λ, which can be solved for small problems, e.g., 2×2 or 3×3 matrices, in closed form.

For larger matrices, iterative algorithms that first reduce the matrix $\boldsymbol{C}$ to a real symmetric tridiagonal form using orthogonal transforms and then perform QR iterations are normally used (Golub and Van Loan 1996; Trefethen and Bau 1997; Björck and Dahlquist 2010). Since these techniques are rather involved, it is best to use a linear algebra package such as LAPACK (Anderson, Bai, Bischof *et al.* 1999)—see Appendix C.2.

Factorization with missing data requires different kinds of iterative algorithms, which often involve either hallucinating the missing terms or minimizing some weighted reconstruction metric, which is intrinsically much more challenging than regular factorization. This area has been widely studied in computer vision (Shum, Ikeuchi, and Reddy 1995; De la Torre and Black 2003; Huynh, Hartley, and Heyden 2003; Buchanan and Fitzgibbon 2005; Gross, Matthews, and Baker 2006; Torresani, Hertzmann, and Bregler 2008) and is sometimes called *generalized PCA*. However, this term is also sometimes used to denote algebraic subspace clustering techniques, which is the subject of a forthcoming monograph by Vidal, Ma, and Sastry (2010).

A.1.3 QR factorization

A widely used technique for stably solving poorly conditioned least squares problems (Björck 1996) and as the basis of more complex algorithms, such as computing the SVD and eigenvalue decompositions, is the QR factorization,

$$\boldsymbol{A} = \boldsymbol{Q}\boldsymbol{R}, \tag{A.17}$$

procedure *Cholesky*($\boldsymbol{C}, \boldsymbol{R}$):

$\boldsymbol{R} = \boldsymbol{C}$

for $i = 0 \ldots n-1$

for $j = i+1 \ldots n-1$

$\boldsymbol{R}_{j,j:n-1} = \boldsymbol{R}_{j,j:n-1} - r_{ij} r_{ii}^{-1} \boldsymbol{R}_{i,j:n-1}$

$\boldsymbol{R}_{i,i:n-1} = r_{ii}^{-1/2} \boldsymbol{R}_{i,i:n-1}$

Algorithm A.1 Cholesky decomposition of the matrix $\boldsymbol{C}$ into its upper triangular form $\boldsymbol{R}$.

where $\boldsymbol{Q}$ is an *orthonormal* (or *unitary*) matrix $\boldsymbol{Q}\boldsymbol{Q}^T = \boldsymbol{I}$ and $\boldsymbol{R}$ is upper triangular.[3] In computer vision, QR can be used to convert a camera matrix into a rotation matrix and an upper-triangular calibration matrix (6.35) and also in various self-calibration algorithms (Section 7.2.2). The most common algorithms for computing QR decompositions, modified Gram–Schmidt, Householder transformations, and Givens rotations, are described by Golub and Van Loan (1996), Trefethen and Bau (1997), and Björck and Dahlquist (2010) and are also found in LAPACK. Unlike the SVD and eigenvalue decompositions, QR factorization does not require iteration and can be computed exactly in $O(MN^2 + N^3)$ operations, where M is the number of rows and N is the number of columns (for a tall matrix).

A.1.4 Cholesky factorization

Cholesky factorization can be applied to any symmetric positive definite matrix $\boldsymbol{C}$ to convert it into a product of symmetric lower and upper triangular matrices,

$$\boldsymbol{C} = \boldsymbol{L}\boldsymbol{L}^T = \boldsymbol{R}^T\boldsymbol{R}, \tag{A.18}$$

where $\boldsymbol{L}$ is a lower-triangular matrix and $\boldsymbol{R}$ is an upper-triangular matrix. Unlike Gaussian elimination, which may require pivoting (row and column reordering) or may become unstable (sensitive to roundoff errors or reordering), Cholesky factorization remains stable for positive definite matrices, such as those that arise from normal equations in least squares problems (Appendix A.2). Because of the form of (A.18), the matrices $\boldsymbol{L}$ and $\boldsymbol{R}$ are sometimes called *matrix square roots*.[4]

The algorithm to compute an upper triangular Cholesky decomposition of $\boldsymbol{C}$ is a straightforward symmetric generalization of Gaussian elimination and is based on the decomposition (Björck 1996; Golub and Van Loan 1996)

$$\boldsymbol{C} = \begin{bmatrix} \gamma & \boldsymbol{c}^T \\ \boldsymbol{c} & \boldsymbol{C}_{11} \end{bmatrix} \tag{A.19}$$

[3] The term "R" comes from the German name for the lower–upper (LU) decomposition, which is LR for "links" and "rechts" (left and right of the diagonal).

[4] In fact, there exists a whole family of matrix square roots. Any matrix of the form $\boldsymbol{L}\boldsymbol{Q}$ or $\boldsymbol{Q}\boldsymbol{R}$, where $\boldsymbol{Q}$ is a unitary matrix, is a square root of $\boldsymbol{C}$.

$$= \begin{bmatrix} \gamma^{1/2} & \mathbf{0}^T \\ \boldsymbol{c}\gamma^{-1/2} & \boldsymbol{I} \end{bmatrix} \begin{bmatrix} 1 & \mathbf{0}^T \\ \mathbf{0} & \boldsymbol{C}_{11} - \boldsymbol{c}\gamma^{-1}\boldsymbol{c}^T \end{bmatrix} \begin{bmatrix} \gamma^{1/2} & \gamma^{-1/2}\boldsymbol{c}^T \\ \mathbf{0} & \boldsymbol{I} \end{bmatrix} \quad (A.20)$$

$$= \boldsymbol{R}_0^T \boldsymbol{C}_1 \boldsymbol{R}_0, \quad (A.21)$$

which, through recursion, can be turned into

$$\boldsymbol{C} = \boldsymbol{R}_0^T \ldots \boldsymbol{R}_{n-1}^T \boldsymbol{R}_{n-1} \ldots \boldsymbol{R}_0 = \boldsymbol{R}^T \boldsymbol{R}. \quad (A.22)$$

Algorithm A.1 provides a more procedural definition, which can store the upper-triangular matrix $\boldsymbol{R}$ in the same space as $\boldsymbol{C}$, if desired. The total operation count for Cholesky factorization is $O(N^3)$ for a dense matrix but can be significantly lower for sparse matrices with low fill-in (Appendix A.4).

Note that Cholesky decomposition can also be applied to block-structured matrices, where the term γ in (A.19) is now a square block sub-matrix and $\boldsymbol{c}$ is a rectangular matrix (Golub and Van Loan 1996). The computation of square roots can be avoided by leaving the γ on the diagonal of the middle factor in (A.20), which results in the $\boldsymbol{C} = \boldsymbol{L}\boldsymbol{D}\boldsymbol{L}^T$ factorization, where $\boldsymbol{D}$ is a diagonal matrix. However, since square roots are relatively fast on modern computers, this is not worth the bother and Cholesky factorization is usually preferred.

A.2 Linear least squares

Least squares fitting problems are pervasive in computer vision. For example, the alignment of images based on matching feature points involves the minimization of a squared distance objective function (6.2),

$$E_{\text{LS}} = \sum_i \|\boldsymbol{r}_i\|^2 = \sum_i \|\boldsymbol{f}(\boldsymbol{x}_i; \boldsymbol{p}) - \boldsymbol{x}'_i\|^2, \quad (A.23)$$

where

$$\boldsymbol{r}_i = \boldsymbol{f}(\boldsymbol{x}_i; \boldsymbol{p}) - \boldsymbol{x}'_i = \hat{\boldsymbol{x}}'_i - \tilde{\boldsymbol{x}}'_i \quad (A.24)$$

is the *residual* between the measured location $\hat{\boldsymbol{x}}'_i$ and its corresponding current *predicted* location $\tilde{\boldsymbol{x}}'_i = \boldsymbol{f}(\boldsymbol{x}_i; \boldsymbol{p})$. More complex versions of least squares problems, such as large-scale structure from motion (Section 7.4), may involve the minimization of functions of thousands of variables. Even problems such as image filtering (Section 3.4.3) and regularization (Section 3.7.1) may involve the minimization of sums of squared errors.

Figure A.2a shows an example of a simple least squares line fitting problem, where the quantities being estimated are the line equation parameters (m, b). When the sampled vertical values y_i are assumed to be noisy versions of points on the line $y = mx + b$, the optimal estimates for (m, b) can be found by minimizing the squared vertical residuals

$$E_{\text{VLS}} = \sum_i |y_i - (mx_i + b)|^2. \quad (A.25)$$

Note that the function being fitted need not itself be linear to use linear least squares. All that is required is that the function be linear in the unknown parameters. For example, polynomial fitting can be written as

$$E_{\text{PLS}} = \sum_i |y_i - (\sum_{j=0}^{p} a_j x_i^j)|^2, \quad (A.26)$$

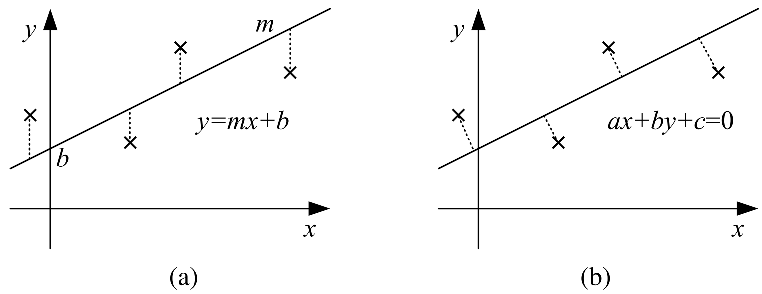


Figure A.2 Least squares regression. (a) The line $y = mx + b$ is fit to the four noisy data points, $\{(x_i, y_i)\}$, denoted by $\times$ by minimizing the squared vertical residuals between the data points and the line, $\sum_i \|y_i - (mx_i + b)\|^2$. (b) When the measurements $\{(x_i, y_i)\}$ are assumed to have noise in all directions, the sum of orthogonal squared distances to the line $\sum_i \|ax_i + by_i + c\|^2$ is minimized using total least squares.

while sinusoid fitting with unknown amplitude A and phase ϕ (but known frequency f) can be written as

$$E_{\text{SLS}} = \sum_i |y_i - A\sin(2\pi f x_i + \phi)|^2 = \sum_i |y_i - (B \sin 2\pi f x_i + C \cos 2\pi f x_i)|^2, \quad \text{(A.27)}$$

which is linear in (B, C).

In general, it is more common to denote the unknown parameters using $\boldsymbol{x}$ and to write the general form of linear least squares as[5]

$$E_{\text{LLS}} = \sum_i |\boldsymbol{a}_i \boldsymbol{x} - b_i|^2 = \|\boldsymbol{A}\boldsymbol{x} - \boldsymbol{b}\|^2. \quad \text{(A.28)}$$

Expanding the above equation gives us

$$E_{\text{LLS}} = \boldsymbol{x}^T(\boldsymbol{A}^T\boldsymbol{A})\boldsymbol{x} - 2\boldsymbol{x}^T(\boldsymbol{A}^T\boldsymbol{b}) + \|\boldsymbol{b}\|^2, \quad \text{(A.29)}$$

whose minimum value for $\boldsymbol{x}$ can be found by solving the associated *normal equations* (Björck 1996; Golub and Van Loan 1996)

$$(\boldsymbol{A}^T\boldsymbol{A})\boldsymbol{x} = \boldsymbol{A}^T\boldsymbol{b}. \quad \text{(A.30)}$$

The preferred way to solve the normal equations is to use Cholesky factorization. Let

$$\boldsymbol{C} = \boldsymbol{A}^T\boldsymbol{A} = \boldsymbol{R}^T\boldsymbol{R}, \quad \text{(A.31)}$$

where $\boldsymbol{R}$ is the upper-triangular Cholesky factor of the Hessian $\boldsymbol{C}$, and

$$\boldsymbol{d} = \boldsymbol{A}^T\boldsymbol{b}. \quad \text{(A.32)}$$

After factorization, the solution for $\boldsymbol{x}$ can be obtained as

$$\boldsymbol{R}^T\boldsymbol{z} = \boldsymbol{d}, \quad \boldsymbol{R}\boldsymbol{x} = \boldsymbol{z}, \quad \text{(A.33)}$$

[5] Be extra careful in interpreting the variable names here. In the 2D line-fitting example, x is used to denote the horizontal axis, but in the general least squares problem, $\boldsymbol{x} = (m, b)$ denotes the unknown parameter vector.

which involves the solution of two triangular systems, i.e., forward and backward substitution (Björck 1996).

In cases where the least squares problem is numerically poorly conditioned (which should generally be avoided by adding sufficient regularization or prior knowledge about the parameters, (Appendix A.3)), it is possible to use QR factorization or SVD directly on the matrix $\boldsymbol{A}$ (Björck 1996; Golub and Van Loan 1996; Trefethen and Bau 1997; Nocedal and Wright 2006; Björck and Dahlquist 2010), e.g.,

$$\boldsymbol{A}\boldsymbol{x} = \boldsymbol{Q}\boldsymbol{R}\boldsymbol{x} = \boldsymbol{b} \quad \longrightarrow \quad \boldsymbol{R}\boldsymbol{x} = \boldsymbol{Q}^T\boldsymbol{b}. \tag{A.34}$$

Note that the upper triangular matrices $\boldsymbol{R}$ produced by the Cholesky factorization of $\boldsymbol{C} = \boldsymbol{A}^T\boldsymbol{A}$ and the QR factorization of $\boldsymbol{A}$ are the same, but that solving (A.34) is generally more stable (less sensitive to roundoff error) but slower (by a constant factor).

A.2.1 Total least squares

In some problems, e.g., when performing geometric line fitting in 2D images or 3D plane fitting to point cloud data, instead of having measurement error along one particular axis, the measured points have uncertainty in all directions, which is known as the *errors-in-variables* model (Van Huffel and Lemmerling 2002; Matei and Meer 2006). In this case, it makes more sense to minimize a set of homogeneous squared errors of the form

$$E_{\text{TLS}} = \sum_i (\boldsymbol{a}_i\boldsymbol{x})^2 = \|\boldsymbol{A}\boldsymbol{x}\|^2, \tag{A.35}$$

which is known as *total least squares* (TLS) (Van Huffel and Vandewalle 1991; Björck 1996; Golub and Van Loan 1996; Van Huffel and Lemmerling 2002).

The above error metric has a trivial minimum solution at $\boldsymbol{x} = 0$ and is, in fact, homogeneous in $\boldsymbol{x}$. For this reason, we augment this minimization problem with the requirement that $\|\boldsymbol{x}\|^2 = 1$. which results in the eigenvalue problem

$$\boldsymbol{x} = \arg\min_{\boldsymbol{x}} \boldsymbol{x}^T(\boldsymbol{A}^T\boldsymbol{A})\boldsymbol{x} \quad \text{such that} \quad \|\boldsymbol{x}\|^2 = 1. \tag{A.36}$$

The value of $\boldsymbol{x}$ that minimizes this constrained problem is the eigenvector associated with the smallest eigenvalue of $\boldsymbol{A}^T\boldsymbol{A}$. This is the same as the last right singular vector of $\boldsymbol{A}$, since

$$\boldsymbol{A} = \boldsymbol{U}\boldsymbol{\Sigma}\boldsymbol{V}, \tag{A.37}$$

$$\boldsymbol{A}^T\boldsymbol{A} = \boldsymbol{V}\boldsymbol{\Sigma}^2\boldsymbol{V}, \tag{A.38}$$

$$\boldsymbol{A}^T\boldsymbol{A}\boldsymbol{v}_k = \sigma_k^2, \tag{A.39}$$

which is minimized by selecting the smallest σ_k value.

Figure A.2b shows a line fitting problem where, in this case, the measurement errors are assumed to be isotropic in (x, y). The solution for the best line equation $ax + by + c = 0$ is found by minimizing

$$E_{\text{TLS-2D}} = \sum_i (ax_i + by_i + c)^2, \tag{A.40}$$

i.e., finding the eigenvector associated with the smallest eigenvalue of[6]

$$\boldsymbol{C} = \boldsymbol{A}^T \boldsymbol{A} = \sum_i \begin{bmatrix} x_i \\ y_i \\ 1 \end{bmatrix} \begin{bmatrix} x_i & y_i & 1 \end{bmatrix}. \tag{A.41}$$

Notice, however, that minimizing $\sum_i (\boldsymbol{a}_i \boldsymbol{x})^2$ in (A.35) is only statistically optimal (Appendix B.1.1) if all of the measured terms in the $\boldsymbol{a}_i$, e.g., the $(x_i, y_i, 1)$ measurements, have equal noise. This is definitely not the case in the line-fitting example of Figure A.2b (A.40), since the 1 values are noise-free. To mitigate this, we first subtract the mean x and y values from all the measured points

$$\hat{x}_i = x_i - \bar{x} \tag{A.42}$$

$$\hat{y}_i = y_i - \bar{y} \tag{A.43}$$

and then fit the 2D line equation $a(x - \bar{x}) + b(y - \bar{y}) = 0$ by minimizing

$$E_{\mathrm{TLS-2Dm}} = \sum_i (a\hat{x}_i + b\hat{y}_i)^2. \tag{A.44}$$

The more general case where each individual measurement component can have different noise level, as is the case in estimating essential and fundamental matrices (Section 7.2), is called the *heteroscedastic* errors-in-variable (HEIV) model and is discussed by Matei and Meer (2006).

A.3 Non-linear least squares

In many vision problems, such as structure from motion, the least squares problem formulated in (A.23) involves functions $\boldsymbol{f}(\boldsymbol{x}_i; \boldsymbol{p})$ that are *not* linear in the unknown parameters $\boldsymbol{p}$. This problem is known as *non-linear least squares* or *non-linear regression* (Björck 1996; Madsen, Nielsen, and Tingleff 2004; Nocedal and Wright 2006). It is usually solved by iteratively re-linearizing (A.23) around the current estimate of $\boldsymbol{p}$ using the gradient derivative (Jacobian) $\boldsymbol{J} = \partial \boldsymbol{f} / \partial \boldsymbol{p}$ and computing an incremental improvement $\Delta \boldsymbol{p}$.

As shown in Equations (6.13–6.17), this results in

$$E_{\mathrm{NLS}}(\Delta \boldsymbol{p}) = \sum_i \|\boldsymbol{f}(\boldsymbol{x}_i; \boldsymbol{p} + \Delta \boldsymbol{p}) - \boldsymbol{x}'_i\|^2 \tag{A.45}$$

$$\approx \sum_i \|\boldsymbol{J}(\boldsymbol{x}_i; \boldsymbol{p}) \Delta \boldsymbol{p} - \boldsymbol{r}_i\|^2, \tag{A.46}$$

where the Jacobians $\boldsymbol{J}(\boldsymbol{x}_i; \boldsymbol{p})$ and residual vectors $\boldsymbol{r}_i$ play the same role in forming the normal equations as $\boldsymbol{a}_i$ and b_i in (A.28).

Because the above approximation only holds near a local minimum or for small values of $\Delta \boldsymbol{p}$, the update $\boldsymbol{p} \leftarrow \boldsymbol{p} + \Delta \boldsymbol{p}$ may not always decrease the summed square residual error (A.45). One way to mitigate this problem is to take a smaller step,

$$\boldsymbol{p} \leftarrow \boldsymbol{p} + \alpha \Delta \boldsymbol{p}, \quad 0 < \alpha \leq 1. \tag{A.47}$$

[6] Again, be careful with the variable names here. The measurement equation is $\boldsymbol{a}_i = (x_i, y_i, 1)$ and the unknown parameters are $\boldsymbol{x} = (a, b, c)$.

A simple way to determine a reasonable value of α is to start with 1 and successively halve the value, which is a simple form of *line search* (Al-Baali and Fletcher. 1986; Björck 1996; Nocedal and Wright 2006).

Another approach to ensuring a downhill step in error is to add a diagonal damping term to the approximate Hessian

$$\boldsymbol{C} = \sum_i \boldsymbol{J}^T(\boldsymbol{x}_i)\boldsymbol{J}(\boldsymbol{x}_i), \tag{A.48}$$

i.e., to solve

$$[\boldsymbol{C} + \lambda\, \text{diag}(\boldsymbol{C})]\Delta\boldsymbol{p} = \boldsymbol{d}, \tag{A.49}$$

where

$$\boldsymbol{d} = \sum_i \boldsymbol{J}^T(\boldsymbol{x}_i)\boldsymbol{r}_i, \tag{A.50}$$

which is called a *damped Gauss–Newton* method. The damping parameter λ is increased if the squared residual is not decreasing as fast as expected, i.e., as predicted by (A.46), and is decreased if the expected decrease is obtained (Madsen, Nielsen, and Tingleff 2004). The combination of the Newton (first-order Taylor series) approximation (A.46) and the adaptive damping parameter λ is commonly known as the Levenberg–Marquardt algorithm (Levenberg 1944; Marquardt 1963) and is an example of more general *trust region methods*, which are discussed in more detail in (Björck 1996; Conn, Gould, and Toint 2000; Madsen, Nielsen, and Tingleff 2004; Nocedal and Wright 2006).

When the initial solution is far away from its quadratic region of convergence around a local minimum, *large residual methods*, e.g., *Newton-type methods*, which add a second-order term to the Taylor series expansion in (A.46), may converge faster. Quasi-Newton methods such as BFGS, which require only gradient evaluations, can also be useful if memory size is an issue. Such techniques are discussed in textbooks and papers on numerical optimization (Toint 1987; Björck 1996; Conn, Gould, and Toint 2000; Nocedal and Wright 2006).

A.4 Direct sparse matrix techniques

Many optimization problems in computer vision, such as bundle adjustment (Szeliski and Kang 1994; Triggs, McLauchlan, Hartley *et al.* 1999; Hartley and Zisserman 2004; Snavely, Seitz, and Szeliski 2008b; Agarwal, Snavely, Simon *et al.* 2009) have Jacobian and (approximate) Hessian matrices that are extremely sparse (Section 7.4.1). For example, Figure 7.9a shows the *bipartite* model typical of structure from motion problems, in which most points are only observed by a subset of the cameras, which results in the sparsity patterns for the Jacobian and Hessian shown in Figure 7.9b–c.

Whenever the Hessian matrix is sparse enough, it is more efficient to use sparse Cholesky factorization instead of regular Cholesky factorization. In such sparse direct techniques, the Hessian matrix $\boldsymbol{C}$ and its associated Cholesky factor $\boldsymbol{R}$ are stored in *compressed form*, in which the amount of storage is proportional to the number of (potentially) non-zero entries (Björck 1996; Davis 2006).[7] Algorithms for computing the non-zero elements in $\boldsymbol{C}$ and $\boldsymbol{R}$

[7] For example, you can store a list of (i, j, c_{ij}) triples. One example of such a scheme is *compressed sparse row (CSR)* storage. An alternative storage method called *skyline*, which stores adjacent vertical spans of non-zero elements (Bathe 2007), is sometimes used in finite element analysis. Banded systems such as snakes (5.3) can store just the non-zero band elements (Björck 1996, Section 6.2) and can be solved in $O(nb^2)$, where n is the number of

from the sparsity pattern of the Jacobian matrix $\boldsymbol{J}$ are given by Björck (1996, Section 6.4), and algorithms for computing the numerical Cholesky and QR decompositions (once the sparsity pattern has been computed and storage allocated) are discussed by Björck (1996, Section 6.5).

A.4.1 Variable reordering

The key to efficiently solving sparse problems using direct (non-iterative) techniques is to determine an efficient *ordering* for the variables, which reduces the amount of *fill-in*, i.e., the number of non-zero entries in $\boldsymbol{R}$ that were zero in the original $\boldsymbol{C}$ matrix. We already saw in Section 7.4.1 how storing the more numerous 3D point parameters before the camera parameters and using the Schur complement (7.56) results in a more efficient algorithm. Similarly, sorting parameters by time in video-based reconstruction problems usually results in lower fill-in. Furthermore, any problem whose adjacency graph (the graph corresponding to the sparsity pattern) is a tree can be solved in linear time with an appropriate reordering of the variables (putting all the children before their parents). All of these are examples of good reordering techniques.

In the general case of unstructured data, there are many heuristics available to find good reorderings (Björck 1996; Davis 2006).[8] For general adjacency (sparsity) graphs, *minimum degree orderings* generally produce good results. For planar graphs, which often arise on image or spline grids (Section 8.3), *nested dissection*, which recursively splits the graph into two equal halves along a *frontier* (or boundary) of small size, generally works well. Such *domain decomposition* (or *multi-frontal*) techniques also enable the use of parallel processing, since independent sub-graphs can be processed in parallel on separate processors (Davis 2008).

The overall set of steps used to perform the direct solution of sparse least squares problems are summarized in Algorithm A.2, which is a modified version of Algorithm 6.6.1 by Björck (1996, Section 6.6)). If a series of related least squares problems is being solved, as is the case in iterative non-linear least squares (Appendix A.3), steps 1–3 can be performed ahead of time and reused for each new invocation with different $\boldsymbol{C}$ and $\boldsymbol{d}$ values. When the problem is block-structured, as is the case in structure from motion where point (structure) variables have dense 3×3 sub-entries in $\boldsymbol{C}$ and cameras have 6×6 (or larger) entries, the cost of performing the reordering computation is small compared to the actual numerical factorization, which can benefit from block-structured matrix operations (Golub and Van Loan 1996). It is also possible to apply sparse reordering and multifrontal techniques to QR factorization (Davis 2008), which may be preferable when the least squares problems are poorly conditioned.

A.5 Iterative techniques

When problems become large, the amount of memory required to store the Hessian matrix $\boldsymbol{C}$ and its factor $\boldsymbol{R}$, and the amount of time it takes to compute the factorization, can become prohibitively large, especially when there are large amounts of fill-in. This is often the case with image processing problems defined on pixel grids, since, even with the optimal reordering (nested dissection) the amount of fill can still be large.

variables and b is the bandwidth.

[8] Finding the optimal reordering with minimal fill-in is provably NP-hard.

procedure *SparseCholeskySolve*$(\boldsymbol{C}, \boldsymbol{d})$:

1. Determine symbolically the structure of $\boldsymbol{C}$, i.e., the adjacency graph.
2. (Optional) Compute a reordering for the variables, taking into account any block structure inherent in the problem.
3. Determine the fill-in pattern for $\boldsymbol{R}$ and allocate the compressed storage for $\boldsymbol{R}$ as well as storage for the permuted right hand side $\hat{\boldsymbol{d}}$.
4. Copy the elements of $\boldsymbol{C}$ and $\boldsymbol{d}$ into $\boldsymbol{R}$ and $\hat{\boldsymbol{d}}$, permuting the values according to the computed ordering.
5. Perform the numerical factorization of $\boldsymbol{R}$ using Algorithm A.1.
6. Solve the factored system (A.33), i.e.,
$$\boldsymbol{R}^T \boldsymbol{z} = \hat{\boldsymbol{d}}, \quad \boldsymbol{R}\boldsymbol{x} = \boldsymbol{z}.$$
7. Return the solution $\boldsymbol{x}$, after undoing the permutation.

Algorithm A.2 Sparse least squares using a sparse Cholesky decomposition of the matrix $\boldsymbol{C}$.

A preferable approach to solving such linear systems is to use iterative techniques, which compute a series of estimates that converge to the final solution, e.g., by taking a series of downhill steps in an energy function such as (A.29).

A large number of iterative techniques have been developed over the years, including such well-known algorithms as successive overrelaxation and multi-grid. These are described in specialized textbooks on iterative solution techniques (Axelsson 1996; Saad 2003) as well as in more general books on numerical linear algebra and least squares techniques (Björck 1996; Golub and Van Loan 1996; Trefethen and Bau 1997; Nocedal and Wright 2006; Björck and Dahlquist 2010).

A.5.1 Conjugate gradient

The iterative solution technique that often performs best is conjugate gradient descent, which takes a series of downhill steps that are *conjugate* to each other with respect to the $\boldsymbol{C}$ matrix, i.e., if the $\boldsymbol{u}$ and $\boldsymbol{v}$ descent directions satisfy $\boldsymbol{u}^T\boldsymbol{C}\boldsymbol{v} = 0$. In practice, conjugate gradient descent outperforms other kinds of gradient descent algorithm because its convergence rate is proportional to the square root of the *condition number* of $\boldsymbol{C}$ instead of the condition number itself.[9] Shewchuk (1994) provides a nice introduction to this topic, with clear intuitive explanations of the reasoning behind the conjugate gradient algorithm and its performance.

Algorithm A.3 describes the conjugate gradient algorithm and its related least squares counterpart, which can be used when the original set of least squares linear equations are

[9] The condition number $\kappa(\boldsymbol{C})$ is the ratio of the largest and smallest eigenvalues of $\boldsymbol{C}$. The actual convergence rate depends on the clustering of the eigenvalues, as discussed in the references cited in this section.

ConjugateGradient$(\boldsymbol{C}, \boldsymbol{d}, \boldsymbol{x}_0)$

1. $\boldsymbol{r}_0 = \boldsymbol{d} - \boldsymbol{C}\boldsymbol{x}_0$
2. $\boldsymbol{p}_0 = \boldsymbol{r}_0$
3. **for** $k = 0 \ldots$
4. $\quad \boldsymbol{w}_k = \boldsymbol{C}\boldsymbol{p}_k$
5. $\quad \alpha_k = \|\boldsymbol{r}_k\|^2 / (\boldsymbol{p}_k \cdot \boldsymbol{w}_k)$
6. $\quad \boldsymbol{x}_{k+1} = \boldsymbol{x}_k + \alpha_k \boldsymbol{p}_k$
7. $\quad \boldsymbol{r}_{k+1} = \boldsymbol{r}_k - \alpha_k \boldsymbol{w}_k$
8.
9. $\quad \beta_{k+1} = \|\boldsymbol{r}_{k+1}\|^2 / \|\boldsymbol{r}_k\|^2$
10. $\quad \boldsymbol{p}_{k+1} = \boldsymbol{r}_{k+1} + \beta_k \boldsymbol{p}_k$

ConjugateGradientLS$(\boldsymbol{A}, \boldsymbol{b}, \boldsymbol{x}_0)$

1. $\boldsymbol{q}_0 = \boldsymbol{b} - \boldsymbol{A}\boldsymbol{x}_0, \quad \boldsymbol{r}_0 = \boldsymbol{A}^T \boldsymbol{q}_0$
2. $\boldsymbol{p}_0 = \boldsymbol{r}_0$
3. **for** $k = 0 \ldots$
4. $\quad \boldsymbol{v}_k = \boldsymbol{A}\boldsymbol{p}_k$
5. $\quad \alpha_k = \|\boldsymbol{r}_k\|^2 / \|\boldsymbol{v}_k\|^2$
6. $\quad \boldsymbol{x}_{k+1} = \boldsymbol{x}_k + \alpha_k \boldsymbol{p}_k$
7. $\quad \boldsymbol{q}_{k+1} = \boldsymbol{q}_k - \alpha_k \boldsymbol{v}_k$
8. $\quad \boldsymbol{r}_{k+1} = \boldsymbol{A}^T \boldsymbol{q}_{k+1}$
9. $\quad \beta_{k+1} = \|\boldsymbol{r}_{k+1}\|^2 / \|\boldsymbol{r}_k\|^2$
10. $\quad \boldsymbol{p}_{k+1} = \boldsymbol{r}_{k+1} + \beta_k \boldsymbol{p}_k$

Algorithm A.3 Conjugate gradient and conjugate gradient least squares algorithms. The algorithm is described in more detail in the text, but in brief, they choose descent directions $\boldsymbol{p}_k$ that are conjugate to each other with respect to $\boldsymbol{C}$ by computing a factor β by which to discount the previous search direction $\boldsymbol{p}_{k-1}$. They then find the optimal step size α and take a downhill step by an amount $\alpha_k \boldsymbol{p}_k$.

available in the form of $\boldsymbol{A}\boldsymbol{x} = \boldsymbol{b}$ (A.28). While it is easy to convince yourself that the two forms are mathematically equivalent, the least squares form is preferable if rounding errors start to affect the results because of poor conditioning. It may also be preferable if, due to the sparsity structure of $\boldsymbol{A}$, multiplies with the original $\boldsymbol{A}$ matrix are faster or more space efficient than multiplies with $\boldsymbol{C}$.

The conjugate gradient algorithm starts by computing the current residual $\boldsymbol{r}_0 = \boldsymbol{d} - \boldsymbol{C}\boldsymbol{x}_0$, which is the direction of steepest descent of the energy function (A.28). It sets the original descent direction $\boldsymbol{p}_0 = \boldsymbol{r}_0$. Next, it multiplies the descent direction by the quadratic form (Hessian) matrix $\boldsymbol{C}$ and combines this with the residual to estimate the optimal step size α_k. The solution vector $\boldsymbol{x}_k$ and the residual vector $\boldsymbol{r}_k$ are then updated using this step size. (Notice how the least squares variant of the conjugate gradient algorithm splits the multiplication by the $\boldsymbol{C} = \boldsymbol{A}^T\boldsymbol{A}$ matrix across steps 4 and 8.) Finally, a new search direction is calculated by first computing a factor β as the ratio of current to previous residual magnitudes. The new search direction $\boldsymbol{p}_{k+1}$ is then set to the residual plus β times the old search direction $\boldsymbol{p}_k$, which keeps the directions conjugate with respect to $\boldsymbol{C}$.

It turns out that conjugate gradient descent can also be directly applied to non-quadratic energy functions, e.g., those arising from non-linear least squares (Appendix A.3). Instead of explicitly forming a local quadratic approximation $\boldsymbol{C}$ and then computing residuals $\boldsymbol{r}_k$, non-linear conjugate gradient descent computes the gradient of the energy function E (A.45) directly inside each iteration and uses it to set the search direction (Nocedal and Wright 2006). Since the quadratic approximation to the energy function may not exist or may be inaccurate, line search is often used to determine the step size α_k. Furthermore, to compensate for errors in finding the true function minimum, alternative formulas for β_{k+1} such as Polak–Ribière,

$$\beta_{k+1} = \frac{\nabla E(\boldsymbol{x}_{k+1})[\nabla E(\boldsymbol{x}_{k+1}) - \nabla E(\boldsymbol{x}_k)]}{\|\nabla E(\boldsymbol{x}_k)\|^2} \tag{A.51}$$

are often used (Nocedal and Wright 2006).

A.5.2 Preconditioning

As we mentioned previously, the rate of convergence of the conjugate gradient algorithm is governed in large part by the condition number $\kappa(\boldsymbol{C})$. Its effectiveness can therefore be increased dramatically by reducing this number, e.g., by rescaling elements in $\boldsymbol{x}$, which corresponds to rescaling rows and columns in $\boldsymbol{C}$.

In general, preconditioning is usually thought of as a change of basis from the vector $\boldsymbol{x}$ to a new vector

$$\hat{x} = \boldsymbol{S}\boldsymbol{x}. \tag{A.52}$$

The corresponding linear system being solved then becomes

$$\boldsymbol{A}\boldsymbol{S}^{-1}\hat{x} = \boldsymbol{S}^{-1}\boldsymbol{b} \quad \text{or} \quad \hat{\boldsymbol{A}}\hat{x} = \hat{\boldsymbol{b}}, \tag{A.53}$$

with a corresponding least squares energy (A.29) of the form

$$E_{\text{PLS}} = \hat{x}^T(\boldsymbol{S}^{-T}\boldsymbol{C}\boldsymbol{S}^{-1})\hat{x} - 2\hat{x}^T(\boldsymbol{S}^{-T}\boldsymbol{d}) + \|\hat{\boldsymbol{b}}\|^2. \tag{A.54}$$

The actual preconditioned matrix $\hat{\boldsymbol{C}} = \boldsymbol{S}^{-T}\boldsymbol{C}\boldsymbol{S}^{-1}$ is usually not explicitly computed. Instead, Algorithm A.3 is extended to insert $\boldsymbol{S}^{-T}$ and $\boldsymbol{S}^T$ operations at the appropriate places (Björck 1996; Golub and Van Loan 1996; Trefethen and Bau 1997; Saad 2003; Nocedal and Wright 2006).

A good preconditioner $\boldsymbol{S}$ is easy and cheap to compute, but is also a decent approximation to a square root of $\boldsymbol{C}$, so that $\kappa(\boldsymbol{S}^{-T}\boldsymbol{C}\boldsymbol{S}^{-1})$ is closer to 1. The simplest such choice is the square root of the diagonal matrix $\boldsymbol{S} = \boldsymbol{D}^{1/2}$, with $\boldsymbol{D} = \text{diag}(\boldsymbol{C})$. This has the advantage that any scalar change in variables (e.g., using radians instead of degrees for angular measurements) has no effect on the range of convergence of the iterative technique. For problems that are naturally block-structured, e.g., for structure from motion, where 3D point positions or 6D camera poses are being estimated, a block diagonal preconditioner is often a good choice.

A wide variety of more sophisticated preconditioners have been developed over the years (Björck 1996; Golub and Van Loan 1996; Trefethen and Bau 1997; Saad 2003; Nocedal and Wright 2006), many of which can be directly applied to problems in computer vision (Byröd and øAström 2009; Jeong, Nistér, Steedly *et al.* 2010; Agarwal, Snavely, Seitz *et al.* 2010). Some of these are based on an *incomplete Cholesky* factorization of $\boldsymbol{C}$, i.e., one in which the amount of fill-in in $\boldsymbol{R}$ is strictly limited, e.g., to just the original non-zero elements in $\boldsymbol{C}$.[10] Other preconditioners are based on a sparsified, e.g., tree-based or clustered, approximation to $\boldsymbol{C}$ (Koutis 2007; Koutis and Miller 2008; Grady 2008; Koutis, Miller, and Tolliver 2009), since these are known to have efficient inversion properties.

[10] If a complete Cholesky factorization $\boldsymbol{C} = \boldsymbol{R}^T\boldsymbol{R}$ is used, we get $\hat{\boldsymbol{C}} = \boldsymbol{R}^{-T}\boldsymbol{C}\boldsymbol{R}^{-1} = \boldsymbol{I}$ and all iterative algorithms converge in a single step, thereby obviating the need to use them, but the complete factorization is often too expensive. Note that incomplete factorization can also benefit from reordering.

For grid-based image-processing applications, *parallel* or *hierarchical* preconditioners often perform extremely well (Yserentant 1986; Szeliski 1990b; Pentland 1994; Saad 2003; Szeliski 2006b). These approaches use a change of basis transformation $\boldsymbol{S}$ that resembles the pyramidal or wavelet representations discussed in Section 3.5, and are hence amenable to parallel and GPU-based implementations. Coarser elements in the new representation quickly converge to the low-frequency components in the solution, while finer-level elements encode the higher-frequency components. Some of the relationships between hierarchical preconditioners, incomplete Cholesky factorization, and multigrid techniques are explored by Saad (2003) and Szeliski (2006b).

A.5.3 Multigrid

One other class of iterative techniques widely used in computer vision is *multigrid* techniques (Briggs, Henson, and McCormick 2000; Trottenberg, Oosterlee, and Schuller 2000), which have been applied to problems such as surface interpolation (Terzopoulos 1986a), optical flow (Terzopoulos 1986a; Bruhn, Weickert, Kohlberger *et al.* 2006), high dynamic range tone mapping (Fattal, Lischinski, and Werman 2002), colorization (Levin, Lischinski, and Weiss 2004), natural image matting (Levin, Lischinski, and Weiss 2008), and segmentation (Grady 2008).

The main idea behind multigrid is to form coarser (lower-resolution) versions of the problems and use them to compute the low-frequency components of the solution. However, unlike simple coarse-to-fine techniques, which use the coarse solutions to initialize the fine solution, multigrid techniques only *correct* the low-frequency component of the current solution and use multiple rounds of coarsening and refinement (in what are often called "V" and "W" patterns of motion across the pyramid) to obtain rapid convergence.

On certain simple homogeneous problems (such as solving Poisson equations), multigrid techniques can achieve optimal performance, i.e., computation times linear in the number of variables. However, for more inhomogeneous problems or problems on irregular grids, variants on these techniques, such as *algebraic multigrid* (AMG) approaches, which look at the structure of $\boldsymbol{C}$ to derive coarse level problems, may be preferable. Saad (2003) has a nice discussion of the relationship between multigrid and parallel preconditioners and on the relative merits of using multigrid or conjugate gradient approaches.

Appendix B

Bayesian modeling and inference

The following problem commonly recurs in this book: Given a number of measurements (images, feature positions, etc.), estimate the values of some unknown structure or parameter (camera positions, object shape, etc.). These kinds of problems are in general called *inverse* problems because they involve estimating unknown model parameters instead of simulating the forward formation equations.[1] Computer graphics is a classic forward modeling problem (given some objects, cameras, and lighting, simulate the images that would result), while computer vision problems are usually of the inverse kind (given one or more images, recover the scene that gave rise to these images).

Given an instance of an inverse problem, there are, in general, several ways to proceed. For instance, through clever (or sometimes straightforward) algebraic manipulation, a closed form solution for the unknowns can sometimes be derived. Consider, for example, the *camera matrix calibration* problem (Section 6.2.1): given an image of a calibration pattern consisting of known 3D point positions, compute the 3×4 camera matrix $\boldsymbol{P}$ that maps these points onto the image plane.

In more detail, we can write this problem as (6.33–6.34)

$$x_i = \frac{p_{00}X_i + p_{01}Y_i + p_{02}Z_i + p_{03}}{p_{20}X_i + p_{21}Y_i + p_{22}Z_i + p_{23}} \tag{B.1}$$

$$y_i = \frac{p_{10}X_i + p_{11}Y_i + p_{12}Z_i + p_{13}}{p_{20}X_i + p_{21}Y_i + p_{22}Z_i + p_{23}}, \tag{B.2}$$

where (x_i, y_i) is the feature position of the ith point measured in the image plane, (X_i, Y_i, Z_i) is the corresponding 3D point position, and the p_{ij} are the unknown entries of the camera matrix $\boldsymbol{P}$. Moving the denominator over to the left hand side, we end up with a set of simultaneous linear equations,

$$x_i(p_{20}X_i + p_{21}Y_i + p_{22}Z_i + p_{23}) = p_{00}X_i + p_{01}Y_i + p_{02}Z_i + p_{03}, \tag{B.3}$$

$$y_i(p_{20}X_i + p_{21}Y_i + p_{22}Z_i + p_{23}) = p_{10}X_i + p_{11}Y_i + p_{12}Z_i + p_{13}, \tag{B.4}$$

which we can solve using linear least squares (Appendix A.2) to obtain an estimate of $\boldsymbol{P}$.

The question then arises: is this set of equations the right ones to be solving? If the measurements are totally noise-free or we do not care about getting the best possible answer, then the answer is yes. However, in general, we cannot be sure that we have a reasonable algorithm unless we make a model of the likely sources of error and devise an algorithm that performs as well as possible given these potential errors.

B.1 Estimation theory

The study of such inference problems from noisy data is often called *estimation theory* (Gelb 1974), and its extension to problems where we explicitly choose a loss function is called *statistical decision theory* (Berger 1993; Hastie, Tibshirani, and Friedman 2001; Bishop 2006; Robert 2007). We first start by writing down the forward process that leads from our unknowns (and knowns) to a set of noise-corrupted measurements. We then devise an algorithm that will give us an estimate (or set of estimates) that are both insensitive to the noise (as best they can be) and also quantify the reliability of these estimates.

[1] In machine learning, these problems are called *regression problems*, because we are trying to estimate a *continuous* quantity from noisy inputs, as opposed to a discrete *classification* task (Bishop 2006).

The specific equations above (B.1) are just a particular instance of a more general set of *measurement equations*,

$$\boldsymbol{y}_i = \boldsymbol{f}_i(\boldsymbol{x}) + \boldsymbol{n}_i. \tag{B.5}$$

Here, the $\boldsymbol{y}_i$ are the noise-corrupted *measurements*, e.g., (x_i, y_i) in Equation (B.1), and $\boldsymbol{x}$ is the unknown *state vector*.[2]

Each measurement comes with its associated *measurement model* $\boldsymbol{f}_i(\boldsymbol{x})$, which maps the unknown into that particular measurement. An alternative formulation would be to have one general function $\boldsymbol{f}(\boldsymbol{x}, \boldsymbol{p}_i)$ and to use a per-measurement parameter vector $\boldsymbol{p}_i$ to distinguish between different measurements, e.g., (X_i, Y_i, Z_i) in Equation (B.1). Note that the use of the $\boldsymbol{f}_i(\boldsymbol{x})$ form makes it straightforward to have measurements of different dimensions, which becomes useful when we start adding in prior information (Appendix B.4).

Each measurement is also contaminated with some noise $\boldsymbol{n}_i$. In Equation (B.5), we have indicated that $\boldsymbol{n}_i$ is a zero-mean normal (Gaussian) random variable with a covariance matrix $\boldsymbol{\Sigma}_i$. In general, the noise need not be Gaussian and, in fact, it is usually prudent to assume that some measurements may be outliers. However, we defer this discussion to Appendix B.3, after we have explored the simpler Gaussian noise case more fully. We also assume that the noise vectors $\boldsymbol{n}_i$ are independent. In the case where they are not (e.g., when some constant gain or offset contaminates all of the pixels in a given image), we can add this effect as a *nuisance parameter* to our state vector $\boldsymbol{x}$ and later estimate its value (and discard it, if so desired).

B.1.1 Likelihood for multivariate Gaussian noise

Given all of the noisy measurements $\boldsymbol{y} = \{\boldsymbol{y}_i\}$, we would like to infer a probability distribution on the unknown $\boldsymbol{x}$ vector. We can write the *likelihood* of having observed the $\{\boldsymbol{y}_i\}$ given a particular value of $\boldsymbol{x}$ as

$$L = p(\boldsymbol{y}|\boldsymbol{x}) = \prod_i p(\boldsymbol{y}_i|\boldsymbol{x}) = \prod_i p(\boldsymbol{y}_i|\boldsymbol{f}_i(\boldsymbol{x})) = \prod_i p(\boldsymbol{n}_i). \tag{B.6}$$

When each noise vector $\boldsymbol{n}_i$ is a multivariate Gaussian with covariance $\boldsymbol{\Sigma}_i$,

$$\boldsymbol{n}_i \sim \mathcal{N}(0, \boldsymbol{\Sigma}_i), \tag{B.7}$$

we can write this likelihood as

$$\begin{aligned} L &= \prod_i |2\pi\boldsymbol{\Sigma}_i|^{-1/2} \exp\left(-\frac{1}{2}(\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x}))^T \boldsymbol{\Sigma}_i^{-1} (\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x}))\right) \\ &= \prod_i |2\pi\boldsymbol{\Sigma}_i|^{-1/2} \exp\left(-\frac{1}{2}\|\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x})\|^2_{\boldsymbol{\Sigma}_i^{-1}}\right), \end{aligned} \tag{B.8}$$

where the matrix norm $\|\boldsymbol{x}\|^2_{\boldsymbol{A}}$ is a shorthand notation for $\boldsymbol{x}^T\boldsymbol{A}\boldsymbol{x}$.

The norm $\|\boldsymbol{y}_i - \overline{\boldsymbol{y}}_i\|_{\boldsymbol{\Sigma}_i^{-1}}$ is often called the *Mahalanobis distance* (5.26 and 14.14) and is used to measure the distance between a measurement and the mean of a multivariate Gaussian distribution. Contours of equal Mahalanobis distance are equi-probability contours. Note

[2] In the Kalman filtering literature (Gelb 1974), it is more common to use $\boldsymbol{z}$ instead of $\boldsymbol{y}$ to denote measurements.

that when the measurement covariance is isotropic (the same in all directions), i.e., when $\mathbf{\Sigma}_i = \sigma_i^2 \boldsymbol{I}$, the likelihood can be written as

$$L = \prod_i (2\pi\sigma_i^2)^{-N_i/2} \exp\left(-\frac{1}{2\sigma_i^2}\|\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x})\|^2\right), \tag{B.9}$$

where N_i is the length of the ith measurement vector $\boldsymbol{y}_i$.

We can more easily visualize the structure of the covariance matrix and the corresponding Mahalanobis distance if we first perform an *eigenvalue* or *principal component* analysis (PCA) of the covariance matrix (A.6),

$$\mathbf{\Sigma} = \mathbf{\Phi}\ \mathrm{diag}(\lambda_0 \ldots \lambda_{N-1})\ \mathbf{\Phi}^T. \tag{B.10}$$

Equal-probability contours of the corresponding multi-variate Gaussian, which are also equi-distance contours in the Mahalanobis distance (Figure 14.14), are multi-dimensional ellipsoids whose axis directions are given by the columns of $\mathbf{\Phi}$ (the *eigenvectors*) and whose lengths are given by the $\sigma_j = \sqrt{\lambda_j}$ (Figure A.1).

It is usually more convenient to work with the negative log likelihood, which we can think of as a *cost* or *energy*

$$E = -\log L \quad = \quad \frac{1}{2}\sum_i (\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x}))^T \mathbf{\Sigma}_i^{-1} (\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x})) + k \tag{B.11}$$

$$= \quad \frac{1}{2}\sum_i \|\boldsymbol{y}_i - \boldsymbol{f}_i(\boldsymbol{x})\|^2_{\mathbf{\Sigma}_i^{-1}} + k, \tag{B.12}$$

where $k = \sum_i \log|2\pi\mathbf{\Sigma}_i|$ is a constant that depends on the measurement variances, but is independent of $\boldsymbol{x}$.

Notice that the inverse covariance $\boldsymbol{C}_i = \mathbf{\Sigma}_i^{-1}$ plays the role of a *weight* on each of the measurement error *residuals*, i.e., the difference between the contaminated measurement $\boldsymbol{y}_i$ and its uncontaminated (predicted) value $\boldsymbol{f}_i(\boldsymbol{x})$. In fact, the inverse covariance is often called the (Fisher) *information matrix* (Bishop 2006), since it tells us how much information is contained in a given measurement, i.e., how well it constrains the final estimate. We can also think of this matrix as denoting the amount of *confidence* to associate with each measurement (hence the letter $\boldsymbol{C}$).

In this formulation, it is quite acceptable for some information matrices to be singular (of degenerate rank) or even zero (if the measurement is missing altogether). Rank-deficient measurements often occur, for example, when using a line feature or edge to measure a 3D edge-like feature, since its exact position along the edge is unknown (of infinite or extremely large variance) §8.1.3.

In order to make the distinction between the noise contaminated measurement and its expected value for a particular setting of $\boldsymbol{x}$ more explicit, we adopt the notation $\tilde{\boldsymbol{y}}$ for the former (think of the tilde as the approximate or noisy value) and $\hat{\boldsymbol{y}} = \boldsymbol{f}_i(\boldsymbol{x})$ for the latter (think of the hat as the predicted or expected value). We can then write the negative log likelihood as

$$E = -\log L = \sum_i \|\tilde{\boldsymbol{y}}_i - \hat{\boldsymbol{y}}_i\|_{\mathbf{\Sigma}_i^{-1}} + k. \tag{B.13}$$

B.2 Maximum likelihood estimation and least squares

Now that we have presented the likelihood and log likelihood functions, how can we find the optimal value for our state estimate $\boldsymbol{x}$? One plausible choice might be to select the value of $\boldsymbol{x}$ that maximizes $L = p(\boldsymbol{y}|\boldsymbol{x})$. In fact, in the absence of any prior model for $\boldsymbol{x}$ (Appendix B.4), we have

$$L = p(\boldsymbol{y}|\boldsymbol{x}) = p(\boldsymbol{y}, \boldsymbol{x}) = p(\boldsymbol{x}|\boldsymbol{y}).$$

Therefore, choosing the value of $\boldsymbol{x}$ that maximizes the likelihood is equivalent to choosing the maximum of our probability density estimate for $\boldsymbol{x}$.

When might this be a good idea? If the data (measurements) constrain the possible values of $\boldsymbol{x}$ so that they all cluster tightly around one value (e.g., if the distribution $p(\boldsymbol{x}|\boldsymbol{y})$ is a unimodal Gaussian), the maximum likelihood estimate is the optimal one in that it is both unbiased and has the least possible variance. In many other cases, e.g., if a single estimate is all that is required, it is still often the best estimate.[3] However, if the probability is multi-modal, i.e., it has several local minima in the log likelihood (Figure 5.7), much more care may be required. In particular, it might be necessary to defer certain decisions (such as the ultimate position of an object being tracked) until more measurements have been taken. The CONDENSATION algorithm presented in Section 5.1.2 is one possible method for modeling and updating such multi-modal distributions but is just one example of more general *particle filtering* and *Markov Chain Monte Carlo* (MCMC) techniques (Andrieu, de Freitas, Doucet *et al.* 2003; Bishop 2006; Koller and Friedman 2009).

Another possible way to choose the best estimate is to maximize the *expected utility* (or, conversely, to minimize the expected risk or loss) associated with obtaining the correct estimate, i.e., by minimizing

$$E_{\text{loss}}(\boldsymbol{x}, \boldsymbol{y}) = \int l(\boldsymbol{x} - \boldsymbol{z}) p(\boldsymbol{z}|\boldsymbol{y}) d\boldsymbol{z}. \tag{B.14}$$

For example, if a robot wants to avoid hitting a wall at all costs, the loss function will be high whenever the estimate underestimates the true distance to the wall. When $l(\boldsymbol{x} - \boldsymbol{y}) = \delta(\boldsymbol{x} - \boldsymbol{y})$, we obtain the maximum likelihood estimate, whereas when $l(\boldsymbol{x} - \boldsymbol{y}) = \|\boldsymbol{x} - \boldsymbol{y}\|^2$, we obtain the *mean square error* (MSE) or *expected value* estimate. The explicit modeling of a utility or loss function is what characterizes *statistical decision theory* (Berger 1993; Hastie, Tibshirani, and Friedman 2001; Bishop 2006; Robert 2007).

How do we find the maximum likelihood estimate? If the measurement noise is Gaussian, we can minimize the quadratic objective function (B.13). This becomes even simpler if the measurement equations are linear, i.e.,

$$\boldsymbol{f}_i(\boldsymbol{x}) = \boldsymbol{H}_i \boldsymbol{x}, \tag{B.15}$$

where $\boldsymbol{H}$ is the *measurement matrix* relating unknown state variables $\boldsymbol{x}$ to measurements $\tilde{\boldsymbol{y}}$. In this case, (B.13) becomes

$$E = \sum_i \|\tilde{\boldsymbol{y}}_i - \boldsymbol{H}_i \boldsymbol{x}\|_{\boldsymbol{\Sigma}_i^{-1}} = \sum_i (\tilde{\boldsymbol{y}}_i - \boldsymbol{H}_i \boldsymbol{x})^T \boldsymbol{C}_i (\tilde{\boldsymbol{y}}_i - \boldsymbol{H}_i \boldsymbol{x}), \tag{B.16}$$

[3] According to the Gauss-Markov theorem, least squares produces the best linear unbiased estimator (BLUE) for a linear measurement model regardless of the actual noise distribution, assuming that the noise is zero mean and uncorrelated.

which is a simple quadratic form in $\boldsymbol{x}$, which can be solved using linear least squares (Appendix A.2). When the measurements are non-linear, the system must be solved iteratively using non-linear least squares (Appendix A.3).

B.3 Robust statistics

In Appendix B.1.1, we assumed that the noise being added to each measurement (B.5) was multivariate Gaussian (B.7). This is an appropriate model if the noise is the result of lots of tiny errors being added together, e.g., from thermal noise in a silicon imager. In most cases, however, measurements can be contaminated with larger *outliers*, i.e., gross failures in the measurement process. Examples of such outliers include bad feature matches (Section 6.1.4), occlusions in stereo matching (Chapter 11), and discontinuities in an otherwise smooth image, depth map, or label image (Sections 3.7.1 and 3.7.2).

In such cases, it makes more sense to model the measurement noise with a long-tailed *contaminated* noise model such as a Laplacian. The negative log likelihood in this case, rather than being quadratic in the measurement residuals (B.12–B.16), has a slower growth in the penalty function to account for the increased likelihood of large errors.

This formulation of the inference problem is called an *M-estimator* in the robust statistics literature (Huber 1981; Hampel, Ronchetti, Rousseeuw *et al.* 1986; Black and Rangarajan 1996; Stewart 1999) and involves applying a robust penalty function $\rho(r)$ to the residuals

$$E_{\text{RLS}}(\Delta\boldsymbol{p}) = \sum_i \rho(\|\boldsymbol{r}_i\|) \tag{B.17}$$

instead of squaring them.

As we mentioned in Section 6.1.4, we can take the derivative of this function with respect to $\boldsymbol{p}$ and set it to 0,

$$\sum_i \psi(\|\boldsymbol{r}_i\|)\frac{\partial\|\boldsymbol{r}_i\|}{\partial\boldsymbol{p}} = \sum_i \frac{\psi(\|\boldsymbol{r}_i\|)}{\|\boldsymbol{r}_i\|}\boldsymbol{r}_i^T\frac{\partial\boldsymbol{r}_i}{\partial\boldsymbol{p}} = 0, \tag{B.18}$$

where $\psi(r) = \rho'(r)$ is the derivative of ρ and is called the *influence function*. If we introduce a *weight function*, $w(r) = \Psi(r)/r$, we observe that finding the stationary point of (B.17) using (B.18) is equivalent to minimizing the *iteratively re-weighted least squares* (IRLS) problem

$$E_{\text{IRLS}} = \sum_i w(\|\boldsymbol{r}_i\|)\|\boldsymbol{r}_i\|^2, \tag{B.19}$$

where the $w(\|\boldsymbol{r}_i\|)$ play the same local weighting role as $\boldsymbol{C}_i = \boldsymbol{\Sigma}_i^{-1}$ in (B.12). Black and Anandan (1996) describe a variety of robust penalty functions and their corresponding influence and weighting function.

The IRLS algorithm alternates between computing the influence functions $w(\|\boldsymbol{r}_i\|)$ and solving the resulting weighted least squares problem (with fixed w values). Alternative incremental robust least squares algorithms can be found in the work of Sawhney and Ayer (1996); Black and Anandan (1996); Black and Rangarajan (1996); Baker, Gross, Ishikawa *et al.* (2003) and textbooks and tutorials on robust statistics (Huber 1981; Hampel, Ronchetti, Rousseeuw *et al.* 1986; Rousseeuw and Leroy 1987; Stewart 1999). It is also possible to apply general optimization techniques (Appendix A.3) directly to the non-linear cost function given in Equation (B.19), which may sometimes have better convergence properties.

Most robust penalty functions involve a scale parameter, which should typically be set to the variance (or standard deviation, depending on the formulation) of the non-contaminated (inlier) noise. Estimating such noise levels directly from the measurements or their residuals, however, can be problematic, as such estimates themselves become contaminated by outliers. The robust statistics literature contains a variety of techniques to estimate such parameters. One of the simplest and most effective is the *median absolute deviation* (MAD),

$$MAD = \text{med}_i \|\boldsymbol{r}_i\|, \tag{B.20}$$

which, when multiplied by 1.4, provides a robust estimate of the standard deviation of the inlier noise process.

As mentioned in Section 6.1.4, it is often better to start iterative non-linear minimization techniques, such as IRLS, in the vicinity of a good solution by first randomly selecting small subsets of measurements until a good set of inliers is found. The best known of these techniques is RANdom SAmple Consensus (RANSAC) (Fischler and Bolles 1981), although even better variants such as Preemptive RANSAC (Nistér 2003) and PROgressive SAmple Consensus (PROSAC) (Chum and Matas 2005) have since been developed.

B.4 Prior models and Bayesian inference

While maximum likelihood estimation can often lead to good solutions, in some cases the range of possible solutions consistent with the measurements is too large to be useful. For example, consider the problem of image denoising (Sections 3.4.4 and 3.7.3). If we estimate each pixel separately based on just its noisy version, we cannot make any progress, as there are a large number of values that could lead to each noisy measurement.[4] Instead, we need to rely on typical properties of images, e.g., that they tend to be piecewise smooth (Section 3.7.1).

The propensity of images to be piecewise smooth can be encoded in a *prior distribution* $p(\boldsymbol{x})$, which measures the likelihood of an image being a natural image. For example, to encode piecewise smoothness, we can use a *Markov random field* model (3.109 and B.24) whose negative log likelihood is proportional to a robustified measure of image smoothness (gradient magnitudes).

Prior models need not be restricted to image processing applications. For example, we may have some external knowledge about the rough dimensions of an object being scanned, the focal length of a lens being calibrated, or the likelihood that a particular object might appear in an image. All of these are examples of prior distributions or probabilities and they can be used to produce more reliable estimates.

As we have already seen in (3.68) and (3.106), Bayes' Rule states that a *posterior* distribution $p(\boldsymbol{x}|\boldsymbol{y})$ over the unknowns $\boldsymbol{x}$ given the measurements $\boldsymbol{y}$ can be obtained by multiplying the measurement likelihood $p(\boldsymbol{y}|\boldsymbol{x})$ by the prior distribution $p(\boldsymbol{x})$,

$$p(\boldsymbol{x}|\boldsymbol{y}) = \frac{p(\boldsymbol{y}|\boldsymbol{x})p(\boldsymbol{x})}{p(\boldsymbol{y})}, \tag{B.21}$$

where $p(\boldsymbol{y}) = \int_{\boldsymbol{x}} p(\boldsymbol{y}|\boldsymbol{x})p(\boldsymbol{x})$ is a normalizing constant used to make the $p(\boldsymbol{x}|\boldsymbol{y})$ distribution *proper* (integrate to 1). Taking the negative logarithm of both sides of Equation (B.21), we

[4] In fact, the maximum likelihood estimate is just the noisy image itself.

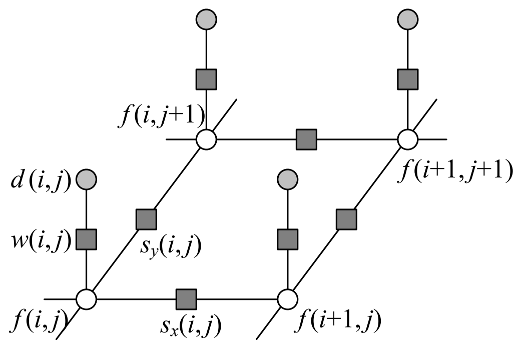


Figure B.1 Graphical model for an $\mathcal{N}_4$ neighborhood Markov random field. The white circles are the unknowns $f(i, j)$, while the dark circles are the input data $d(i, j)$. The $s_x(i, j)$ and $s_y(i, j)$ black boxes denote arbitrary *interaction potentials* between adjacent nodes in the random field, and the $w(i, j)$ denote the *data penalty* functions. They are all examples of the general potentials $V_{i,j,k,l}(f(i, j), f(k, l))$ used in Equation (B.24).

get

$$-\log p(\boldsymbol{x}|\boldsymbol{y}) = -\log p(\boldsymbol{y}|\boldsymbol{x}) - \log p(\boldsymbol{x}) + \log p(\boldsymbol{y}), \tag{B.22}$$

which is the *negative posterior log likelihood*. It is common to drop the constant $\log p(\boldsymbol{y})$ because its value does not matter during energy minimization. However, if the prior distribution $p(\boldsymbol{x})$ depends on some unknown parameters, we may wish to keep $\log p(\boldsymbol{y})$ in order to compute the most likely value of these parameters using *Occam's razor*, i.e., by maximizing the likelihood of the observations, or to select the correct number of free parameters using *model selection* (Hastie, Tibshirani, and Friedman 2001; Torr 2002; Bishop 2006; Robert 2007).

To find the most likely (*maximum a posteriori* or MAP) solution $\boldsymbol{x}$ given some measurements $\boldsymbol{y}$, we simply minimize this negative log likelihood, which can also be thought of as an *energy*,

$$E(\boldsymbol{x}, \boldsymbol{y}) = E_d(\boldsymbol{x}, \boldsymbol{y}) + E_p(\boldsymbol{x}). \tag{B.23}$$

The first term $E_d(\boldsymbol{x}, \boldsymbol{y})$ is the *data energy* or *data penalty* and measures the negative log likelihood that the measurements $\boldsymbol{y}$ were observed given the unknown state $\boldsymbol{x}$. The second term $E_p(\boldsymbol{x})$ is the *prior energy* and it plays a role analogous to the smoothness energy in regularization. Note that the MAP estimate may not always be desirable, since it selects the "peak" in the posterior distribution rather than some more stable statistic such as MSE—see the discussion in Appendix B.2 about loss functions and decision theory.

B.5 Markov random fields

Markov random fields (Blake, Kohli, and Rother 2010) are the most popular types of prior model for gridded image-like data,[5] which include not only regular natural images (Section 3.7.2) but also two-dimensional fields such as optic flow (Chapter 8) or depth maps (Chapter 11), as well as binary fields, such as segmentations (Section 5.5).

[5] Alternative formulations include power spectra (Section 3.4.3) and non-local means (Buades, Coll, and Morel 2008).

As we discussed in Section 3.7.2, the prior probability $p(\boldsymbol{x})$ for a Markov random field is a *Gibbs* or *Boltzmann distribution*, whose negative log likelihood (according to the Hammersley–Clifford Theorem) can be written as a sum of pairwise *interaction potentials*,

$$E_p(\boldsymbol{x}) = \sum_{\{(i,j),(k,l)\} \in \mathcal{N}} V_{i,j,k,l}(f(i,j), f(k,l)), \tag{B.24}$$

where $\mathcal{N}(i,j)$ denotes the *neighbors* of pixel (i,j). In the more general case, MRFs can also contain unary potentials, as well as *higher-order potentials* defined over larger cardinality *cliques* (Kindermann and Snell 1980; Geman and Geman 1984; Bishop 2006; Potetz and Lee 2008; Kohli, Kumar, and Torr 2009; Kohli, Ladický, and Torr 2009; Rother, Kohli, Feng *et al.* 2009; Alahari, Kohli, and Torr 2011). They can also contain *line processes*, i.e., additional binary variables that mediate discontinuities between adjacent elements (Geman and Geman 1984). Black and Rangarajan (1996) show how independent line process variables can be eliminated and incorporated into regular MRFs using robust pairwise penalty functions.

The most commonly used neighborhood in Markov random field modeling is the $\mathcal{N}_4$ neighborhood, where each pixel in the field $f(i,j)$ interacts only with its immediate neighbors—Figure B.1 shows such an $\mathcal{N}_4$ MRF. The $s_x(i,j)$ and $s_y(i,j)$ black boxes denote arbitrary interaction potentials between adjacent nodes in the random field and the $w(i,j)$ denote the elemental data penalty terms in E_d (B.23). These square nodes can also be interpreted as *factors* in a *factor graph* version of the undirected graphical model (Bishop 2006; Wainwright and Jordan 2008; Koller and Friedman 2009), which is another name for interaction potentials. (Strictly speaking, the factors are improper probability functions whose product is the un-normalized posterior distribution.)

More complex and higher-dimensional interaction models and neighborhoods are also possible. For example, 2D grids can be enhanced with the addition of diagonal connections (an $\mathcal{N}_8$ neighborhood) or even larger numbers of pairwise terms (Boykov and Kolmogorov 2003; Rother, Kolmogorov, Lempitsky *et al.* 2007). 3D grids can be used to compute globally optimal segmentations in 3D volumetric medical images (Boykov and Funka-Lea 2006) (Section 5.5.1). Higher-order cliques can also be used to develop more sophisticated models (Potetz and Lee 2008; Kohli, Ladický, and Torr 2009; Kohli, Kumar, and Torr 2009).

One of the biggest challenges in using MRF models is to develop efficient *inference algorithms* that will find low-energy solutions (Veksler 1999; Boykov, Veksler, and Zabih 2001; Kohli 2007; Kumar 2008). Over the years, a large variety of such algorithms have been developed, including simulated annealing, graph cuts, and loopy belief propagation. The choice of inference technique can greatly affect the overall performance of a vision system. For example, most of the top-performing algorithms on the Middlebury Stereo Evaluation page either use belief propagation or graph cuts.

In the next few subsections, we review some of the more widely used MRF inference techniques. More in-depth descriptions of most of these algorithms can be found in a recently published book on advances in MRF techniques (Blake, Kohli, and Rother 2010). Experimental comparisons, along with test datasets and reference software, are provided by Szeliski, Zabih, Scharstein *et al.* (2008).[6]

[6] http://vision.middlebury.edu/MRF/.

B.5.1 Gradient descent and simulated annealing

The simplest optimization technique is gradient descent, which minimizes the energy by changing independent subsets of nodes to take on lower-energy configurations. Such techniques go under a variety of names, including *contextual classification* (Kittler and Föglein 1984) and *iterated conditional modes* (ICM) (Besag 1986).[7] Variables can either be updated sequentially, e.g., in raster scan, or in parallel, e.g., using red–black coloring on a checkerboard. Chou and Brown (1990) suggests using highest confidence first (HCF), i.e., choosing variables based on how large a difference they make in reducing the energy.

The problem with gradient descent is that it is prone to getting stuck in local minima, which is almost always the case with MRF problems. One way around this is to use *stochastic gradient descent* or *Markov chain Monte Carlo* (MCMC) (Metropolis, Rosenbluth, Rosenbluth *et al.* 1953), i.e., to randomly take occasional uphill steps in order to get out of such minima. One popular update rule is the *Gibbs sampler* (Geman and Geman 1984); rather than choosing the lowest energy state for a variable being updated, it chooses the state with probability

$$p(\boldsymbol{x}) \propto e^{-E(\boldsymbol{x})/T}, \tag{B.25}$$

where T is called the *temperature* and controls how likely the system is to choose a more random update. Stochastic gradient descent is usually combined with *simulated annealing* (Kirkpatrick, Gelatt, and Vecchi 1983), which starts at a relatively high temperature, thereby randomly exploring a large part of the state space, and gradually cools (anneals) the temperature to find a good local minimum. During the late 1980s, simulated annealing was the method of choice for solving MRF inference problems (Szeliski 1986; Marroquin, Mitter, and Poggio 1985; Barnard 1989).

Another variant on simulated annealing is the Swendsen–Wang algorithm (Swendsen and Wang 1987; Barbu and Zhu 2003, 2005). Here, instead of "flipping" (changing) single variables, a connected subset of variables, chosen using a random walk based on MRF connectively strengths, is selected as the basic update unit. This can sometimes help make larger state changes, and hence find better-quality solutions in less time.

While simulated annealing has largely been superseded by the newer graph cuts and loopy belief propagation techniques, it still occasionally finds use, especially in highly connected and highly non-submodular graphs (Rother, Kolmogorov, Lempitsky *et al.* 2007).

B.5.2 Dynamic programming

Dynamic programming (DP) is an efficient inference procedure that works for any tree-structured graphical model, i.e., one that does not have any cycles. Given such a tree, pick any node as the root r and figuratively pick up the tree by its root. The depth or distance of all the other nodes from this root induces a partial ordering over the vertices, from which a total ordering can be obtained by arbitrarily breaking ties. Let us now lay out this graph as a tree with the root on the right and indices increasing from left to right, as shown in Figure B.2a.

Before describing the DP algorithm, let us re-write the potential function of Equation (B.24)

[7] The name comes from iteratively setting variables to the mode (most likely, i.e., lowest energy) state conditioned on its currently fixed neighbors.

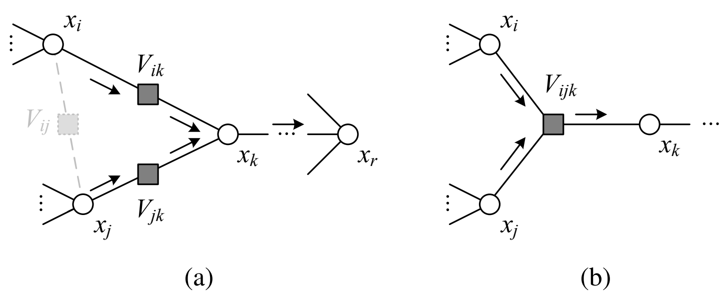


Figure B.2 Dynamic programming over a tree drawn as a factor graph. (a) To compute the lowest energy solution $\hat{E}_k(x_k)$ at node x_k conditioned on the best solutions to the left of this node, we enumerate all possible values of $\hat{E}_i(x_i) + V_{ik}(x_i, x_k)$ and pick the smallest one (and similarly for j). (b) For higher-order cliques, we need to try all combinations of (x_i, x_j) in order to select the best possible configuration. The arrows show the basic flow of the computation. The lightly shaded factor V_{ij} in (a) shows an additional connection that turns the tree into a cyclic graph, for which exact inference cannot be efficiently computed.

in a more general but succinct form,

$$E(\boldsymbol{x}) = \sum_{(i,j)\in\mathcal{N}} V_{i,j}(x_i, x_j) + \sum_i V_i(x_i), \tag{B.26}$$

where instead of using pixel indices (i, j) and (k, l), we just use scalar index variables i and j. We also replace the function value $f(i, j)$ with the more succinct notation x_i, with the $\{x_i\}$ variables making up the state vector $\boldsymbol{x}$. We can simplify this function even further by adding dummy nodes (vertices) i^- for every node that has a non-zero $V_i(x_i)$ and setting $V_{i,i^-}(x_i, x_{i^-}) = V_i(x_i)$, which lets us drop the V_i terms from (B.26).

Dynamic programming proceeds by computing partial sums in a left-to-right fashion, i.e., in order of increasing variable index. Let $\mathcal{C}_k$ be the children of k, i.e., $i < k, (i, k) \in \mathcal{N}$). Then, define

$$\tilde{E}_k(\boldsymbol{x}) = \sum_{i<k,\ j\leq k} V_{i,j}(x_i, x_j) = \sum_{i\in\mathcal{C}_k} \left[V_{i,k}(x_i, x_k) + \tilde{E}_i(\boldsymbol{x})\right], \tag{B.27}$$

as a partial sum of (B.26) over all variables up to and including k, i.e., over all parts of the graph shown in Figure B.2a to the left of x_k. This sum depends on the state of all the unknown variables in $\boldsymbol{x}$ with $i \leq k$.

Now suppose we wish to find the setting for all variables $i < k$ that minimizes this sum. It turns out that we can use a simple recursive formula

$$\hat{E}_k(x_k) = \min_{\{x_i,\ i<k\}} \tilde{E}_k(\boldsymbol{x}) = \sum_{i\in\mathcal{C}_k} \min_{x_i} \left[V_{i,k}(x_i, x_k) + \hat{E}_i(x_i)\right] \tag{B.28}$$

to find this minimum. Visually, this is easy to understand. Looking at Figure B.2a, associate an energy $\hat{E}_k(x_k)$ with each node k and each possible setting of its value x_k that is based on the *best* possible setting of variables to the left of that node. It is easy to convince yourself that in this figure, you only need to know $\hat{E}_i(x_i)$ and $\hat{E}_j(x_j)$ in order to compute this value.

Once the flow of information in the tree has been processed from left to right, the minimum value of $\hat{E}_r(x_r)$ at the root gives the MAP (lowest-energy) solution for $E(\boldsymbol{x})$. The root node is set to the choice of x_r that minimizes this function, and other nodes are set in a *backward chaining* pass by selecting the values of child nodes $i \in \mathcal{C}_k$ that were minimal in the original recursion (B.28).

Dynamic programming is not restricted to trees with pairwise potentials. Figure B.2b shows an example of a three-way potential $V_{ijk}(x_i, x_j, x_k)$ inside a tree. To compute the optimum value of $\hat{E}_k(x_k)$, the recursion formula in (B.28) now has to evaluate the minimum over all combinations of possible state values leading into a factor node (gray box). For this reason, dynamic programming is normally exponential in complexity in the order of the clique size, i.e., a clique of size n with l labels at each node requires the evaluation of l^{n-1} possible states (Potetz and Lee 2008; Kohli, Kumar, and Torr 2009). However, for certain kinds of potential functions $V_{i,k}(x_i, x_k)$, including the Potts model (delta function), absolute values (total variation), and quadratic (Gaussian MRF), Felzenszwalb and Huttenlocher (2006) show how to reduce the complexity of the min-finding step (B.28) from $O(l^2)$ to $O(l)$. In Appendix B.5.3, we also discuss how Potetz and Lee (2008) reduce the complexity for special kinds of higher-order clique, i.e., linear summations followed by non-linearities.

Figure B.2a also shows what happens if we add an extra factor between nodes i and j. In this case, the graph is no longer a tree, i.e., it contains a cycle. It is no longer possible to use the recursion formula (B.28), since $\hat{E}_i(x_i)$ now appears in two different terms inside the summation, i.e., as a child of both nodes j and k, and the same setting for x_i may not minimize both. In other words, when loops exist, there is no ordering of the variables that allows the recursion (elimination) in (B.28) to be well-founded.

It is, however, possible to convert small loops into higher-order factors and to solve these as shown in Figure B.2b. However, graphs with long loops or meshes result in extremely large clique sizes and hence an amount of computation potentially exponential in the size of the graph.

B.5.3 Belief propagation

Belief propagation is an inference technique originally developed for trees (Pearl 1988) but more recently extended to "loopy" (cyclic) graphs such as MRFs (Frey and MacKay 1997; Freeman, Pasztor, and Carmichael 2000; Yedidia, Freeman, and Weiss 2001; Weiss and Freeman 2001a,b; Yuille 2002; Sun, Zheng, and Shum 2003; Felzenszwalb and Huttenlocher 2006). It is closely related to dynamic programming, in that both techniques pass messages forward and backward over a tree or graph. In fact, one of the two variants of belief propagation, the *max-product rule*, performs the exact same computation (inference) as dynamic programming, albeit using probabilities instead of energies.

Recall that the energy we are minimizing in MAP estimation (B.26) is the negative log likelihood (B.12, B.13, and B.22) of a factored Gibbs posterior distribution,

$$p(\boldsymbol{x}) = \prod_{(i,j)\in\mathcal{N}} \phi_{i,j}(x_i, x_j), \tag{B.29}$$

where

$$\phi_{i,j}(x_i, x_j) = e^{-V_{i,j}(x_i,x_j)} \tag{B.30}$$

are the pairwise *interaction potentials*. We can rewrite (B.27) as

$$\tilde{p}_k(\boldsymbol{x}) = \prod_{i<k,\ j\leq k} \phi_{i,j}(x_i, x_j) = \prod_{i\in\mathcal{C}_k} \tilde{p}_{i,k}(\boldsymbol{x}), \tag{B.31}$$

where

$$\tilde{p}_{i,k}(\boldsymbol{x}) = \phi_{i,k}(x_i, x_k)\tilde{p}_i(\boldsymbol{x}). \tag{B.32}$$

We can therefore rewrite (B.28) as

$$\hat{p}_k(x_k) = \max_{\{x_i,\ i<k\}} \tilde{p}_k(\boldsymbol{x}) = \prod_{i \in \mathcal{C}_k} \hat{p}_{i,k}(\boldsymbol{x}), \tag{B.33}$$

with

$$\hat{p}_{i,k}(\boldsymbol{x}) = \max_{x_i} \phi_{i,k}(x_i, x_k)\hat{p}_i(\boldsymbol{x}). \tag{B.34}$$

Equation (B.34) is the *max* update rule evaluated at all square box factors in Figure B.2a, while (B.33) is the *product* rule evaluated at the nodes. The probability distribution $\hat{p}_{i,k}(\boldsymbol{x})$ is often interpreted as a *message* passing information about child i to parent k and is hence written as $m_{i,k}(x_k)$ (Yedidia, Freeman, and Weiss 2001) or $\mu_{i\to k}(x_k)$ (Bishop 2006).

The max-product rule can be used to compute the MAP estimate in a tree using the same kind of forward and backward sweep as in dynamic programming (which is sometimes called the *max-sum* algorithm (Bishop 2006)). An alternative rule, known as the *sum–product*, sums over all possible values in (B.34) rather than taking the maximum, in essence computing the *expected* distribution rather than the *maximum likelihood* distribution. This produces a set of probability estimates that can be used to compute the *marginal* distributions $b_i(x_i) = \sum_{\boldsymbol{x}\setminus x_i} p(\boldsymbol{x})$ (Pearl 1988; Yedidia, Freeman, and Weiss 2001; Bishop 2006).

Belief propagation may not produce optimal estimates for cyclic graphs for the same reason that dynamic programming fails to work, i.e., because a node with multiple parents may take on different optimal values for each of the parents, i.e., there is no unique elimination ordering. Early algorithms for extending belief propagation to graphs with cycles, dubbed *loopy belief propagation*, performed the updates in parallel over the graph, i.e., using *synchronous updates* (Frey and MacKay 1997; Freeman, Pasztor, and Carmichael 2000; Yedidia, Freeman, and Weiss 2001; Weiss and Freeman 2001a,b; Yuille 2002; Sun, Zheng, and Shum 2003; Felzenszwalb and Huttenlocher 2006).

For example, Felzenszwalb and Huttenlocher (2006) split an $\mathcal{N}_4$ graph into its red and black (checkerboard) components and alternate between sending messages from the red nodes to the black and vice versa. They also use multi-grid (coarser level) updates to speed up the convergence. As discussed previously, to reduce the complexity of the basic max-product update rule (B.28) from $O(l^2)$ to $O(l)$, they develop specialized update algorithms for several cost functions $V_{i,k}(x_i, x_k)$, including the Potts model (delta function), absolute values (total variation), and quadratic (Gaussian MRF). A related algorithm, *mean field diffusion* (Scharstein and Szeliski 1998), also uses synchronous updates between nodes to compute marginal distributions. Yuille (2010) discusses the relationships between mean field theory and loopy belief propagation.

More recent loopy belief propagation algorithms and their variants use sequential scans through the graph (Szeliski, Zabih, Scharstein *et al.* 2008). For example, Tappen and Freeman (2003) pass messages from left to right along each row and then reverse the direction once they reach the end. This is similar to treating each row as an independent tree (chain), except that messages from nodes above and below the row are also incorporated. They then perform similar computations along columns. These sequential updates allow the information to propagate much more quickly across the image than synchronous updates.

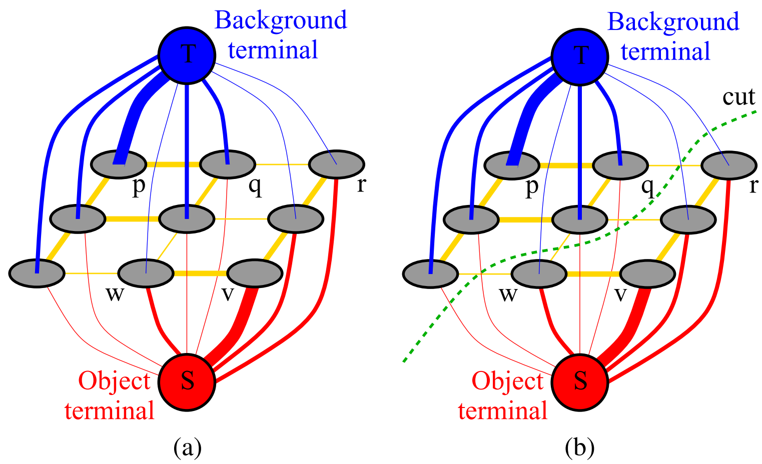


Figure B.3 Graph cuts for minimizing binary sub-modular MRF energies (Boykov and Jolly 2001) © 2001 IEEE: (a) energy function encoded as a max flow problem; (b) the minimum cut determines the region boundary.

The other belief propagation variant tested by Szeliski, Zabih, Scharstein *et al.* (2008), which they call BP-S or TRW-S, is based on Kolmogorov's (2006) sequential extension of the *tree-reweighted message passing* of Wainwright, Jaakkola, and Willsky (2005). TRW first selects a set of trees from the neighborhood graph and computes a set of probability distributions over each tree. These are then used to reweight the messages being passed during loopy belief propagation. The sequential version of TRW, called TRW-S, processed nodes in scan-line order, with a forward and backward pass. In the forward pass, each node sends messages to its right and bottom neighbors. In the backward pass, messages are sent to the left and upper neighbors. TRW-S also computes a lower bound on the energy, which is used by Szeliski, Zabih, Scharstein *et al.* (2008) to estimate how close to the best possible solution all of the MRF inference algorithms being evaluated get.

As with dynamic programming, belief propagation techniques also become less efficient as the order of each factor clique increases. Potetz and Lee (2008) shows how this complexity can be reduced back to linear in the clique order for continuous-valued problems where the factors involve linear summations followed by a non-linearity, which is typical of more sophisticated MRF models such as fields of experts (Roth and Black 2009) and steerable random fields (Roth and Black 2007b). Kohli, Kumar, and Torr (2009) and Alahari, Kohli, and Torr (2011) develop alternative ways for dealing with higher-order cliques in the context of graph cut algorithms.

B.5.4 Graph cuts

The computer vision community has adopted "graph cuts" as an informal name to describe a large family of MRF inference algorithms based on solving one or more min-cut or max-flow problems (Boykov, Veksler, and Zabih 2001; Boykov and Kolmogorov 2010; Boykov, Veksler, and Zabih 2010; Ishikawa and Veksler 2010).

The simplest example of an MRF graph cut is the polynomial-time algorithm for performing exact minimization of a binary MRF originally developed by Greig, Porteous, and Seheult

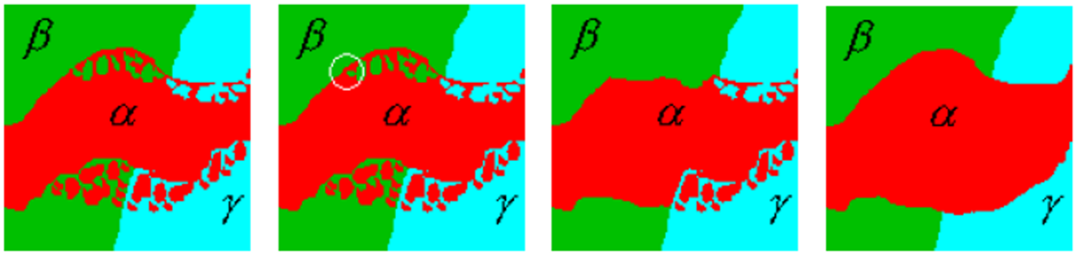
(1989) and brought to the attention of the computer vision community by Boykov, Veksler, and Zabih (2001) and Boykov and Jolly (2001). The basic construction of the min-cut graph from an MRF energy function is shown in Figure B.3 and described in Sections 3.7.2 and 5.5. In brief, the nodes in an MRF are connected to special source and sink nodes, and the minimum cut between these two nodes, whose cost is exactly that of the MRF energy under a binary assignment of labels, is computed using a polynomial-time max flow algorithm (Goldberg and Tarjan 1988; Boykov and Kolmogorov 2004).

As discussed in Section 5.5, important extensions of this basic algorithm have been made for the case of directed edges (Kolmogorov and Boykov 2005), larger neighborhoods (Boykov and Kolmogorov 2003; Kolmogorov and Boykov 2005), connectivity priors (Vicente, Kolmogorov, and Rother 2008), and shape priors (Lempitsky and Boykov 2007; Lempitsky, Blake, and Rother 2008). Kolmogorov and Zabih (2004) formally characterize the class of binary energy potentials (*regularity conditions*) for which these algorithms find the global minimum. Komodakis, Tziritas, and Paragios (2008) and Rother, Kolmogorov, Lempitsky *et al.* (2007) provide good algorithms for the cases when they do not.

Binary MRF problems can also be approximately solved by turning them into continuous $[0, 1]$ problems, solving them either as linear systems (Grady 2006; Sinop and Grady 2007; Grady and Alvino 2008; Grady 2008; Grady and Ali 2008; Singaraju, Grady, and Vidal 2008; Couprie, Grady, Najman *et al.* 2009) (the *random walker model*) or by computing geodesic distances (Bai and Sapiro 2009; Criminisi, Sharp, and Blake 2008) and then thresholding the results. More details on these techniques are provided in Section 5.5 and a nice review can be found in the work of Singaraju, Grady, Sinop *et al.* (2010). A different connection to continuous segmentation techniques, this time to the literature on level sets (Section 5.1.4), is made by Boykov, Kolmogorov, Cremers *et al.* (2006), who develop an approach to solving surface propagation PDEs based on combinatorial graph cut algorithms—Boykov and Funka-Lea (2006) discuss this and related techniques.

Multi-valued MRF inference problems usually require solving a series of related binary MRF problems (Boykov, Veksler, and Zabih 2001), although for special cases, such as some convex functions, a single graph cut may suffice (Ishikawa 2003; Schlesinger and Flach 2006). The seminal work in this area is that of Boykov, Veksler, and Zabih (2001), who introduced two algorithms, called the *swap move* and the *expansion move*, which are sketched in Figure B.4. The α–β-swap move selects two labels (usually by cycling through all possible pairings) and then formulates a binary MRF problem that allows any pixels currently labeled as either α or β to optionally switch their values to the other label. The α-expansion move allows any pixel in the MRF to take on the α label or to keep its current identity. It is easy to see by inspection that both of these moves result in binary MRFs with well-defined energy functions.

Because these algorithms use a binary MRF optimization inside their inner loop, they are subject to the constraints on the energy functions that occur in the binary labeling case (Kolmogorov and Zabih 2004). However, more recent algorithms such as those developed by Komodakis, Tziritas, and Paragios (2008) and Rother, Kolmogorov, Lempitsky *et al.* (2007) can be used to provide approximate solutions for more general energy functions. Efficient algorithms for re-using previous solutions (*flow-* and *cut-recycling*) have been developed for on-line applications such as *dynamic MRFs* (Kohli and Torr 2005; Juan and Boykov 2006; Alahari, Kohli, and Torr 2011) and coarse-to-fine banded graph cuts (Agarwala, Zheng, Pal *et*



(a) initial labeling (b) standard move (c) α-β-swap (d) α-expansion

Figure B.4 Multi-level graph optimization from (Boykov, Veksler, and Zabih 2001) © 2001 IEEE: (a) initial problem configuration; (b) the standard move changes only one pixel; (c) the α–β-swap optimally exchanges all α- and β-labeled pixels; (d) the α-expansion move optimally selects among current pixel values and the α label.

al. 2005; Lombaert, Sun, Grady *et al.* 2005; Juan and Boykov 2006). It is also now possible to minimize the number of labels used as part of the alpha-expansion process (Delong, Osokin, Isack *et al.* 2010).

In experimental comparisons, α-expansions usually converge faster to a good solution than α–β-swaps (Szeliski, Zabih, Scharstein *et al.* 2008), especially for problems that involve large regions of identical labels, such as the labeling of source imagery in image stitching (Figure 3.60). For truncated convex energy functions defined over ordinal values, more accurate algorithms that consider complete ranges of labels inside each min-cut and often produce lower energies have been developed (Veksler 2007; Kumar and Torr 2008; Kumar, Veksler, and Torr 2010). The whole field of efficient MRF inference algorithms is rapidly developing, as witnessed by a recent special journal issue (Kohli and Torr 2008; Komodakis, Tziritas, and Paragios 2008; Olsson, Eriksson, and Kahl 2008; Potetz and Lee 2008), articles (Alahari, Kohli, and Torr 2011), and a forthcoming book (Blake, Kohli, and Rother 2010).

B.5.5 Linear programming

[8] Many successful algorithms for MRF optimization are based on the *linear programming* (LP) relaxation of the energy function (Weiss, Yanover, and Meltzer 2010). For some practical MRF problems, LP-based techniques can produce globally minimal solutions (Meltzer, Yanover, and Weiss 2005), even though MRF inference is in general NP-hard. In order to describe this relaxation, let us first rewrite the energy function (B.26) as

$$\begin{aligned} E(\boldsymbol{x}) &= \sum_{(i,j)\in\mathcal{N}} V_{i,j}(x_i,x_j) + \sum_i V_i(x_i) && \text{(B.35)} \\ &= \sum_{i,j,\alpha,\beta} V_{i,j}(\alpha,\beta) x_{i,j;\alpha,\beta} + \sum_{i,\alpha} V_i(\alpha) x_{i;\alpha} && \text{(B.36)} \\ \text{subject to} \quad x_{i;\alpha} &= \sum_\beta x_{i,j;\alpha,\beta} \quad \forall (i,j)\in\mathcal{N},\alpha, && \text{(B.37)} \\ x_{j;\beta} &= \sum_\alpha x_{i,j;\alpha,\beta} \quad \forall (i,j)\in\mathcal{N},\beta, \quad \text{and} && \text{(B.38)} \\ x_{i,\alpha},\ x_{i,j;\alpha,\beta} &\in \{0,1\}. && \text{(B.39)} \end{aligned}$$

[8] This section was contributed by Vladimir Kolmogorov. Thanks!

Here, α and β range over label values and $x_{i;\alpha} = \delta(x_i - \alpha)$ and $x_{ij;\alpha\beta} = \delta(x_i - \alpha)\delta(x_j - \beta)$ are indicator variables of assignments $x_i = \alpha$ and $(x_i, x_j) = (\alpha, \beta)$, respectively. The LP relaxation is obtained by replacing the discreteness constraints (B.39) with linear constraints $x_{ij;\alpha\beta} \in [0, 1]$. It is easy to show that the optimal value of (B.36) is a lower bound on (B.26).

This relaxation has been extensively studied in the literature, starting with the work of Schlesinger (1976). An important question is how to solve this LP efficiently. Unfortunately, general-purpose LP solvers cannot handle large problems in vision (Yanover, Meltzer, and Weiss 2006). A large number of customized iterative techniques have been proposed. Most of these solve the dual problem, i.e., they formulate a lower bound on (B.36) and then try to maximize this bound. The bound is often formulated using a convex combination of trees, as proposed in (Wainwright, Jaakkola, and Willsky 2005).

The LP lower bound can be maximized via a number of techniques, such as *max-sum diffusion* (Werner 2007), *tree-reweighted message passing* (TRW) (Wainwright, Jaakkola, and Willsky 2005; Kolmogorov 2006), subgradient methods (Schlesinger and Giginyak 2007a,b; Komodakis, Paragios, and Tziritas 2007), and Bregman projections (Ravikumar, Agarwal, and Wainwright 2008). Note that the max-sum diffusion and TRW algorithms are not guaranteed to converge to a global maximum of LP—they may get stuck at a suboptimal point (Kolmogorov 2006; Werner 2007). However, in practice, this does not appear to be a problem (Kolmogorov 2006).

For some vision applications, algorithms based on relaxation (B.36) produce excellent results. However, this is not guaranteed in all cases—after all, the problem is NP-hard. Recently, researchers have investigated alternative linear programming relaxations (Sontag and Jaakkola 2007; Sontag, Meltzer, Globerson *et al.* 2008; Komodakis and Paragios 2008; Schraudolph 2010). These algorithms are capable of producing tighter bounds compared to (B.36) at the expense of additional computational cost.

LP relaxation and alpha expansion. Solving a linear program produces primal and dual solutions that satisfy *complementary slackness conditions*. In general, the primal solution of (B.36) does not have to be integer-valued so, in practice, we may have to round it to obtain a valid labeling $\boldsymbol{x}$. An alternative proposed by Komodakis and Tziritas (2007a); Komodakis, Tziritas, and Paragios (2007) is to search for primal and dual solutions such that they satisfy *approximate* complementary slackness conditions and the primal solution is already integer-valued. Several max-flow-based algorithms are proposed by (Komodakis and Tziritas 2007a; Komodakis, Tziritas, and Paragios 2007) for this purpose and the *Fast-PD* method (Komodakis, Tziritas, and Paragios 2007) is shown to perform best. In the case of metric interactions, the default version of Fast-PD produces the same primal solution as the alpha-expansion algorithm (Boykov, Veksler, and Zabih 2001). This provides an interesting interpretation of the alpha expansion algorithm as trying to approximately solve relaxation (B.36).

Unlike the standard alpha expansion algorithm, Fast-PD also maintains a dual solution and thus runs faster in practice. Fast-PD can be extended to the case of semi-metric interactions (Komodakis, Tziritas, and Paragios 2007). The primal version of such extension was also given by Rother, Kumar, Kolmogorov *et al.* (2005).

B.6 Uncertainty estimation (error analysis)

In addition to computing the most likely estimate, many applications require an estimate for the *uncertainty* in this estimate.[9] The most general way to do this is to compute a complete probability distribution over all of the unknowns but this is generally intractable. The one special case where it is easy to obtain a simple description for this distribution is linear estimation problems with Gaussian noise, where the joint energy function (negative log likelihood of the posterior estimate) is a quadratic. In this case, the posterior distribution is a multi-variate Gaussian and the covariance can be computed directly from the inverse of the problem Hessian. (Another name for the inverse covariance matrix, which is equal to the Hessian in such simple cases, is the *information matrix*.)

Even here, however, the full covariance matrix may be too large to compute and store. For example, in large structure from motion problems, a large sparse Hessian normally results in a full dense covariance matrix. In such cases, it is often considered acceptable to report only the variance in the estimated quantities or simple covariance estimates on individual parameters, such as 3D point positions or camera pose estimates (Szeliski 1990a). More insight into the problem, e.g., the dominant *modes* of uncertainty, can be obtained using eigenvalue analysis (Szeliski and Kang 1997).

For problems where the posterior energy is non-quadratic, e.g., in non-linear or robustified least squares, it is still often possible to obtain an estimate of the Hessian in the vicinity of the optimal solution. In this case, the *Cramer–Rao lower bound* on the uncertainty (covariance) can be computed as the inverse of the Hessian. Another way of saying this is that while the local Hessian can underestimate how "wide" the energy function can be, the covariance can never be smaller than the estimate based on this local quadratic approximation. It is also possible to estimate a different kind of uncertainty (min-marginal energies) in general MRFs where the MAP inference is performed using graph cuts (Kohli and Torr 2008).

While many computer vision applications ignore uncertainty modeling, it is often useful to compute these estimates just to get an intuitive feeling for the reliability of the estimates. Certain applications, such as Kalman filtering, require the computation of this uncertainty (either explicitly as posterior covariances or implicitly as inverse covariances) in order to optimally integrate new measurements with previously computed estimates.

[9] This is particularly true of classic photogrammetry applications, where the reporting of precision is almost always considered mandatory (Förstner 2005).

Appendix C

Supplementary material

In this final appendix, I summarize some of the supplementary materials that may be useful to students, instructors, and researchers. The book's Web site at http://szeliski.org/Book contains updated lists of datasets and software, so please check there as well.

C.1 Data sets

One of the keys to developing reliable vision algorithms is to test your procedures on challenging and representative data sets. When ground truth or other people's results are available, such test can be even more informative (and quantitative).

Over the years, a large number of datasets have been developed for testing and evaluating computer vision algorithms. A number of these datasets (and software) are indexed on the Computer Vision Homepage.[1] Some newer Web sites, such as CVonline (http://homepages.inf.ed.ac.uk/rbf/CVonline/), VisionBib.Com (http://datasets.visionbib.com/), and Computer Vision online (http://computervisiononline.com/), have more recent pointers.

Below, I list some of the more popular data sets, grouped by the book chapters to which they most closely correspond:

Chapter 2: Image formation

CUReT: Columbia-Utrecht Reflectance and Texture Database, http://www1.cs.columbia.edu/CAVE/software/curet/ (Dana, van Ginneken, Nayar *et al.* 1999).

Middlebury Color Datasets: registered color images taken by different cameras to study how they transform gamuts and colors, http://vision.middlebury.edu/color/data/ (Chakrabarti, Scharstein, and Zickler 2009).

Chapter 3: Image processing

Middlebury test datasets for evaluating MRF minimization/inference algorithms, http://vision.middlebury.edu/MRF/results/ (Szeliski, Zabih, Scharstein *et al.* 2008).

Chapter 4: Feature detection and matching

Affine Covariant Features database for evaluating feature detector and descriptor matching quality and repeatability, http://www.robots.ox.ac.uk/~vgg/research/affine/ (Mikolajczyk and Schmid 2005; Mikolajczyk, Tuytelaars, Schmid *et al.* 2005).

Database of matched image patches for learning and feature descriptor evaluation, http://cvlab.epfl.ch/~brown/patchdata/patchdata.html (Winder and Brown 2007; Hua, Brown, and Winder 2007).

Chapter 5: Segmentation

Berkeley Segmentation Dataset and Benchmark of 1000 images labeled by 30 humans, along with an evaluation, http://www.eecs.berkeley.edu/Research/Projects/CS/vision/grouping/segbench/ (Martin, Fowlkes, Tal *et al.* 2001).

[1] http://www.cs.cmu.edu/~cil/vision.html, although it has not been maintained since 2004.

Weizmann segmentation evaluation database of 100 grayscale images with ground truth segmentations, http://www.wisdom.weizmann.ac.il/~vision/Seg_Evaluation_DB/index.html (Alpert, Galun, Basri *et al.* 2007).

Chapter 8: Dense motion estimation

The Middlebury optic flow evaluation Web site, http://vision.middlebury.edu/flow/data (Baker, Scharstein, Lewis *et al.* 2009).

The Human-Assisted Motion Annotation database, http://people.csail.mit.edu/celiu/motionAnnotation/ (Liu, Freeman, Adelson *et al.* 2008)

Chapter 10: Computational photography

High Dynamic Range radiance maps, http://www.debevec.org/Research/HDR/ (Debevec and Malik 1997).

Alpha matting evaluation Web site, http://alphamatting.com/ (Rhemann, Rother, Wang *et al.* 2009).

Chapter 11: Stereo correspondence

Middlebury Stereo Datasets and Evaluation, http://vision.middlebury.edu/stereo/ (Scharstein and Szeliski 2002).

Stereo Classification and Performance Evaluation of different aggregation costs for stereo matching, http://www.vision.deis.unibo.it/spe/SPEHome.aspx (Tombari, Mattoccia, Di Stefano *et al.* 2008).

Middlebury Multi-View Stereo Datasets, http://vision.middlebury.edu/mview/data/ (Seitz, Curless, Diebel *et al.* 2006).

Multi-view and Oxford Colleges building reconstructions, http://www.robots.ox.ac.uk/~vgg/data/data-mview.html.

Multi-View Stereo Datasets, http://cvlab.epfl.ch/data/strechamvs/ (Strecha, Fransens, and Van Gool 2006).

Multi-View Evaluation, http://cvlab.epfl.ch/~strecha/multiview/ (Strecha, von Hansen, Van Gool *et al.* 2008).

Chapter 12: 3D reconstruction

HumanEva: synchronized video and motion capture dataset for evaluation of articulated human motion, http://vision.cs.brown.edu/humaneva/ (Sigal, Balan, and Black 2010).

Chapter 13: Image-based rendering

The (New) Stanford Light Field Archive, http://lightfield.stanford.edu/ (Wilburn, Joshi, Vaish *et al.* 2005).

Virtual Viewpoint Video: multi-viewpoint video with per-frame depth maps, http://research.microsoft.com/en-us/um/redmond/groups/ivm/vvv/ (Zitnick, Kang, Uyttendaele *et al.* 2004).

Chapter 14: Recognition

For a list of visual recognition datasets, see Tables 14.1–14.2. In addition to those, there are also:

Buffy pose classes, http://www.robots.ox.ac.uk/~vgg/data/buffy_pose_classes/ and Buffy stickmen V2.1, http://www.robots.ox.ac.uk/~vgg/data/stickmen/index.html (Ferrari, Marin-Jimenez, and Zisserman 2009; Eichner and Ferrari 2009).

H3D database of pose/joint annotated photographs of humans, http://www.eecs.berkeley.edu/~lbourdev/h3d/ (Bourdev and Malik 2009).

Action Recognition Datasets, http://www.cs.berkeley.edu/projects/vision/action, has pointers to several datasets for action and activity recognition, as well as some papers. The human action database at http://www.nada.kth.se/cvap/actions/ contains more action sequences.

C.2 Software

One of the best sources for computer vision algorithms is the Open Source Computer Vision (OpenCV) library (http://opencv.willowgarage.com/wiki/), which was developed by Gary Bradski and his colleagues at Intel and is now being maintained and extended at Willow Garage (Bradsky and Kaehler 2008). A partial list of the available functions, taken from http://opencv.willowgarage.com/documentation/cpp/ includes:

- image processing and transforms (filtering, morphology, pyramids);
- geometric image transformations (rotations, resizing);
- miscellaneous image transformations (Fourier transforms, distance transforms);
- histograms;
- segmentation (watershed, mean shift);
- feature detection (Canny, Harris, Hough, MSER, SURF);
- motion analysis and object tracking (Lucas–Kanade, mean shift);
- camera calibration and 3D reconstruction;
- machine learning (k nearest neighbors, support vector machines, decision trees, boosting, random trees, expectation-maximization, and neural networks).

The Intel Performance Primitives (IPP) library, http://software.intel.com/en-us/intel-ipp/, contains highly optimized code for a variety of image processing tasks. Many of the routines in OpenCV take advantage of this library, if it is installed, to run even faster. In terms of functionality, it has many of the same operators as those found in OpenCV, plus additional libraries for image and video compression, signal and speech processing, and matrix algebra.

The MATLAB Image Processing Toolbox, http://www.mathworks.com/products/image/, contains routines for spatial transformations (rotations, resizing), normalized cross-correlation, image analysis and statistics (edges, Hough transform), image enhancement (adaptive histogram equalization, median filtering) and restoration (deblurring), linear filtering (convolution), image transforms (Fourier and DCT), and morphological operations (connected components and distance transforms).

Two older libraries, which no longer appear to be under active development but contain many useful routines, are VXL (C++ Libraries for Computer Vision Research and Implementation, http://vxl.sourceforge.net/) and LTI-Lib 2 (http://www.ie.itcr.ac.cr/palvarado/ltilib-2/homepage/).

Photo editing and viewing packages, such as Windows Live Photo Gallery, iPhoto, Picasa, GIMP, and IrfanView, can be useful for performing common processing tasks, converting formats, and viewing your results. They can also serve as interesting reference implementations for image processing algorithms (such as tone correction or denoising) that you are trying to develop from scratch.

There are also software packages and infrastructure that can be helpful for building real-time video processing demos. Vision on Tap (http://www.visionontap.com/) provides a Web service that will process your webcam video in real time (Chiu and Raskar 2009). VideoMan (VideoManager, http://videomanlib.sourceforge.net/) can be useful for getting real-time video-based demos and applications running. You can also use `imread` in MATLAB to read directly from any URL, such as a webcam.

Below, I list some additional software that can be found on the Web, grouped by the book chapters to which they most correspond:

Chapter 3: Image processing

matlabPyrTools—MATLAB source code for Laplacian pyramids, QMF/Wavelets, and steerable pyramids, http://www.cns.nyu.edu/~lcv/software.php (Simoncelli and Adelson 1990a; Simoncelli, Freeman, Adelson *et al.* 1992).

BLS-GSM image denoising, http://decsai.ugr.es/~javier/denoise/ (Portilla, Strela, Wainwright *et al.* 2003).

Fast bilateral filtering code, http://people.csail.mit.edu/jiawen/#code (Chen, Paris, and Durand 2007).

C++ implementation of the fast distance transform algorithm, http://people.cs.uchicago.edu/~pff/dt/ (Felzenszwalb and Huttenlocher 2004a).

GREYC's Magic Image Converter, including image restoration software using regularization and anisotropic diffusion, http://gmic.sourceforge.net/gimp.shtml (Tschumperlé and Deriche 2005).

Chapter 4: Feature detection and matching

VLFeat, an open and portable library of computer vision algorithms, http://vlfeat.org/ (Vedaldi and Fulkerson 2008).

SiftGPU: A GPU Implementation of Scale Invariant Feature Transform (SIFT), http://www.cs.unc.edu/~ccwu/siftgpu/ (Wu 2010).

SURF: Speeded Up Robust Features, http://www.vision.ee.ethz.ch/~surf/ (Bay, Tuytelaars, and Van Gool 2006).

FAST corner detection, http://mi.eng.cam.ac.uk/~er258/work/fast.html (Rosten and Drummond 2005, 2006).

Linux binaries for affine region detectors and descriptors, as well as MATLAB files to compute repeatability and matching scores, http://www.robots.ox.ac.uk/~vgg/research/affine/.

Kanade–Lucas–Tomasi feature trackers: KLT, http://www.ces.clemson.edu/~stb/klt/ (Shi and Tomasi 1994); GPU-KLT, http://cs.unc.edu/~cmzach/opensource.html (Zach, Gallup, and Frahm 2008); and Lucas–Kanade 20 Years On, http://www.ri.cmu.edu/projects/project_515.html (Baker and Matthews 2004).

Chapter 5: Segmentation

Efficient graph-based image segmentation, http://people.cs.uchicago.edu/~pff/segment/ (Felzenszwalb and Huttenlocher 2004b).

EDISON, edge detection and image segmentation, http://coewww.rutgers.edu/riul/research/code/EDISON/ (Meer and Georgescu 2001; Comaniciu and Meer 2002).

Normalized cuts segmentation including intervening contours, http://www.cis.upenn.edu/~jshi/software/ (Shi and Malik 2000; Malik, Belongie, Leung *et al.* 2001).

Segmentation by weighted aggregation (SWA), http://www.cs.weizmann.ac.il/~vision/SWA/ (Alpert, Galun, Basri *et al.* 2007).

Chapter 6: Feature-based alignment and calibration

Non-iterative PnP algorithm, http://cvlab.epfl.ch/software/EPnP/ (Moreno-Noguer, Lepetit, and Fua 2007).

Tsai Camera Calibration Software, http://www-2.cs.cmu.edu/~rgw/TsaiCode.html (Tsai 1987).

Easy Camera Calibration Toolkit, http://research.microsoft.com/en-us/um/people/zhang/Calib/ (Zhang 2000).

Camera Calibration Toolbox for MATLAB, http://www.vision.caltech.edu/bouguetj/calib_doc/; a C version is included in OpenCV.

MATLAB functions for multiple view geometry, http://www.robots.ox.ac.uk/~vgg/hzbook/code/ (Hartley and Zisserman 2004).

Chapter 7: Structure from motion

SBA: A generic sparse bundle adjustment C/C++ package based on the Levenberg–Marquardt algorithm, http://www.ics.forth.gr/~lourakis/sba/ (Lourakis and Argyros 2009).

Simple sparse bundle adjustment (SSBA), http://cs.unc.edu/~cmzach/opensource.html.

Bundler, structure from motion for unordered image collections, http://phototour.cs.washington.edu/bundler/ (Snavely, Seitz, and Szeliski 2006).

Chapter 8: Dense motion estimation

Optical flow software, http://www.cs.brown.edu/~black/code.html (Black and Anandan 1996).

Optical flow using total variation and conjugate gradient descent, http://people.csail.mit.edu/celiu/OpticalFlow/ (Liu 2009).

TV-L1 optical flow on the GPU, http://cs.unc.edu/~cmzach/opensource.html (Zach, Pock, and Bischof 2007a).

elastix: a toolbox for rigid and nonrigid registration of images, http://elastix.isi.uu.nl/ (Klein, Staring, and Pluim 2007).

Deformable image registration using discrete optimization, http://www.mrf-registration.net/deformable/index.html (Glocker, Komodakis, Tziritas *et al.* 2008).

Chapter 9: Image stitching

Microsoft Research Image Compositing Editor for stitching images, http://research.microsoft.com/en-us/um/redmond/groups/ivm/ice/.

Chapter 10: Computational photography

HDRShop software for combining bracketed exposures into high-dynamic range radiance images, http://projects.ict.usc.edu/graphics/HDRShop/.

Super-resolution code, http://www.robots.ox.ac.uk/~vgg/software/SR/ (Pickup 2007; Pickup, Capel, Roberts *et al.* 2007, 2009).

Chapter 11: Stereo correspondence

StereoMatcher, standalone C++ stereo matching code, http://vision.middlebury.edu/stereo/code/ (Scharstein and Szeliski 2002).

Patch-based multi-view stereo software (PMVS Version 2), http://grail.cs.washington.edu/software/pmvs/ (Furukawa and Ponce 2011).

Chapter 12: 3D reconstruction

Scanalyze: a system for aligning and merging range data, http://graphics.stanford.edu/software/scanalyze/ (Curless and Levoy 1996).

MeshLab: software for processing, editing, and visualizing unstructured 3D triangular meshes, http://meshlab.sourceforge.net/.

VRML viewers (various) are also a good way to visualize texture-mapped 3D models.

Section 12.6.4: Whole body modeling and tracking

Bayesian 3D person tracking, http://www.cs.brown.edu/~black/code.html (Sidenbladh, Black, and Fleet 2000; Sidenbladh and Black 2003).

HumanEva: baseline code for the tracking of articulated human motion, http://vision.cs.brown.edu/humaneva/ (Sigal, Balan, and Black 2010).

Section 14.1.1: Face detection

Sample face detection code and evaluation tools, http://vision.ai.uiuc.edu/mhyang/face-detection-survey.html.

Section 14.1.2: Pedestrian detection

A simple object detector with boosting, http://people.csail.mit.edu/torralba/shortCourseRLOC/boosting/boosting.html (Hastie, Tibshirani, and Friedman 2001; Torralba, Murphy, and Freeman 2007).

Discriminatively trained deformable part models, http://people.cs.uchicago.edu/~pff/latent/ (Felzenszwalb, Girshick, McAllester *et al.* 2010).

Upper-body detector, http://www.robots.ox.ac.uk/~vgg/software/UpperBody/ (Ferrari, Marin-Jimenez, and Zisserman 2008).

2D articulated human pose estimation software, http://www.vision.ee.ethz.ch/~calvin/articulated_human_pose_estimation_code/ (Eichner and Ferrari 2009).

Section 14.2.2: Active appearance and 3D shape models

AAMtools: An active appearance modeling toolbox, http://cvsp.cs.ntua.gr/software/AAMtools/ (Papandreou and Maragos 2008).

Section 14.3: Instance recognition

FASTANN and FASTCLUSTER for approximate k-means (AKM), http://www.robots.ox.ac.uk/~vgg/software/ (Philbin, Chum, Isard *et al.* 2007).

Feature matching using fast approximate nearest neighbors, http://people.cs.ubc.ca/~mariusm/index.php/FLANN/FLANN (Muja and Lowe 2009).

Section 14.4.1: Bag of words

Two bag of words classifiers, http://people.csail.mit.edu/fergus/iccv2005/bagwords.html (Fei-Fei and Perona 2005; Sivic, Russell, Efros *et al.* 2005).

Bag of features and hierarchical k-means, http://www.vlfeat.org/ (Nistér and Stewénius 2006; Nowak, Jurie, and Triggs 2006).

Section 14.4.2: Part-based models

A simple parts and structure object detector, http://people.csail.mit.edu/fergus/iccv2005/partsstructure.html (Fischler and Elschlager 1973; Felzenszwalb and Huttenlocher 2005).

Section 14.5.1: Machine learning software

Support vector machines (SVM) software (http://www.support-vector-machines.org/SVM_soft.html) has pointers to lots of SVM libraries, including SVM^{light}, http://svmlight.joachims.org/; LIBSVM, http://www.csie.ntu.edu.tw/~cjlin/libsvm/ (Fan, Chen, and Lin 2005); and LIBLINEAR, http://www.csie.ntu.edu.tw/~cjlin/liblinear/ (Fan, Chang, Hsieh *et al.* 2008).

Kernel Machines: links to SVM, Gaussian processes, boosting, and other machine learning algorithms, http://www.kernel-machines.org/software.

Multiple kernels for image classification, http://www.robots.ox.ac.uk/~vgg/software/MKL/ (Varma and Ray 2007; Vedaldi, Gulshan, Varma *et al.* 2009).

Appendix A.1–A.2: Matrix decompositions and linear least squares[2]

BLAS (Basic Linear Algebra Subprograms), http://www.netlib.org/blas/ (Blackford, Demmel, Dongarra *et al.* 2002).

LAPACK (Linear Algebra PACKage), http://www.netlib.org/lapack/ (Anderson, Bai, Bischof *et al.* 1999).

GotoBLAS, http://www.tacc.utexas.edu/tacc-projects/.

ATLAS (Automatically Tuned Linear Algebra Software), http://math-atlas.sourceforge.net/ (Demmel, Dongarra, Eijkhout *et al.* 2005).

Intel Math Kernel Library (MKL), http://software.intel.com/en-us/intel-mkl/.

AMD Core Math Library (ACML), http://developer.amd.com/cpu/Libraries/acml/Pages/default.aspx.

Robust PCA code, http://www.salle.url.edu/~ftorre/papers/rpca2.html (De la Torre and Black 2003).

Appendix A.3: Non-linear least squares

MINPACK, http://www.netlib.org/minpack/.

levmar: Levenberg–Marquardt nonlinear least squares algorithms, http://www.ics.forth.gr/~lourakis/levmar/ (Madsen, Nielsen, and Tingleff 2004).

Appendix A.4–A.5: Direct and iterative sparse matrix solvers

SuiteSparse (various reordering algorithms, CHOLMOD) and SuiteSparse QR, http://www.cise.ufl.edu/research/sparse/SuiteSparse/ (Davis 2006, 2008).

PARDISO (iterative and sparse direct solution), http://www.pardiso-project.org/.

TAUCS (sparse direct, iterative, out of core, preconditioners), http://www.tau.ac.il/~stoledo/taucs/.

HSL Mathematical Software Library, http://www.hsl.rl.ac.uk/index.html.

[2] Thanks to Sameer Agarwal for suggesting and describing most of these sites.

Templates for the solution of linear systems, http://www.netlib.org/linalg/html_templates/Templates.html (Barrett, Berry, Chan *et al.* 1994). Download the PDF for instructions on how to get the software.

ITSOL, MIQR, and other sparse solvers, http://www-users.cs.umn.edu/~saad/software/ (Saad 2003).

ILUPACK, http://www-public.tu-bs.de/~bolle/ilupack/.

Appendix B: Bayesian modeling and inference

Middlebury source code for MRF minimization, http://vision.middlebury.edu/MRF/code/ (Szeliski, Zabih, Scharstein *et al.* 2008).

C++ code for efficient belief propagation for early vision, http://people.cs.uchicago.edu/~pff/bp/ (Felzenszwalb and Huttenlocher 2006).

FastPD MRF optimization code, http://www.csd.uoc.gr/~komod/FastPD (Komodakis and Tziritas 2007a; Komodakis, Tziritas, and Paragios 2008)

Gaussian noise generation. A lot of basic software packages come with a uniform random noise generator (e.g., the `rand()` routine in Unix), but not all have a Gaussian random noise generator. To compute a normally distributed random variable, you can use the Box–Muller transform (Box and Muller 1958), whose C code is given in Algorithm C.1—note that this routine returns pairs of random variables. Alternative methods for generating Gaussian random numbers are given by Thomas, Luk, Leong *et al.* (2007).

Pseudocolor generation. In many applications, it is convenient to be able to visualize the set of labels assigned to an image (or to image features such as lines). One of the easiest ways to do this is to assign a unique color to each integer label. In my work, I have found it convenient to distribute these labels in a quasi-uniform fashion around the RGB color cube using the following idea.

For each (non-negative) label value, consider the bits as being split among the three color channels, e.g., for a nine-bit value, the bits could be labeled RGBRGBRGB. After collecting each of the three color values, *reverse* the bits so that the low-order bits vary the most quickly. In practice, for eight-bit color channels, this bit reverse can be stored in a table or a complete table mapping from labels to pseudocolors (say with 4092 entries) can be pre-computed. Figure 8.16 shows an example of such a pseudo-color mapping.

GPU implementation

The advent of programmable GPUs with capabilities such as pixel shaders and compute shaders has led to the development of fast computer vision algorithms for real-time applications such as segmentation, tracking, stereo, and motion estimation (Pock, Unger, Cremers *et al.* 2008; Vineet and Narayanan 2008; Zach, Gallup, and Frahm 2008). A good source for learning about such algorithms is the CVPR 2008 workshop on Visual Computer Vision on GPUs (CVGPU), http://www.cs.unc.edu/~jmf/Workshop_on_Computer_Vision_on_GPU.html, whose papers can be found on the CVPR 2008 proceedings DVD. Additional sources

```
double urand()
{
  return ((double) rand()) / ((double) RAND_MAX);
}
void grand(double& g1, double& g2)
{
#ifndef M_PI
#define M_PI 3.14159265358979323846
#endif // M_PI

  double n1 = urand();
  double n2 = urand();
  double x1 = n1 + (n1 == 0); /* guard against log(0) */
  double sqlogn1 = sqrt(-2.0 * log (x1));
  double angl = (2.0 * M_PI) * n2;
  g1 = sqlogn1 * cos(angl);
  g2 = sqlogn1 * sin(angl);
}
```

Algorithm C.1 C algorithm for Gaussian random noise generation, using the Box–Muller transform.

for GPU algorithms include the GPGPU Web site and workshops, http://gpgpu.org/, and the OpenVIDIA Web site, http://openvidia.sourceforge.net/index.php/OpenVIDIA.

C.3 Slides and lectures

As I mentioned in the preface, I hope to post slides corresponding to the material in the book. Until these are ready, your best bet is to look at the slides from the courses I have co-taught at the University of Washington, as well as related courses that have used a similar syllabus. Here is a partial list of such courses:

UW 455: Undergraduate Computer Vision, http://www.cs.washington.edu/education/courses/455/.

UW 576: Graduate Computer Vision, http://www.cs.washington.edu/education/courses/576/.

Stanford CS233B: Introduction to Computer Vision, http://vision.stanford.edu/teaching/cs223b/.

MIT 6.869: Advances in Computer Vision, http://people.csail.mit.edu/torralba/courses/6.869/6.869.computervision.htm.

Berkeley CS 280: Computer Vision, http://www.eecs.berkeley.edu/~trevor/CS280.html.

UNC COMP 776: Computer Vision, http://www.cs.unc.edu/~lazebnik/spring10/.

Middlebury CS 453: Computer Vision, http://www.cs.middlebury.edu/~schar/courses/cs453-s10/.

Related courses have also been taught on the topic of Computational Photography, e.g.,

CMU 15-463: Computational Photography, http://graphics.cs.cmu.edu/courses/15-463/.

MIT 6.815/6.865: Advanced Computational Photography, http://stellar.mit.edu/S/course/6/sp09/6.815/.

Stanford CS 448A: Computational photography on cell phones, http://graphics.stanford.edu/courses/cs448a-10/.

SIGGRAPH courses on Computational Photography, http://web.media.mit.edu/~raskar/photo/.

There is also an excellent set of on-line lectures available on a range of computer vision topics, such as belief propagation and graph cuts, at the UW-MSR Course of Vision Algorithms http://www.cs.washington.edu/education/courses/577/04sp/.

C.4 Bibliography

While a bibliography (BibTex .bib file) for all of the references cited in this book is available on the book's Web site, a much more comprehensive partially annotated bibliography of nearly *all* computer vision publications is maintained by Keith Price at http://iris.usc.edu/Vision-Notes/bibliography/contents.html. There is also a searchable computer graphics bibliography at http://www.siggraph.org/publications/bibliography/. Additional good sources for technical papers are Google Scholar and CiteSeer^{X}.

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