

APPLICATIONS OF A NONNEGATIVELY CONSTRAINED ITERATIVE METHOD WITH STATISTICALLY BASED STOPPING RULES TO CT, PET, AND SPECT IMAGING *

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Abstract. In this paper, we extend a nonnegatively constrained iterative method and three stopping rules for its iterations to the medical imaging inverse problems of computed tomography (CT), positron emission tomography (PET), and single photon emission computed tomography (SPECT); the iterative method and stopping rules were introduced for use in astronomical imaging. The paper begins with a brief introduction to the CT, PET, and SPECT mathematical and statistical models.

Key words. nonnegatively constrained iterative methods, inverse problems, statistical methods, medical imaging

AMS subject classifications. 65J22, 65K10, 65F22

1. Introductory Material. The medical imaging modalities of computed tomography (CT), positron emission tomography (PET), and single photon emission computed tomography (SPECT) are widely used in the medical professions. Because of the unique set of strengths and weakness of each of these methods, they are utilized in different settings. However, mathematically they are closely related.

In this introductory section, we set the stage for the algorithmic discussion that constitutes the main result of the paper by briefly introducing the mathematical models for CT, PET, and SPECT imaging, their numerical discretization, and the associated statistical models. The mathematical discussion is included because it is accessible and will be of interest to the unfamiliar reader, while the statistical models are integral to the development of the computational methods that are our focus.

1.1. Mathematical Models. CT is the most widely used of the three methods and has the simplest mathematical model. In the two dimensional case, which is our focus in this paper, CT involves the reconstruction of the mass absorption function μ of a body from one-dimensional projections of that body. A particular one-dimensional projection is obtained by integrating μ along all parallel lines making a given angle ω with an axis in a fixed coordinate system. Each line L can be uniquely represented in this coordinate system by ω together with its perpendicular distance y to the origin.

Suppose $L(\omega, y) = \{x(s) \mid 0 \leq s \leq S\}$, with an X-ray source located at $s = 0$ and a sensor at $s = S$. The standard assumption is that the intensity I of the X-ray along a line segment ds is attenuated via the model [7]

$$dI = -\mu(s)I ds.$$

The resulting ordinary differential equation can be solved using the method of separation of variables to obtain

$$I(S) = I(0)e^{-\int_0^S \mu(s) ds},$$

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where $I(0)$ is the intensity at the source and $I(S)$ the intensity at the receiver. Letting $z = -\ln(I(S)/I(0))$, we obtain the Radon transform model for CT:

$$z(\omega, y) = \int_{L(\omega, y)} \mu(s) ds. \quad (1.1)$$

A discretized version of (1.1) is what is solved in the CT inverse problem, where z corresponds to collected data, and μ is the unknown.

In both PET and SPECT, a somewhat different problem is solved. In both cases, a radioactive tracer element is injected into the body. The tracer then exhibits radioactive decay, resulting in photon emission. The emitted photons that leave the body are, in theory, all recorded by a photon detector, which also determines the line of response (LOR) $L(\omega, y)$. In PET, two photons are emitted, and if they reach the detector ring at the same time (i.e. within a few nanoseconds of each other), an event is registered along the connecting line, which is also the LOR. In SPECT, single photons are emitted and detected. The LOR is determined using a method known as collimation. In both cases, the task is to reconstruct the tracer density distribution u within the subject given the collected, photon count data.

In both PET and SPECT, the data $z(\omega, y)$ for the line $L(\omega, y)$ corresponds to the number of detected incidents along that line. The model relating the tracer density u to the data is similar to (1.1) and is given by

$$z(\omega, y) = \int_{L(\omega, y)} g_{\omega, y}(x(s))u(x(s))ds,$$

where the impulse response function $g_{\omega, y}(x(r))$ can be viewed as the probability that an emission event located at $x(r)$ along $L(\omega, y)$ is detected.

For SPECT, we assume that the detector is located at $x(S)$. Then, making assumptions for probabilities analogous to those made for intensities in the derivation of the CT model above, and assuming probability of 1 at the $x(r)$, one can obtain $g_{\omega, y}(x(r)) = e^{-\int_r^S \mu(x(t)) dt}$, so that the full model becomes

$$z(\omega, y) = \int_{L(\omega, y)} e^{-\int_s^S \mu(x(t)) dt} u(x(s)) ds, \quad (1.2)$$

where the interior integral is along the line $L(\omega, y)$.

For PET, since there are two photons that have to reach respective detectors at $x(0)$ and $x(S)$, the impulse response is the product of the probabilities,

$$g_{\omega, y}(x(r)) = e^{-\int_0^r \mu(x(t)) dt} e^{-\int_r^S \mu(x(t)) dt} = e^{-\int_{L(\omega, y)} \mu(x(t)) dt},$$

which doesn't depend on r , and hence we have the somewhat simpler mathematical model

$$z(\omega, y) = e^{-\int_{L(\omega, y)} \mu(t) dt} \int_{L(\omega, y)} u(x(s)) ds. \quad (1.3)$$

A discussion of the PET mathematical and statistical models is given in [23]

Note the appearance of the absorption density μ in both (1.2) and (1.3), which must be known before hand in order to solve the PET and SPECT inverse problems. Estimates of μ can be obtained using, for example, CT. Note also that brief derivations of all of these models can be found in [15], whereas as [7] focuses on CT, [16] on PET, and [4] on SPECT.

1.2. Numerical Discretization. After discretization, each of (1.1), (1.2), and (1.3) can be written as a system of linear equations. The discretization occurs both in the spatial domain, where μ and u are defined, as well as in the Radon transform domain, where the independent variables are ω and y . We will use a uniform $n \times n$ spatial grid, and a grid for the transform domain with n_ω angles and n_s sensors, both uniformly spaced. Then, after column-stacking the resulting two-dimensional grids, we obtain a matrix-vector system

$$\mathbf{z} = \mathbf{A}\mathbf{u}, \quad (1.4)$$

where the data vector $\mathbf{z} \in \mathbb{R}^{n_\theta n_s}$, the unknown vector $\mathbf{u} \in \mathbb{R}^{n^2}$, and the forward model matrix $\mathbf{A} \in \mathbb{R}^{n_\theta n_s \times (n_\theta n_s)}$.

In the case of CT, for the i th line L_i , we have the discrete model

$$z_i = \sum_{j=1}^{n^2} a_{ij}^{\text{Radon}} \mu_j,$$

where a_{ij}^{Radon} is the intersection length of L_i with pixel j . Written as (1.4), we have $[\mathbf{A}]_{ij} = a_{ij}^{\text{Radon}}$ and $u_j = \mu_j$.

For both PET and SPECT, the system of linear equations instead has the form

$$z_i = \sum_{j=1}^{n^2} g_{ij} a_{ij}^{\text{Radon}} u_j.$$

where g_{ij} is the discrete impulse response function, which for PET is

$$g_{ij} = \exp \left(- \sum_{k=1}^{n^2} a_{ik}^{\text{Radon}} \mu_k \right), \quad (1.5)$$

(note, no dependence on j) and for SPECT is

$$g_{ij} = \exp \left(- \sum_{k=j}^{n^2} a_{ik}^{\text{Radon}} \mu_k \right). \quad (1.6)$$

Written as (1.4), we have $[\mathbf{A}]_{ij} = \exp \left(- \sum_{k=1}^{n^2} a_{ik}^{\text{Radon}} \mu_k \right) a_{ij}^{\text{Radon}}$ for PET, and $[\mathbf{A}]_{ij} = \exp \left(- \sum_{k=j}^{n^2} a_{ik}^{\text{Radon}} \mu_k \right) a_{ij}^{\text{Radon}}$ for SPECT.

1.3. Statistical Models. The character of the noise in the data \mathbf{z} is an important consideration, particularly in the cases of PET and SPECT.

In CT, because intensities are typically high, a statistical model of the form

$$\mathbf{z} = \mathbf{A}\mathbf{u} + \mathbf{n}, \quad (1.7)$$

where \mathbf{n} is a zero mean, independent and identically distributed normal distribution with variance σ^2 , is not uncommon. The resulting likelihood function takes the form

$$p_{\mathbf{z}}(\mathbf{z}; \mathbf{u}) \propto \exp \left(- \frac{1}{2\sigma^2} \|\mathbf{A}\mathbf{u} - \mathbf{z}\|^2 \right). \quad (1.8)$$

PET and SPECT data are typically much more noisy, and hence, it is important to accurately model noise statistics in these cases. We follow [16, 4], and use a Poisson statistical model

$$\mathbf{z} = \text{Poiss}(\mathbf{A}\mathbf{u} + \boldsymbol{\gamma}). \quad (1.9)$$

In this case, the likelihood function takes the form

$$p_{\mathbf{z}}(\mathbf{z}; \mathbf{u}) = \prod_{i=1}^n \frac{([\mathbf{A}\mathbf{u}]_i + \gamma_i)^{z_i} \exp[-([\mathbf{A}\mathbf{u}]_i + \gamma_i)]}{z_i!}. \quad (1.10)$$

Given image data \mathbf{z} arising from model (1.7) or (1.9), the maximum likelihood estimate of \mathbf{u} is obtained by maximizing $p_{\mathbf{z}}(\mathbf{z}; \mathbf{u})$ with respect to $\mathbf{u} \geq \mathbf{0}$, or equivalently by solving

$$\mathbf{u}_{\text{ML}} = \arg \min_{\mathbf{u} \geq \mathbf{0}} T(\mathbf{u}; \mathbf{z}), \quad (1.11)$$

where for likelihood (1.8),

$$T(\mathbf{u}; \mathbf{z}) = \frac{1}{2\sigma^2} \|\mathbf{A}\mathbf{u} - \mathbf{z}\|^2, \quad (1.12)$$

whereas for likelihood (1.10),

$$T(\mathbf{u}; \mathbf{z}) = \sum_{i=1}^n \{([\mathbf{A}\mathbf{u}]_i + \gamma_i) - z_i \ln([\mathbf{A}\mathbf{u}]_i + \gamma_i)\}. \quad (1.13)$$

Solutions of (1.11) tend to be noise-corrupted due both to random errors in \mathbf{z} and ill-conditioning of the matrix \mathbf{A} , which in all cases is the discretization of a compact operator [14]. Thus some form of regularization is needed. One way that this can be accomplished is by truncating an iterative method applied to (1.11) [5]. When this approach is taken, the choice of stopping iteration becomes extremely important and is akin to the choice of regularization parameter in the standard Tikhonov approach to regularization [5, 24].

In the context of PET imaging, the Richardson-Lucy algorithm (RL) is widely used. RL is an iterative method for solving (1.11), (1.13) [11, 20], and stopping rules for its iterations have been given [10, 17, 18, 19]. Much effort has gone into the development of efficient iterative methods for PET; see, e.g., the review paper [16] and the references therein, and also [9]. In this paper, we apply the iterative method and stopping rules of [1, 3], developed in the context of astronomical imaging, to (1.11) for both (1.12) and (1.13). The iterative method, called modified residual norm steepest descent (MRNSD) in [13], was originally introduced in [8] in the context of PET.

The remainder of the paper is organized as follows. In Section 2, we present the iterative method and stopping rules that we will use for the image reconstruction step, and then in Section 3, we test our methods on some synthetically generated examples. Finally, we end with conclusions in Section 4.

2. An Iterative Method and Stopping Rules. It is now time to present our numerical method and iteration stopping rules for approximately solving (1.11). The methods require a least-squares formulation of the nonnegatively constrained

optimization problem (1.11). For noise model (1.7) and T defined by (1.12), this is already the case. However, for noise model (1.9) an approximation of (1.13) must be computed. For this, we follow [1, 2], where a Taylor series argument is used to motivate the following quadratic approximation of T :

$$T(\mathbf{u}; \mathbf{z}) \approx T(\mathbf{u}_e; \mathbf{z}) + T_{\text{wls}}(\mathbf{u}; \mathbf{z}), \quad (2.1)$$

where

$$T_{\text{wls}}(\mathbf{u}; \mathbf{z}) \stackrel{\text{def}}{=} \frac{1}{2} \|\mathbf{C}^{-1/2}(\mathbf{A}\mathbf{u} - (\mathbf{z} - \boldsymbol{\gamma}))\|^2, \quad (2.2)$$

with $\mathbf{C} = \text{diag}(\mathbf{z})$. Here we assume that $\mathbf{z} > \mathbf{0}$. This leads to the following approximation of (1.11):

$$\mathbf{u}_{\text{wls}} = \arg \min_{\mathbf{u} \geq \mathbf{0}} T_{\text{wls}}(\mathbf{u}; \mathbf{z}). \quad (2.3)$$

Before continuing, we note that T defined by (1.12) can also be written as (2.2), with $\mathbf{C} = \sigma^2 \mathbf{I}$ and $\boldsymbol{\gamma} = \mathbf{0}$. In what follows we will use this convention in order to unify notation. However we note that this implies that the user knows the noise level $\|\mathbf{n}\|^2$ in (1.7) a priori.

2.1. The Iterative Method. The algorithm of [3] for the numerical solution of (2.3) has the form

$$\mathbf{u}_{k+1} = \mathbf{u}_k - \tau_k \mathbf{u}_k \odot \mathbf{A}^T \mathbf{C}^{-1}(\mathbf{A}\mathbf{u}_k - (\mathbf{z} - \boldsymbol{\gamma})), \quad (2.4)$$

where “ \odot ” denotes Hadamard (component-wise) multiplication, and the line search parameter τ_k in (2.4) is given by

$$\tau_k = \min\{\tau_{\text{uc}}, \tau_{\text{bd}}\}.$$

Here, if $\mathbf{v}_k = \mathbf{u}_k \odot \nabla T_{\text{wls}}(\mathbf{u}_k)$,

$$\tau_{\text{uc}} = \frac{\langle \mathbf{v}_k, \nabla T_{\text{wls}}(\mathbf{u}_k) \rangle_2}{\langle \mathbf{v}_k, \mathbf{A}^T \mathbf{C}^{-1} \mathbf{A} \mathbf{v}_k \rangle_2}, \quad (2.5)$$

and

$$\tau_{\text{bd}} = \min \{ [\mathbf{u}_k]_i / [\mathbf{v}_k]_i \mid [\mathbf{v}_k]_i > 0, [\mathbf{u}_k]_i \neq 0 \}.$$

This method has been shown to be effective on several astronomical imaging examples. For more details, see [1, 3]. In this paper, we will refer to this technique as weighted MRNSD, or WMRNSD.

2.2. The Stopping Rules. Next, we introduce three stopping rules for (2.4). Each can be motivated from the assumption that our statistical model has the form

$$\mathbf{z} - \boldsymbol{\gamma} = \mathbf{A}\mathbf{u} + \mathbf{n}, \quad (2.6)$$

where \mathbf{n} is distributed as a zero-mean Gaussian random vector with covariance matrix \mathbf{C} . For (1.7), $\boldsymbol{\gamma} = \mathbf{0}$, $\mathbf{C} = \sigma^2 \mathbf{I}$, and model (2.6) is exact. For (1.9), on the other hand, we take $\mathbf{C} = \text{diag}(\mathbf{z})$, and the negative-log likelihood function (2.2) results. Note alternative to the mathematical derivation of (2.2) above, one can use the statistical approximation (2.6) to derive the approximate maximum likelihood problem (2.2).

More detailed derivations of these stopping rules can be found in [1].

2.2.1. The Discrepancy Principle. Assuming that (2.6) holds, $\mathbf{C}^{-1/2}(\mathbf{A}\mathbf{u}_e - (\mathbf{z} - \boldsymbol{\gamma}))$, where \mathbf{u}_e is the true image, is approximately normally distributed with covariance \mathbf{I} . Then by a standard result

$$2T_{\text{wls}}(\mathbf{u}_e) \sim \chi^2(n), \quad (2.7)$$

where $\chi^2(n)$ denotes the chi-squared distribution with n degrees of freedom, and hence

$$E(T_{\text{wls}}(\mathbf{u}_e)) \approx \frac{1}{2}E(\chi^2(n)) = \frac{n}{2}.$$

Since in early iterations $\frac{2}{n}T_{\text{wls}}(\mathbf{u}_k)$ is typically much larger than 1, a stopping rule of the form

$$\frac{2}{n}T_{\text{wls}}(\mathbf{u}_k; \mathbf{z}) \leq 1 + \epsilon_n \quad (2.8)$$

is therefore reasonable. We note that $\epsilon_n = 0$ corresponds to Morozov's discrepancy principle [12, 24], and we recommend its use unless (2.8) isn't satisfied in a feasible number of iterations or if it uniformly yields over-regularized reconstructed images. Otherwise, ϵ_n can be taken to be, for example, $\pm\sqrt{2n}/n$, or $\pm 2\sqrt{2n}/n$, i.e. \pm one or two times the standard deviation of $\chi^2(n)$.

We note that for model (1.7), this stopping rule is equivalent to that presented in [22].

2.2.2. Generalized Cross Validation. In [17, 19] it is shown that the generalized cross validation (GCV) method [5, 24] can be used to develop iteration dependent stopping rules for the steepest descent and RL iterations. Following their approach, in [1] a GCV method is developed for (2.4).

The GCV function for (2.2) at iteration k is defined by

$$\text{GCV}(k) = n \|\mathbf{C}^{-1/2}(\mathbf{A}\mathbf{u}_k - (\mathbf{z} - \boldsymbol{\gamma}))\|^2 / \text{trace}(\mathbf{I}_n - \mathbf{C}^{-1/2}\mathbf{A}\mathbf{A}_k)^2, \quad (2.9)$$

where \mathbf{A}_k is the iterative regularization matrix satisfying

$$\mathbf{A}_k(\mathbf{z} - \boldsymbol{\gamma}) = \mathbf{u}_k,$$

with \mathbf{u}_k the k th WMRNSD iterate. The idea is then to stop WMRNSD at the iteration k that results in an increase in the GCV function.

In order to evaluate $\text{GCV}(k)$ in practice $\text{trace}(\mathbf{I}_n - \mathbf{C}^{-1/2}\mathbf{A}\mathbf{A}_k)$ must be approximated. This can be accomplished using the Trace Lemma [24]: given $\mathbf{B} \in \mathbb{R}^{n \times n}$ and \mathbf{v} a discrete white noise vector, $E(\mathbf{v}^T \mathbf{B} \mathbf{v}) = \text{trace}(\mathbf{B})$. Thus given a realization \mathbf{v} from a white noise process,

$$\text{trace}(\mathbf{I}_n - \mathbf{C}^{-1/2}\mathbf{A}\mathbf{A}_k) \approx \mathbf{v}^T \mathbf{v} - \mathbf{v}^T \mathbf{C}^{-1/2}\mathbf{A}\mathbf{A}_k \mathbf{v}.$$

Thus, if we know \mathbf{A}_k , we can efficiently estimate $\text{GCV}(k)$ at each iteration. However we don't know \mathbf{A}_k , nor do we want to compute it. Instead, we follow [17] and define

$$\mathbf{w}_k = \mathbf{A}_k \mathbf{v},$$

which yields the following approximation of (2.9):

$$\widetilde{\text{GCV}}(k) = n \|\mathbf{C}^{-1/2}(\mathbf{A}\mathbf{u}_k - (\mathbf{z} - \boldsymbol{\gamma}))\|^2 / (\mathbf{v}^T \mathbf{v} - \mathbf{v}^T \mathbf{C}^{-1/2}\mathbf{A}\mathbf{w}_k). \quad (2.10)$$

An iterative for \mathbf{w}_k can be derived, following [1], and is given by

$$\begin{aligned} \mathbf{w}_{k+1} = & \mathbf{w}_k - \tau_k [\mathbf{w}_k \odot \mathbf{A}^T \mathbf{C}^{-1} (\mathbf{A} \mathbf{u}_k - (\mathbf{z} - \boldsymbol{\gamma})) \\ & + \mathbf{u}_k \odot \mathbf{A}^T \mathbf{C}^{-1} (\mathbf{A} \mathbf{w}_k - \mathbf{v})], \end{aligned} \quad (2.11)$$

where $\mathbf{w}_0 = (\mathbf{u}_0 \odot \mathbf{v}) / (\mathbf{z} - \boldsymbol{\gamma})$.

Thus we immediately have a stopping rule for WMRNSD iterations; namely, iterate (2.4) and (2.11) simultaneously, and stop iterations once $\widetilde{\text{GCV}}(k) > \widetilde{\text{GCV}}(k-1)$, where $\widetilde{\text{GCV}}(k)$ is defined in (2.10). As is standard [24], we choose \mathbf{v} so that its components are either -1 or 1 with equal probability.

2.2.3. The Unbiased Predictive Risk Estimator. Similar to GCV is the unbiased predictive risk estimator (UPRE) [24]. With UPRE, the goal is to choose the iteration k for which the predictive risk $E\left(\frac{2}{n} T_{wls}(\mathbf{u}_k; \mathbf{z}_e)\right)$, where $\mathbf{z}_e = \mathbf{A} \mathbf{u}_e + \boldsymbol{\gamma}$, is smallest. The UPRE function for (2.2) is

$$\text{UPRE}(k) = \frac{2}{n} T_{wls}(\mathbf{u}_k; \mathbf{z}) + \frac{2}{n} \text{trace} \left(\mathbf{C}^{-1/2} \mathbf{A} \mathbf{A}_k \right) - 1. \quad (2.12)$$

It is derived as in [24] for regular least-squares problems and is an unbiased estimator of the predictive risk, hence its name. Following the same approach as for GCV, we can approximate (2.12) by

$$\widetilde{\text{UPRE}}(k) = \frac{2}{n} T_{wls}(\mathbf{u}_k; \mathbf{z}) + \frac{2}{n} \mathbf{v}^T \mathbf{C}^{-1/2} \mathbf{A} \mathbf{w}_k - 1, \quad (2.13)$$

where \mathbf{v} and \mathbf{w}_k are as above.

Thus we have our third stopping rule for WMRNSD iterations; namely, iterate (2.4) and (2.11) simultaneously, and stop iterations once $\widetilde{\text{UPRE}}(k) > \widetilde{\text{UPRE}}(k-1)$, where $\widetilde{\text{UPRE}}(k)$ is defined in (2.13).

3. Numerical Results. We now demonstrate the effectiveness of our methods on synthetically generated examples for each of the CT, PET, and SPECT imaging problems. For each of our tests we use the Shepp-Vardi phantom [21], given on the left in Figure 3.1, as the true image, generated using MATLAB's `phantom` function. For data generation in CT, PET, and SPECT, we use the discretization of models (1.1), (1.3), and (1.2), respectively, described in Section 1.2. For PET, we ignore attenuation, corresponding to $\mu = 0$ in (1.3), which is common in synthetic numerical experiments done in the PET literature. For SPECT, we follow [4], and take $\mu = 1$ where the absorption density of the body is positive and $\mu = 0$ otherwise. The statistical model used for generating the CT data is (1.7), while for PET and SPECT it is (1.9). The noisy sinogram data for CT and SPECT are given in the middle and on the left in Figure 3.1. The sinogram for PET looks structurally very similar to the CT sinogram, with noise more characteristic of the SPECT sinogram, thus we do not include it. The signal-to-noise level for these examples is approximately 30.

The inverse problem is to reconstruct the Shepp-Vardi phantom given the respective sinogram data \mathbf{z} and forward model matrix \mathbf{A} . We do this using the iterative method and stopping rule presented in Section 2. With an initial guess of $\mathbf{u}_0 = \mathbf{1}$ and the three stopping rules, with $\epsilon_n = 0$ in (2.8). The computations were done in MATLAB.

For the CT example, the reconstruction given by the DP and UPRE stopping rules are given on the left and middle, respectively, in Figure 3.2. On the right is a

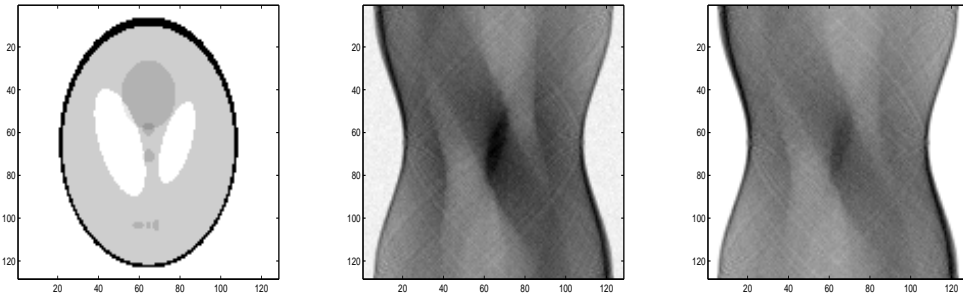


FIG. 3.1. The Shepp-Vardi phantom is pictured in the upper-left. The simulated sinogram for CT and SPECT are given, respectively, in the middle and right.

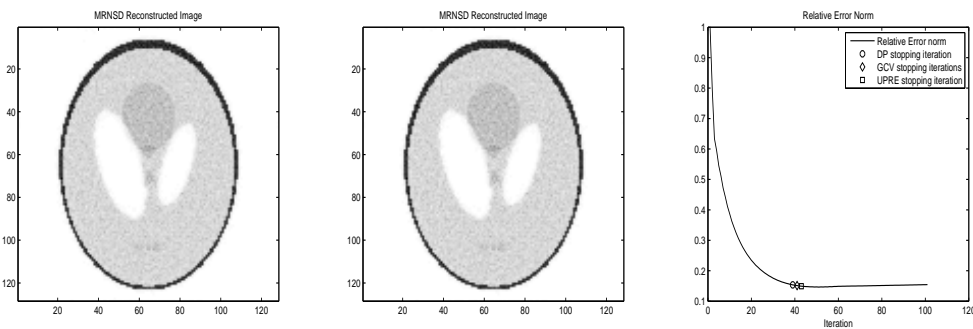


FIG. 3.2. CT Example. On the left and in the middle are the reconstructions obtained using the DP and UPRE stopping rules, respectively, and on the right is a plot of the relative error with the stopping iterations labeled.

plot of the relative error $\|\mathbf{u}_k - \mathbf{u}_{\text{true}}\|/\|\mathbf{u}_{\text{true}}\|$ with the stopping iterations for DP, GCV, and UPRE labeled. In this example, the reconstructions for the three methods are visually very similar.

Before continuing, we note that GCV and UPRE depend, through iteration (2.11), upon the particular randomly drawn vector \mathbf{v} . We have observed that different \mathbf{v} yield different stopping iterations. Though the methods seem to be relatively stable with respect to the choice of \mathbf{v} , additional stability can be obtained through averaging if multiple values of \mathbf{v} are chosen, and multiple iterations of the form (2.11) implemented.

Additionally, we have found that regularly restarting the iteration (2.11) within the WMRNSD iterations yields more effective stopping rules. In the results shown in Figure 3.2, as well as those that follow, we restart (2.11) every ten WMRNSD iterations by setting $\mathbf{w}_k = (\mathbf{u}_k \odot \mathbf{v})/(\mathbf{z} - \gamma)$.

For the PET example, the reconstruction given by the DP and GCV stopping rules are given on the left and middle in Figure 3.3. On the right is a plot of the relative error with the stopping iterations for DP, GCV, and UPRE labeled. In this case, the GCV and UPRE reconstructions appear slightly sharper than the DP reconstruction, and have a slightly smaller relative error..

For the SPECT example, the reconstruction given by the DP and GCV stopping rules are given on the left and center in Figure 3.3. On the right is a plot of the relative error with the stopping iterations for DP, GCV, and UPRE labeled. In this

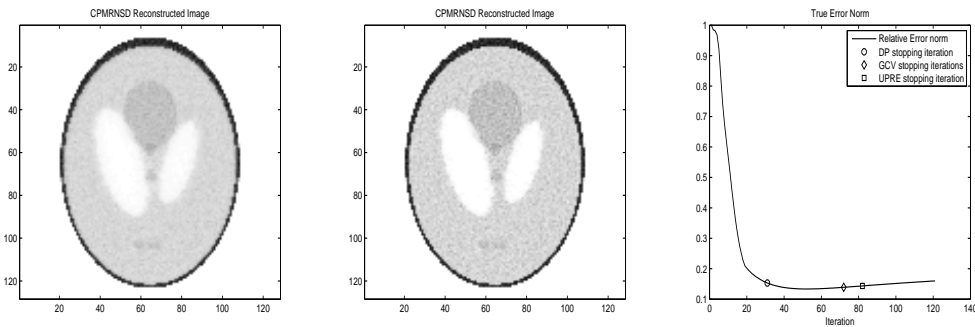


FIG. 3.3. *PET Example.* On the left and in the middle are the reconstructions obtained using the DP and GCV stopping rules, respectively, and on the right is a plot of the relative error with the stopping iterations labeled.

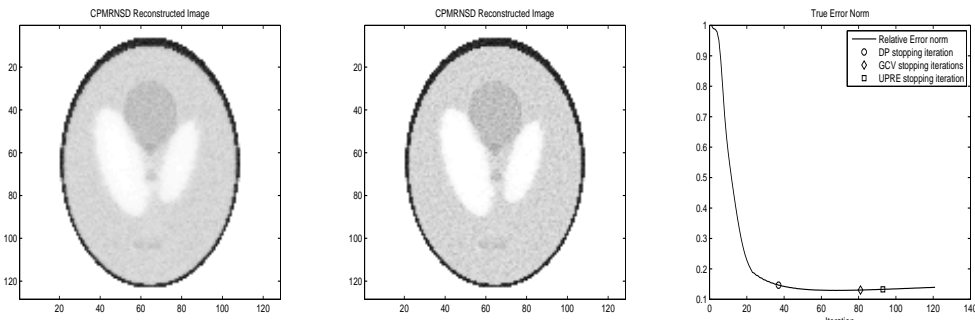


FIG. 3.4. *SPECT Example.* On the left and in the middle are the reconstructions obtained using the DP and GCV stopping rules, respectively, and on the right is a plot of the relative error with the stopping iterations labeled.

case, once again, the GCV and UPRE reconstructions appear slightly sharper than the DP reconstruction, and have a slightly smaller relative error.

As is the case for the discrepancy principle for regularization parameter selection in the case of Tikhonov regularization, the discrepancy principle consistently underestimates the stopping iteration. On the other hand, where we've chosen $\epsilon_n = 0$ in (2.8), a negative value could reasonably be chosen, e.g. one standard deviation below the mean of the $\chi^2(n)$, or $\epsilon_n = -\sqrt{2n}/n$.

4. Conclusions. We have presented an iterative method and three statistically motivated stopping rules for solving inverse problems arising in the applications of CT, PET, and SPECT imaging. For PET and SPECT, a quadratic approximation of the negative-log Poisson likelihood function is needed in order to motivate the use of (2.2), whereas in the CT example, Gaussian data, and hence a least-squares likelihood, is assumed. This allows for the implementation of the simple, nonnegatively constrained WMRNSD algorithm of [1, 3] to be applied in all cases.

Stopping rules for WMRNSD follow from a Gaussian approximation of the data-noise model. For CT, such a model is assumed, whereas for for PET and SPECT, approximation (2.6) of a Poisson statistical model of the form (1.9) is used. The Gaussian/least-squares assumptions allow for the development of three stopping rules: the discrepancy principle, generalized cross validation, and unbiased predictive risk

estimation. All three of these methods work in practice, as the numerical experiments show.

The codes used to perform the numerical experiments in this paper can be obtained from the author.

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