Iterative Optimization in Medical Imaging

Charles Byrne (Charles_Byrne@uml.edu) http://faculty.uml.edu/cbyrne/cbyrne.html Department of Mathematical Sciences University of Massachusetts Lowell Lowell, MA 01854, USA

March 12, 2008



This work was supported, in part, by the National Institutes of Health (NIH), under grant CA23452. The contents of this presentation are solely the responsibility of the author and do not necessarily reflect the official views of NIH.



This slide presentation and accompanying article are available on my web site, http://faculty.uml.edu/cbyrne/cbyrne.html ; click on "Talks".



・ロト ・ 四 ト ・ 回 ト ・ 回

Overview

- 1. transmission tomography and non-iterative filtered backprojection;
- 2. discretization and iteration- ART and MART;
- 3. emission tomography and iterative likelihood maximization;
- 4. the EMML algorithm for emission tomography;
- 5. acceleration through block-iterative methods;
- 6. iterative entropy maximization;
- 7. the split feasibility problem and the CQ algorithm;
- 8. intensity-modulated radiation therapy (IMRT).



In transmission tomography, radiation, usually x-ray, is transmitted along many lines through the object of interest and the initial and final intensities are measured. The intensity drop associated with a given line indicates the amount of attenuation the ray encountered as it passed along the line. It is this distribution of attenuating matter within the patient, described by a function of two or three spatial variables, that is the object of interest. Unexpected absence of attenuation can indicate a break in a bone, for example. The data are usually modeled as line integrals of that function. The Radon transform is the function that associates with each line its line integral.



The intensity of the x-ray beam upon entry is I_{in} and I_{out} is its lower intensity after passing through the body, along line *L*. Then we have

$$I_{out} = I_{in} e^{-\int_L t}, \qquad (1)$$

where $f = f(x, y) \ge 0$ is the *attenuation function* describing the two-dimensional distribution of matter within the slice of the body being scanned and $\int_L f$ is the integral of the function f over the line L along which the x-ray beam has passed.



The line *L* is parameterized by the variable *s* and the intensity function is I(s). For small $\Delta s > 0$, the drop in intensity from the start to the end of the interval $[s, s + \Delta s]$ is approximately proportional to the intensity I(s), to the attenuation f(s) and to Δs , the length of the interval; that is,

$$l(s) - l(s + \Delta s) \approx f(s)l(s)\Delta s.$$
 (2)

Dividing by Δs and letting Δs approach zero, we get

$$I'(s) = -f(s)I(s), \tag{3}$$

and so

$$I(s) = I(0) \exp(-\int_{u=0}^{u=s} f(u) du).$$



Radon Transform



For each fixed value of t, we compute the integral

$$\int_{L} f(x, y) ds = \int f(t \cos \theta - s \sin \theta, t \sin \theta + s \cos \theta) ds \qquad (5)$$

along the single line *L* corresponding to the fixed values of θ and *t*. We repeat this process for every value of *t* and then change the angle θ and repeat again. We denote by $r_f(\theta, t)$ the integral

$$r_f(\theta, t) = \int_L f(x, y) ds.$$
(6)

The function $r_f(\theta, t)$ is called the *Radon transform* of *f*.



For fixed θ the function $r_f(\theta, t)$ is a function of the single real variable *t*; let $R_f(\theta, \omega)$ be its Fourier transform. Then

$$R_{f}(\theta,\omega) = \int r_{f}(\theta,t) e^{i\omega t} dt$$
(7)

$$= \int \int f(t\cos\theta - s\sin\theta, t\sin\theta + s\cos\theta) e^{i\omega t} ds dt$$
 (8)

$$= \int \int f(x, y) e^{i\omega(x\cos\theta + y\sin\theta)} dx dy = F(\omega\cos\theta, \omega\sin\theta), \quad (9)$$

where $F(\omega \cos \theta, \omega \sin \theta)$ is the two-dimensional Fourier transform of the function f(x, y), evaluated at the point $(\omega \cos \theta, \omega \sin \theta)$; this relationship is called the *Central Slice Theorem*. For fixed θ , as we change the value of ω , we obtain the values of the function *F* along the points of the line making the angle θ with the horizontal axis. As θ varies in $[0, \pi)$, we get all the values of the function *F*. Once we have *F*, we can obtain *f* using the formula for the two-dimensional inverse Fourier transform:

$$f(x,y) = \frac{1}{4\pi^2} \int \int F(u,v) e^{-i(xu+yv)} du dv.$$
 (10)

The *filtered backprojection* methods commonly used in the clinic are derived from different ways of calculating the double integral in Equation (10).



The Discrete Model





The estimated attenuation function will ultimately be reduced to a finite array of numbers prior to display. This discretization can be performed at the end, or can be made part of the problem model from the start. In the latter case, the attenuation function is assumed to be constant over small pixels or voxels; these constants are the object of interest now. The problem has been reduced to solving a large system of linear equations, possibly subject to non-negativity or other constraints.



If the physical nature of the radiation is described using a statistical model, then the pixel values can be viewed as parameters to be estimated. The well-known maximum likelihood parameter estimation method can then be employed to obtain these pixel values. This involves a large-scale optimization of the likelihood function.



(日)

For j = 1, ..., J, let x_j be the unknown constant value of the attenuation function within the *j*th pixel or voxel.

For i = 1, ..., I, let L_i be the set of pixel indices j for which the jth pixel intersects the *i*-th line segment, let $|L_i|$ be the cardinality of the set L_j .

Let $b_i > 0$ be the measured approximation of the line integral of *f* along L_i .

Let $A_{ij} = 1$ for *j* in L_i , and $A_{ij} = 0$ otherwise.

The line integral is replaced by $(Ax)_i = \sum_{j \in L_i} A_{ij} x_j$.

The problem is then to solve Ax = b.



With $i = k \pmod{l} + 1$, the iterative step of the ART algorithm is

$$x_{j}^{k+1} = x_{j}^{k} + \frac{1}{|L_{i}|}(b_{j} - (Ax^{k})_{i}), \qquad (11)$$

for *j* in L_i , and

$$x_j^{k+1} = x_j^k, \tag{12}$$

(a)

if *j* is not in L_i . In each step of ART, we take the error, $b_i - (Ax^k)_i$, associated with the current x^k and the *i*-th equation, and distribute it equally over each of the pixels that intersects L_i . For the ART we do not require that the A_{ij} , b_i or the x_i be non-negative.



The ART can be used to solve any system of linear equations Ax = b. The iterative step of ART is

$$x_{j}^{k+1} = x_{j}^{k} + \frac{1}{||a^{i}||^{2}}(b_{j} - (Ax^{k})_{j})a^{i}, \qquad (13)$$

where a^i denotes the *i*th column of A^{\dagger} .



In the consistent case, the ART converges to the solution closest to the starting vector.





ART: The Inconsistent Case

In the inconsistent case, ART exhibits subsequential convergence to a limit cycle of distinct vectors.



The Multiplicative ART (MART)

Suppose, now, that we have $A_{ij} \ge 0$, $b_i > 0$ and we know that the desired image we wish to reconstruct must be nonnegative. We can begin with $x^0 > 0$, but as we compute the ART steps, we may lose nonnegativity. One way to avoid this loss is to correct the current x^k multiplicatively, rather than additively, as in ART. This leads to the *multiplicative* ART (MART). The MART, in this case, has the iterative step

$$x_j^{k+1} = x_j^k \Big(\frac{b_j}{(Ax^k)_j}\Big),\tag{14}$$

for those j in L_i , and

$$x_j^{k+1} = x_j^k, \tag{15}$$

otherwise. Therefore, we can write the iterative step as

$$x_j^{k+1} = x_j^k \left(\frac{b_i}{(Ax^k)_i}\right)^{A_{ij}}$$



The MART can be used to solve systems of the form y = Px, where y has positive entries, P has non-negative entries, and we seek a non-negative solution. The iterative step of MART is

$$x_{j}^{k+1} = x_{j}^{k} \left(\frac{y_{i}}{(Px^{k})_{i}}\right)^{P_{i,j}/m_{i}},$$
(17)

where $m_i = \max\{P_{i,j} | j = 1, ..., J\}$. If y = Px has non-negative solutions, then MART converges to such a solution; if not, MART exhibits subsequential convergence to a limit cycle, similar to ART.



If we take *J*, the number of pixels, to be larger than *I*, the number of measurements, then we have an under-determined problem, with multiple solutions. In such cases, prior knowledge can be used effectively to produce a reasonable reconstruction.





In emission tomography, a carefully designed chemical tagged with a radioisotope is introduced into the body of the patient. The chemical is selected to accumulate in a specific organ or region of the body, such as the brain, or the heart wall. On the basis of emissions from the radioisotope that are detected outside the body, the distribution of the chemical within the body is estimated. Unexpected absence of the radionuclide from a given region, or a higher than expected concentration, can indicate a medical problem.



There are two basic types of emission tomography:

- single photon emission computed tomography (SPECT);
- positron emission tomography (PET).

In SPECT the radioisotope emits a single photon, while in PET a positron is emitted, which shortly meets an electron and the resulting annihilation produces two gamma-ray photons traveling in essentially opposite directions.



In both SPECT and PET the data can be approximated as integrals along lines through the body and FBP used in reconstruction. However, more sophisticated models that more accurately describe the physics of the situation are preferred.

The photons that travel through the body toward the external detectors are sometimes absorbed by the body itself and not detected. The probability of being detected depends on the attenuation presented by the body. This attenuation, while not the object of interest now, is an important part of the physical model and needs to be included in the reconstruction method.

The randomness inherent in emission can also be included, leading once again to probabilistic models and a maximum likelihood approach to reconstruction.



The discrete model for emission tomography is the following:

- for *j* = 1,..., *J*, *x_j* ≥ 0 is the unknown expected number of photons emitted from the *j*th pixel during the scan;
- for *i* = 1, ..., *I*, *y_i* > 0 is the number of photons detected at the *i*th detector;
- *P_{ij}* ≥ 0 is the probability that a photon emitted at *j* will be detected at *i*, which we shall assume is known;
- $s_j = \sum_{i=1}^{l} P_{ij}$ is the sensitivity to *j*, that is, probability that a photon emitted at *j* will be detected;
- the y_i are realizations of independent Poisson random variables with expected values $(Px)_i = \sum_{i=1}^{J} P_{ij}x_j$.



We view the unknown values $x_j \ge 0$ as parameters to be estimated. To within a constant, the log of the likelihood function is then

$$LL(x) = \sum_{i=1}^{l} y_i \log(Px)_i - (Px)_i.$$
 (18)

The EMML algorithm for maximizing LL(x) over $x \ge 0$ has the iterative step

$$x_{j}^{k+1} = x_{j}^{k} s_{j}^{-1} \sum_{i=1}^{l} P_{ij} \left(\frac{y_{i}}{(Px^{k})_{i}} \right).$$
(19)



Although the EM algorithm allows for more accurate description of the physical situation, there are several disadvantages that must be removed before the EM algorithm can be a useful clinical tool:

- Calculating $(Px^k)_i = \sum_{j=1}^J P_{ij}x_j^k$, for each *i*, at each step of the iteration is expensive, since *I* and *J* can be in the tens of thousands;
- The sequence {x^k} usually converges quite slowly to the maximizer of LL(x);
- The maximum-likelihood (ML) solution will be a non-negative solution of y = Px, in the consistent case, that is, if such solutions exist, so may overfit noisy data;
- The ML solution may not be a good choice, in the inconsistent case, either.



・ コ ト ・ 雪 ト ・ 目 ト

It can be shown that, when the system y = Px has no non-negative solutions, the maximum-likelihood solution will have at most I - 1 non-zero pixel values, so, if J is greater than I, the ML solution may be useless. To control noise and obtain a useful image, one usually uses *regularization*, which means maximizing the sum of the likelihood function and another penalty function that is larger when the image is smooth.



In the early 1990's it was noticed that if, when performing one step of the EM iteration, one summed only over some of the detector indices, instead of over all of them, one could usually obtain a useful reconstruction more quickly.

Suppose that we take a partition $B_1 \cup B_2 \cup \cdots \cup B_N$ of the set $\{i = 1, ..., I\}$, and, at the *k*th step of the iteration, we use only a single B_n .



At the *k*th step of the OSEM we compute

$$x_{j}^{k+1} = x_{j}^{k} \mathbf{s}_{n,j}^{-1} \sum_{i \in B_{n}} P_{ij} \Big(\frac{y_{i}}{(Px^{k})_{i}} \Big),$$
(20)

for $n = k \pmod{N} + 1$ and $s_{n,j} = \sum_{i \in B_n} P_{ij}$. Although its mathematical foundations are a bit shaky, it has proven to be a useful clinical tool.



Limit Cycle





ヘロト ヘ節ト ヘヨト ヘヨト

Without strong under-relaxation, algorithms such as ART, MART and the OSEM that use only some of the data at each step of the iteration cannot converge to a single vector in the inconsistent case. For MART and OSEM this means there is no non-negative solution of y = Px, while for ART it simply means Ax = b has no solution. In such cases, these algorithms exhibit subsequential convergence to a limit cycle of (usually) Ndistinct vectors. One problem with OSEM is that it sometimes produces a limit cycle, even when there is a non-negative solution of y = Px. This makes the OSEM images noisier than they need to be, when the data is noisy.



The *rescaled block-iterative* EMML (RBI-EMML) is similar to the OSEM, but converges to a non-negative solution of y = Px, whenever such solutions exist, for every starting vector $x^0 > 0$ and every choice of blocks. Let x^0 be an arbitrary positive vector. For k = 0, 1, ..., let $n = k \pmod{N} + 1$. Then let

$$x_{j}^{k+1} = (1 - m_{n}^{-1} s_{j}^{-1} s_{n,j}) x_{j}^{k} + m_{n}^{-1} s_{j}^{-1} x_{j}^{k} \sum_{i \in B_{n}} (P_{ij} \frac{y_{i}}{(Px^{k})_{i}}), \quad (21)$$

with

$$m_n = \max\{s_{n,j}s_j^{-1} | j = 1, ..., J\}.$$



When there are multiple non-negative solutions of y = Px, it makes sense to select the solution closest to a prior estimate of x, according to some measure of distance. The *cross-entropy* or Kullback-Leibler distance is frequently used. As we shall see, this distance is also closely related to the EMML algorithm.



The Kullback-Leibler distance between positive numbers α and β is

$$KL(\alpha,\beta) = \alpha \log \frac{\alpha}{\beta} + \beta - \alpha.$$

We also define $KL(\alpha, 0) = +\infty$ and $KL(0, \beta) = \beta$. Extending to non-negative vectors $\mathbf{a} = (a_1, ..., a_J)^T$ and $\mathbf{b} = (b_1, ..., b_J)^T$, we have

$$\mathcal{KL}(a,b) = \sum_{j=1}^{J} \mathcal{KL}(a_j,b_j) = \sum_{j=1}^{J} \left(a_j \log \frac{a_j}{b_j} + b_j - a_j\right).$$

With $a_+ = \sum_{j=1}^J a_j$, and $b_+ > 0$, we have

$$KL(a,b) = KL(a_+,b_+) + KL(a,\frac{a_+}{b_+}b).$$



The EMML algorithm has the iterative step

$$x_{j}^{k+1} = x_{j}^{k} s_{j}^{-1} \sum_{i=1}^{l} P_{ij} \left(\frac{y_{i}}{(Px^{k})_{i}} \right).$$
(23)

It is interesting to compare this iteration with that of the *simultaneous* MART (SMART):

$$x_{j}^{k+1} = x_{j}^{k} \exp\left[s_{j}^{-1} \sum_{i=1}^{l} P_{ij} \log\left(\frac{y_{i}}{(Px^{k})_{i}}\right)\right].$$
 (24)



Theorem

The SMART sequence $\{x^k\}$ converges to the non-negative minimizer of KL(Px, y) for which $KL(x, x^0)$ is minimized, for any choice of $x^0 > 0$. The EMML sequence $\{x^k\}$ converges to a non-negative minimizer of KL(y, Px), for any choice of $x^0 > 0$.

It is an open question to which minimizer the EMML sequence converges. In the consistent case, the limit is a non-negative solution of y = Px. If there are multiple non-negative solutions of y = Px, the limit will depend on $x^0 > 0$, but we do not know how it depends on x^0 .



• • • • • • • • • • • • •

When y = Px has non-negative solutions, the SMART and MART algorithms produce sequences that converge to the unique non-negative solution that minimizes $KL(x, x^0)$, for any $x^0 > 0$. If x^0 is the vector whose entries are all one, then minimizing $KL(x, x^0)$ is equivalent to maximizing the *Shannon entropy*

$$SE(x) = \sum_{j=1}^J x_j(\log x_j) - x_j.$$

So the SMART and MART can be used to maximize entropy.



Let *A* be a real *I* by *J* matrix, and *C* and *Q* non-empty closed, convex sets in R^J and R^I , respectively.

The *split feasibility problem* (SFP) is to find a vector x in C, such that Ax is in Q.



When the SFP has no solution, it is sensible to seek a minimizer of the function

$$f(x) = \frac{1}{2} ||P_Q A x - A x||_2^2, \qquad (25)$$

over x in C; P_Q denotes the orthogonal projection onto Q.



For arbitrary x^0 and k = 0, 1, ..., and γ in the interval $(0, 2/\rho(A^T A))$, where $\rho(A^T A)$ denotes the largest eigenvalue of the matrix $A^T A$, let

$$x^{k+1} = P_C(x^k - \gamma A^T (I - P_Q) A x^k).$$
⁽²⁶⁾

This is the CQ algorithm. The CQ algorithm converges to a solution of the SFP, whenever solutions exist. When there are no solutions of the SFP, the CQ algorithm converges to a minimizer, over x in C, of the function

$$f(x) = \frac{1}{2} ||P_Q A x - A x||_2^2, \qquad (27)$$

whenever such minimizers exist.



The CQ algorithm employs the relaxation parameter γ in the interval $(0, 2/\rho(A^T A))$, where $\rho(A^T A)$ is the largest eigenvalue of the matrix $A^{T}A$. Choosing the best relaxation parameter in any algorithm is a nontrivial procedure. Generally speaking, we want to select γ near to $1/\rho(A^T A)$. A simple estimate for $\rho(A^T A)$ that is particularly useful when A is sparse is the following: if A is normalized so that each row has length one, then the spectral radius of $A^{T}A$ does not exceed the maximum number of nonzero elements in any column of A. A similar upper bound on $\rho(A^T A)$ was obtained for non-normalized, ϵ -sparse A.



A D F A P F A B F A B

Recently, Censor, Elfving, Kopf and Bortfeld have extended the CQ algorithm to the case in which the sets C and Q are the intersections of finitely many other convex sets. The new algorithm employs the orthogonal projections onto these other convex sets.



Censor, Bortfeld, Martin, and Trofimov use this new algorithm to determine intensity-modulation protocols for radiation therapy. The issue here is to determine the intensities of the radiation sources external to the patient, subject to constraints on how spatially varying the machinery permits these intensities to be, on the maximum dosage directed to healthy areas, and on the minimum dosage directly to the targets.



It is easy to find important examples of the SFP: if $C = R^J$ and $Q = \{b\}$ then solving the SFP amounts to solving the linear system of equations Ax = b; if *C* is a proper subset of R^J , such as the nonnegative cone, then we seek solutions of Ax = b that lie within *C*, if there are any. Generally, we cannot solve the SFP in closed form and iterative methods are needed.



A number of well known iterative algorithms, such as the Landweber and projected Landweber methods, are particular cases of the CQ algorithm.



With x^0 arbitrary and k = 0, 1, ..., the Landweber algorithm for finding a (possibly least-squares) solution of Ax = b has the iterative step

$$x^{k+1} = x^k + \gamma A^T (b - A x^k).$$
⁽²⁸⁾



(日)

For a general nonempty closed convex C, x^0 arbitrary, and k = 0, 1, ..., the projected Landweber algorithm for finding a (possibly constrained least-squares) solution of Ax = b in C has the iterative step

$$x^{k+1} = P_C(x^k + \gamma A^T(b - Ax^k)).$$
⁽²⁹⁾



Another example of the CQ algorithm is the *simultaneous* algebraic reconstruction technique (SART) of Anderson and Kak for solving Ax = b, for nonnegative matrix A. Let A be an M by N matrix with nonnegative entries. Let $A_{m+} > 0$ be the sum of the entries in the *m*th row of A and $A_{+n} > 0$ be the sum of the entries in the *n*th column of A. Consider the (possibly inconsistent) system Ax = b. For x^0 arbitrary and k = 0, 1, ..., let

$$x_n^{k+1} = x_n^k + \frac{1}{A_{+n}} \sum_{m=1}^M A_{mn}(b_m - (Ax^k)_m)/A_{m+1}.$$
 (30)

This is the SART algorithm. With a change of variables, the SART becomes a particular case of the Landweber iteration

Changing Variables

We make the following changes of variables:

$$B_{mn} = A_{mn}/(A_{m+})^{1/2}(A_{+n})^{1/2}, \qquad (31)$$

$$z_n = x_n (A_{+n})^{1/2},$$
 (32)

and

$$c_m = b_m / (A_{m+})^{1/2}.$$
 (33)

Then the SART iterative step can be written as

$$z^{k+1} = z^k + B^T (c - B z^k).$$
 (34)

This is a particular case of the Landweber algorithm, with $\gamma = 1$. The convergence of SART follows, once we know the largest eigenvalue of $B^T B$ is less than two; in fact, it is one should be a solution of $B^T B$ is less than two; in fact, it is one should be a solution of the largest eigenvalue of $B^T B$ is less than two; in fact, it is one should be a solution of the largest eigenvalue of $B^T B$ is less than two; in fact, it is one should be a solution of the largest eigenvalue of $B^T B$ is less than two; in fact, it is one should be a solution of the largest eigenvalue of $B^T B$ is less than two solutions are should be a solution of the largest eigenvalue of $B^T B$ is less than two solutions are should be a solution of $B^T B$ is less than two solutions are should be a solution of the largest eigenvalue of $B^T B$ is less than two solutions are should be a solution of $B^T B$ is less than two solutions are should be a solution of $B^T B$ is less than two solutions are solutions are solutions at the solution of $B^T B$ is less than two solutions are solutions are solutions.

The CQ algorithm is a particular case of an iterative algorithm based on Moreau's notion of proximity operator.



The Moreau envelope of a convex function f is the function

$$m_f(z) = \inf_x \{f(x) + \frac{1}{2} ||x - z||_2^2\},$$
(35)

which is also the infimal convolution of the functions f(x) and $\frac{1}{2}||x||_2^2$. It can be shown that the infimum is uniquely attained at the point denoted $x = \text{prox}_f z$. The function $m_f(z)$ is differentiable and $\nabla m_f(z) = z - \text{prox}_f z$. The point $x = \text{prox}_f z$ is characterized by the property $z - x \in \partial f(x)$. Consequently, x is a global minimizer of f if and only if $x = \text{prox}_f x$.



The conjugate function associated with *f* is the function $f^*(x^*) = \sup_x(\langle x^*, x \rangle - f(x) \rangle)$. In similar fashion, we can define $m_{f^*}z$ and $\operatorname{prox}_{f^*}z$. Both m_f and m_{f^*} are convex and differentiable.



Theorem

Let f be a closed, proper, convex function with conjugate f*. Then

$$m_{f}z + m_{f^{*}}z = \frac{1}{2}||z||^{2};$$

$$\operatorname{prox}_{f}z + \operatorname{prox}_{f^{*}}z = z;$$

$$\operatorname{prox}_{f^{*}}z \in \partial f(\operatorname{prox}_{f}z);$$

$$\operatorname{prox}_{f^{*}}z = \nabla m_{f}(z), \text{ and}$$

$$\operatorname{prox}_{f}z = \nabla m_{f^{*}}(z).$$
(36)

(日) (四) (日) (日) (日)

isetts

An Example

For example, consider the indicator function of the convex set C, $f(x) = \iota_C(x)$ that is zero if x is in the closed convex set C and $+\infty$ otherwise. Then $m_f z$ is the minimum of $\frac{1}{2}||x - z||_2^2$ over all x in C, and $\operatorname{prox}_f z = P_C z$, the orthogonal projection of z onto the set C. The operators $\operatorname{prox}_f : z \to \operatorname{prox}_f z$ are proximity operators. These operators generalize the projections onto convex sets, and, like those operators, are firmly non-expansive (Combettes and Wajs).

The support function of the convex set C is

 $\sigma_C(x) = \sup_{u \in C} \langle x, u \rangle$. It is easy to see that $\sigma_C = \iota_C^*$. For $f^*(z) = \sigma_C(z)$, we can find $m_{f^*}z$ using Moreau's Theorem:

$$\operatorname{prox}_{\sigma_C} z = z - \operatorname{prox}_{\iota_C} z = z - P_C z$$



The minimizers of m_f and the minimizers of f are the same. From Moreau's Theorem we know that

$$\nabla m_f(z) = \operatorname{prox}_{f^*} z = z - \operatorname{prox}_f z, \qquad (38)$$

so $\nabla m_f z = 0$ is equivalent to $z = \text{prox}_f z$.



Because the minimizers of m_f are also minimizers of f, we can find global minimizers of f using gradient descent iterative methods on m_f .

Let x^0 be arbitrary. Then let

$$x^{k+1} = x^k - \gamma_k \nabla m_f(x^k). \tag{39}$$

We know from Moreau's Theorem that

$$\nabla m_f z = \operatorname{prox}_{f^*} z = z - \operatorname{prox}_f z, \qquad (40)$$

so that Equation (39) can be written as

$$x^{k+1} = x^k - \gamma_k (x^k - \operatorname{prox}_f x^k)$$

$$= (1 - \gamma_k) x^k + \gamma_k \operatorname{prox}_f x^k.$$

University of Massachusetts

It follows from the definition of $\partial f(x^{k+1})$ that $f(x^k) \ge f(x^{k+1})$.

Minimizing $F(x) = f_1(x) + f_2(x)$

Combettes and Wajs consider the problem of minimizing the function $F(x) = f_1(x) + f_2(x)$, where $f_2(x)$ is differentiable and its gradient is λ -Lipschitz continuous. The function F is minimized at the point x if and only if

$$0 \in \partial F(x) = \partial f_1(x) + \nabla f_2(x), \tag{42}$$

so we have

$$-\gamma \nabla f_2(\mathbf{x}) \in \gamma \partial f_1(\mathbf{x}), \tag{43}$$

for any $\gamma > 0$. Therefore

$$\mathbf{x} - \gamma \nabla f_2(\mathbf{x}) - \mathbf{x} \in \gamma \partial f_1(\mathbf{x}).$$
(44)

From Equation (44) we conclude that

$$\boldsymbol{x} = \operatorname{prox}_{\gamma f_1}(\boldsymbol{x} - \gamma \nabla f_2(\boldsymbol{x})).$$

This suggests an algorithm, called the *forward-backward* splitting for minimizing the function F(x).



Beginning with an arbitrary x^0 , and having calculated x^k , we let

$$x^{k+1} = \operatorname{prox}_{\gamma f_1}(x^k - \gamma \nabla f_2(x^k)), \tag{46}$$

with γ chosen to lie in the interval $(0, 2/\lambda)$. The operator $I - \gamma \nabla f_2$ is then averaged. Since the operator $\operatorname{prox}_{\gamma f_1}$ is firmly non-expansive, the sequence $\{x^k\}$ converges to a minimizer of the function F(x), whenever minimizers exist. It is also possible to allow γ to vary with the *k*.



(□) (圖) (E) (E)

Recall that the split-feasibility problem (SFP) is to find x in C with Ax in Q. The CQ algorithm minimizes the function

$$f(x) = ||P_Q A x - A x||_2^2,$$
(47)

over $x \in C$, whenever such minimizers exist, and so solves the SFP whenever it has solutions. The CQ algorithm therefore minimizes the function

$$F(x) = \iota_C(x) + f(x), \tag{48}$$

・ コ ト ・ 雪 ト ・ 目 ト

where ι_C is the indicator function of the set *C*. With $f_1(x) = \iota_C(x)$ and $f_2(x) = f(x)$, the function F(x) has the form considered by Combettes and Wajs, and the CQ algorithm becomes a special case of their forward-backward splitting method.



THE END

