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Solution of a Complex Least Squares Problem with Constrained Phase

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Abstract

The least squares solution of a complex linear equation is in general a complex vector with independent real and imaginary parts. In certain applications in magnetic resonance imaging, a solution is desired such that each element has the same phase. A direct method for obtaining the least squares solution to the phase constrained problem is described.

Keywords

Matrix equation; Phase constraint; Magnetic resonance imaging

I Introduction

Consider the linear equation given in Eq 1

$$\mathbf{Ax}=\mathbf{b} \quad (1)$$

where \mathbf{A} is a complex $m \times n$ matrix, \mathbf{b} is a complex m -vector and \mathbf{x} is a complex n -vector. The minimum norm least squares solution to Eq 1 has $2n$ independent variables: the real and imaginary parts of \mathbf{x} , which may also be represented in polar form as the amplitude and phase. However in certain applications in magnetic resonance imaging, it is reasonable to expect the phase of all elements of \mathbf{x} to be the same and thus a phase constrained solution is desired.

This is a nonlinear optimization problem that has been approached previously using iterative Gauss-Newton search [1]. The present study derives an alternate, direct method for solving the phase constrained problem in which the minimum norm least squares solution is obtained such that the phase of every element of \mathbf{x} is identical.

II Direct Method

A solution of the desired form is assumed, $\mathbf{x}_{real}e^{i\phi}$, which comprises a real n -vector \mathbf{x}_{real} and a real scalar ϕ . Eq 1 is then re-written as in Eq 2.

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$$\mathbf{A}\mathbf{x}_{real}e^{i\phi}=\mathbf{b} \quad (2)$$

The goal is to minimize the sum of squares of the residual $\mathbf{r} = \mathbf{b} - \mathbf{A}\mathbf{x}_{real}e^{i\phi}$ over \mathbf{x}_{real} and ϕ . Using separable least squares [2] to isolate the linear terms, the optimal \mathbf{x}_{real} can be obtained for any ϕ by equating $d(\mathbf{r}^H\mathbf{r})/d\mathbf{x}_{real}$ to zero. This leads to the expression $\mathbf{M}\mathbf{x}_{real} = \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi})$, where $\mathbf{M} \equiv \text{Re}(\mathbf{A}^H\mathbf{A})$. Taking the pseudoinverse \mathbf{M}^\dagger yields the minimum norm least squares solution,

$$\widehat{\mathbf{x}}_{real} = \mathbf{M}^\dagger \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi}). \quad (3)$$

Note that the rank and condition number of \mathbf{M} are not necessarily the same as those of $\mathbf{A}^H\mathbf{A}$.

The residual may now be expressed as function of ϕ only and it remains to minimize $\mathbf{r}^H\mathbf{r}$ over ϕ .

$$\mathbf{r} = \mathbf{b} - \mathbf{A}\mathbf{M}^\dagger \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi})e^{i\phi} \quad (4)$$

Making use of the identities $\mathbf{A}^H\mathbf{A} = \mathbf{M} + i \text{Im}(\mathbf{A}^H\mathbf{A})$ and $\mathbf{M}^\dagger\mathbf{M}\mathbf{M}^\dagger = \mathbf{M}^\dagger$ and dropping imaginary terms (since $\mathbf{r}^H\mathbf{r}$ is real),

$$\mathbf{r}^H\mathbf{r} = \mathbf{b}^H\mathbf{b} - \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi})^T \mathbf{M}^\dagger \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi}). \quad (5)$$

Equating $d(\mathbf{r}^H\mathbf{r})/d\phi$ to zero yields the necessary condition for obtaining a minimum.

$$-2\text{Im}(\mathbf{A}^H\mathbf{b}e^{-i\phi})^T \mathbf{M}^\dagger \text{Re}(\mathbf{A}^H\mathbf{b}e^{-i\phi}) = 0 \quad (6)$$

Eq 6 can be seen to be the imaginary part of $(\mathbf{A}^H\mathbf{b})^T \mathbf{M}^\dagger (\mathbf{A}^H\mathbf{b})e^{-2i\phi}$. For the imaginary part to be zero, the phase must also be zero which requires

$$\widehat{\phi} = \frac{1}{2} \angle (\mathbf{A}^H\mathbf{b})^T \mathbf{M}^\dagger (\mathbf{A}^H\mathbf{b}). \quad (7)$$

Thus the least squares solution to the phase constrained problem is $\widehat{\mathbf{x}}_{real}e^{i\widehat{\phi}}$ with the phase given by Eq 7 and the real vector given by Eq 3.

III Application to Magnetic Resonance Imaging

In magnetic resonance imaging, methods for separating water and fat signals commonly exploit the characteristic resonant frequencies of the protons in water and fat molecules [3-5]. Differences in frequency come about because electron shielding around the functional groups (-OH, -CH₂, -CH₃, etc.) causes the protons to experience slightly different magnetic fields and thus precess at different speeds, typically of a few parts per million of the main field.

In an imaging experiment data is typically sampled at three time points to detect changes in signal. The relevant matrix for this situation is given by Eq 8, taking the sampling times from Ref [3] and the fat spectrum from Ref [5].

$$A = \begin{bmatrix} 1.000 & 0.881 - 0.443i \\ 1.000 & 0.119 + 0.895i \\ 1.000 & -0.701 - 0.381i \end{bmatrix} \quad (8)$$

Simulated data were generated for range of water and fat combinations with water + fat = 1 and phase 0. Gaussian random noise with standard deviation 0.1 was added to the real and imaginary parts. Estimates were calculated using unconstrained linear least squares and by phase constrained least squares (Eq 3 and Eq 7). The means and standard deviations were computed from 10^6 trials. Table I indicates mean values are identical for both methods but the standard deviations are up to 41% higher when using the unconstrained method.

IV Conclusion

A direct method has been derived for solving a complex least squares problem with constrained phase. In application to water/fat separation in magnetic resonance imaging, the advantage over unconstrained linear least squares is reduced standard deviation in the estimated variables.

Acknowledgments

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Simulation results for the unconstrained and phase constrained estimation of water and fat based on Eq 8. Results indicate mean values are identical for both methods while standard deviations are up to 41% higher in the unconstrained case.

Table 1

Water Fat	Mean (unconstrained)	Mean (constrained)	Std. Dev. (unconstrained)	Std. Dev. (constrained)	Ratio
1.0	1.000-0.000i	1.000-0.000i	0.0822	0.0820	1.002
0.0	0.000-0.000i	-0.000-0.000i	0.0914	0.0649	1.408
0.8	0.800+0.000i	0.800+0.000i	0.0822	0.0801	1.026
0.2	0.200-0.000i	0.200-0.000i	0.0914	0.0664	1.376
0.6	0.600-0.000i	0.600+0.000i	0.0822	0.0751	1.094
0.4	0.400-0.000i	0.400-0.000i	0.0914	0.0722	1.266
0.4	0.400-0.000i	0.400+0.000i	0.0822	0.0670	1.227
0.6	0.600-0.000i	0.600-0.000i	0.0914	0.0814	1.123
0.2	0.200+0.000i	0.200+0.000i	0.0822	0.0603	1.363
0.8	0.800+0.000i	0.800+0.000i	0.0914	0.0884	1.034
0.0	0.000-0.000i	0.000+0.000i	0.0822	0.0584	1.408
1.0	1.000+0.000i	1.000+0.000i	0.0914	0.0912	1.002