Improving the quality of quantitative susceptibility maps

Jürgen R. Reichenbach, Ferdinand Schweser, Karsten Sommer, Andreas Deistung
Medical Physics Group, Institute for Diagnostic and Interventional Radiology, Jena University Clinics, Friedrich-Schiller-University, Jena, Germany

Quantitative susceptibility mapping (QSM) has only recently entered the ever increasing armamentarium of magnetic resonance imaging. It represents a novel quantitative contrast of an intrinsic physical tissue property that may be regarded as one of the most fundamental properties in the context of magnetic resonance imaging because it reflects the reaction of the tissue to the static main magnetic field. Despite its young age, QSM has already unfolded an enormous scientific and clinical potential, which will be certainly explored in detail in the coming years. In particular, since phase contrast can exceed the magnitude contrast by up to an order of magnitude with gradient-echo imaging (GRE) at high field, transforming the GRE phase information into quantitative susceptibility maps will become increasingly more attractive with increasing field strengths.

Among the many potential future applications, susceptibility contrast and susceptibility mapping is foreseen to be applied for risk assessment and therapy monitoring by examining iron deposition, demyelination and connectivity disruption in neurodegenerative diseases, microhemorrhages in traumatic brain injury (TBI), stroke assessment, bone mineralization, as well as atherosclerotic plaque composition and vulnerability. QSM will also enable non-invasive measurements of oxygen saturation in vivo [1] and will offer new contrast for studying nerve bundles and white matter fibre tracts that is important for quantitative connectivity studies or biophysical studies in neuroimaging [2,3]. If changes in susceptibility can be measured reliably based on GRE-EPI data, it will become possible to predict changes in blood susceptibility not only in single, large macro vessels [4], but also in regions containing randomly orientated blood vessels. Future avenues of QSM will further encompass applications to tissues and organs other than the brain (e.g., abdominal or breast imaging), which will have clinical implications and will open possibilities for future research.

QSM is a novel contrast mechanism in MRI compared to conventional hypointensity contrast in SWI or T2*-weighted images and employs small magnetic field variations to compute quantitative maps of the corresponding underlying magnetic susceptibility distribution. Although QSM has been successfully demonstrated by using conventional clinical GRE data of single-angle acquisition, the applied algorithms rely on strong numerical regularization either of generic type [5-8] or by inclusion of spatial a priori information derived from associated magnitude images [9-12]. Consequently, the resulting susceptibility maps may suffer from streaking artefacts [9], underestimation of the susceptibility values [7,10,12,13], over-smoothing [10], or artefacts due to inconsistency between a priori information and the actual susceptibility distribution [14].

We have recently developed an improved QSM algorithm, Homogeneity Enabled Incremental Dipole Inversion (HEIDI), which utilizes a sophisticated problem-specific incremental inversion procedure and a priori information on the homogeneity of the susceptibility distribution. This approach adopts the incremental inversion strategy by Li et al. [15] and Wu et al. [16], extends it by introducing transitional sub-domains, and exploits a priori information on the homogeneity of the susceptibility distribution for reconstructing the ill-conditioned sub-domain. Extracting a priori information is based on the assumption that a small spatial gradient of the background-field corrected GRE phase images \( \phi \) coincides with a small gradient of the magnetic susceptibility \( \chi \), i.e.

\[
\left| \hat{\nabla}_j \phi \right| \approx 0 \rightarrow \left| \hat{\nabla}_j \chi \right| \approx 0 \quad j = x, y, z
\]  

(Eq. 1)

With this assumption a binary mask \( M \) can be generated by thresholding the gradient of the phase images. Refinements of this mask are achieved by applying additional constraints including the Laplacian of the phase and the gradient of the magnitude image \( m \). Thresholding
both the Laplacian of the phase and the gradient in the magnitude image then allows determination and exclusion of regions with strong susceptibility variations.

The incremental inversion is based on subdividing Fourier space into three sub-domains $A$, $B$, and $C$. In sub-domain $A$ the inversion is ill-conditioned, in $B$ inversion is well-conditioned, and $C$ represents an interim region. Inversion in sub-domain $A$ requires \textit{a priori} information because the GRE phase does not contain information about $\chi$ in these regions. A special weighted total variation (TV) norm is defined as a scalar measure that ensures that only susceptibility in low gradient, smooth regions contributes to this quality measure and that can be used for reconstructing the susceptibility by solving the following constrained optimization problem:

$$\min_{\chi_{\text{interm}}} \| \tilde{\chi}_{\text{HEIDI}} \|_{F-TV} \quad \text{subject to} \quad P \tilde{\chi}_{\text{HEIDI}} = P \tilde{\chi}_{\text{interm}} \quad \text{and} \quad \| \tilde{\chi}_{\text{HEIDI}} \| < E_{\text{total}} \quad (\text{Eq. 2})$$

where $P$ is a projection operator that restricts minimization of the quality measure to Fourier coefficients in the ill-conditioned sub-domain and prevents changes of Fourier coefficients in the well-conditioned and transitional sub-domains, and $E_{\text{total}}$ is an \textit{a priori} estimate of the total image energy of the susceptibility map. $\chi_{\text{interm}}$ is a susceptibility distribution with well-conditioned and pre-estimated transitional coefficients. Sub-domains $B$ and $C$ are reconstructed by using a literature algorithm [17; $\beta=0$], followed by additional image-domain denoising of sub-domain $C$.

\begin{figure}[h]
\centering
\includegraphics[width=0.4\textwidth]{Fig_1.png}
\caption{Transverse slice of a HEIDI reconstructed susceptibility map from a single-angle high resolution 3D data set acquired with a dual-echo gradient echo sequence [18].}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=0.4\textwidth]{Fig_2.png}
\caption{Sagittal slice of the susceptibility map reconstructed with HEIDI. Streaking artifacts are mostly suppressed.}
\end{figure}

Figure 1 shows an exemplarily susceptibility map calculated with HEIDI algorithm. The new algorithm improves spatial depiction of subtle magnetic susceptibility variations in the human brain. HEIDI overcomes several pitfalls of other recently published algorithms (Fig. 2), including streaking artefacts, severe noise amplification, excessive smoothing, and sensitive dependence of the reconstruction quality on regularization parameters by applying different solution strategies to three sub-domains of the Fourier space. It is anticipated that HEIDI will be instrumental for investigating occurrence and origin of subtle pathological susceptibility variations in clinical settings.
References


