

## Tomo-V: a new tool for Doppler tomography

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Abstract. The paper presents a new tool for constructing Doppler tomograms: Tomo-V (https://tomo-v.inasan.ru), developed on the basis of the Algebraic Reconstruction Technique (ART). Previously, the ART method was not widely used in tomography since its direct implementation had high computational complexity. The author developed a fast version of this algorithm, which made it possible to implement it as a web application that runs at an acceptable speed in a browser on a personal computer. Using this method, it is possible to obtain sharp tomographic images from blurred profiles; in addition, the method has shown good results in restoring images from noisy data, from a small number of profiles, and from profiles contaminated with absorption lines and the emission of an expanding envelope. Tomo-V also includes tools for analysing the obtained tomograms, allowing one to display accretion disks and Roche lobes on the tomogram as well as the back projection of the tomographic image onto the flow elements in spatial coordinates.

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## 1 Introduction

To construct Doppler tomograms, methods are used similar to those utilized to construct tomographic images in other fields: medicine, defectoscopy, etc. The input data for constructing Doppler tomograms is a set of spectral line profiles obtained from observations of binary stars. The peculiarity of these data is their heterogeneity (the state of the object can change during the observations), noise, fairly low resolution, and a relatively small number of profiles that can be obtained for one object. To obtain tomograms from such data, it is necessary to use special methods, including regularization methods that allow one to restore the lost information from inconsistent input data. The most commonly used method is the maximum entropy method (MEM, Marsh & Horne 1988), which allows one to obtain images with the least possible amount of detail, which is important for interpretation. Also, to construct tomograms, the radio astronomical approach (CLEAN method, Agafonov 1997) is used, which is well suited for identifying the boundaries of the elements. These methods use a property of tomograms called the "central theorem," which allows searching for a solution in Fourier space, filling in the areas missing in the original data following a certain algorithm. In contrast, the Algebraic Reconstruction Techinque (ART, Gordon et al. 1970) uses minimization methods to find a solution directly (for Doppler tomography) in the velocity space without using the Fourier transform. Until now, this method has not been used to obtain Doppler tomograms, probably due to its high computational complexity: it requires minimization in a space with a dimension equal to the number of pixels in the desired image. For example, for an image with a resolution of  $50 \times 50$  pixels, it is necessary to minimize (for example, by gradient descent) in a space with a dimension of 2500. In Tomo-V we precalculate some data that can then be reused during all of the steps, which allows us to achieve good performance of the ART method even without using a graphics processing unit. This made it possible to create a web application open for public use.<sup>1</sup>

## 2 The ART method

With the ART method we are trying to find a two-dimensional brightness distribution in the velocity space such that the projections of this distribution taken for the phases corresponding to the phases of the observed profiles has the best conformance with the observed profiles. The standard deviation  $\chi^2$  is used as a criterion. In Tomo-V each pixel in the image contributes to the luminance as a point source convolved with a Gaussian profile having a certain full width at half maximum (FWHM). Due

<sup>&</sup>lt;sup>1</sup> https://tomo-v.inasan.ru

to the overlap of the Gaussian profiles of the points, nonlinearity appears which does not allow the solution to degenerate into a set of superimposed bands.

#### 3 Working with Tomo-V

All of the computations are performed in the user's browser without any significant CPU load on the server side. On the web page, the user will see a screen divided into two parts. In the left column (initially empty) one can see a list of saved images, an area for loading previously exported data (files with the .tmv extension, see below), and a button for creating a new image. By clicking this button, the user is offered a choice: to create a test image ("Sample data...") for mastering the program as well as for experimenting with the settings or create an image built from real data ("Real data...").

If the user selects "Sample data," a window opens on the right side of the screen with an image of a test symbol and a block of settings. Next to this block is a graph for displaying the profiles. By comparing the "real" (red) profiles with the "synthetic" (blue) ones, the user can control the quality of the tomogram reconstruction. The right part of the window shows the reconstructed image, a graph with the absorption line (blue) and an additional emission (red), and elements related to the settings and control of the solution search process. To take into account the weights (for very noisy source data), one can enable the "Low SNR mode" option. The "Noize treshhold" and "Low-SNR degree" parameters can be used to adjust the weights when the low SNR mode is enabled. The "Start reconstruction" button is used to start the image construction process. In addition, on the block header there is a button for setting general parameters—the velocity range, FWHM, and resolution of the tomogram—as well as the buttons to save/export/delete the solver state and a "close" button.

The method shows rather good results in restoring images from a low number of profiles (see Fig. 1a–1d). Even complex shapes like the symbols "@" and "\*" are reconstructed well from 5 profiles. Also it works well with highly blurred profiles (Fig. 1e–1i). It can also reconstruct images with satisfactory quality from highly noisy data (up to SNR = 2), but the results cannot be included in this paper due to the page limits.

If the user selects "Real data..." when creating a new image, a window for constructing an image based on real data opens. In general, it is similar to working with the test data, but on the left side there will be a button for selecting the files, a table of the loaded files, and input fields for setting the continuum level (1 by default) and system parameters (component masses and orbital period). The loaded files must be text files and contain two columns: velocity (in km/s) and intensity.



Fig. 1. The reconstruction of the symbol "A" by 11 profiles (a), the symbol "A" by 5 profiles (b), the symbol "@" by 5 profiles (c), and the symbol "\*" by 5 profiles (d) with FWHM = 100; image reconstruction with FWHM = 300 km/s (e, g, i—500 iterations) and 600 km/s (f, h—1000 iterations). In the first row there are the original images (convolved with a Gaussian with the corresponding FWHM), the second row demonstrates the restored images, the third row shows the profiles by which the reconstruction was performed.

The intensities must be normalized to the continuum level, preferably so that the continuum intensity is taken as one. For each loaded file it is necessary to specify the phase (in the right part of the table, then click the "update" button), also in the right part of the table of the loaded files there is a check mark against each file, by unchecking which one can remove the corresponding profile from the calculations. The loaded profiles (the part of them that fits into the specified speed range) are immediately shown on the graph to the right of the file table. One can also load a file by specifying the phases for each profile ("Load phases from file").

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## References

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