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Overview of LOPSIMUL software, quick ray-tracing simulator of multi-foil reflective optical system

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Abstract. This paper presents description of LOPSIMUL ray-tracing simulation software that offers extremely high computational rate. LOPSIMUL has not a specific requirements for computer hardware and the computing time is less than one second or few seconds on a common personal computer. The software is optimized for lobster eye reflective optics (Angel as well as Schmidt variants) and various types of multi-foil optics. These systems are commonly used for X-rays. As the optimization supposes a specific optics design, the software cannot be used for a generic optics. Lopsimul draws focal image and x and y profiles. LOPSIMUL calculates FWHM, effective collecting area and other principal results.

Key words: multi-foil optics – lobster eye – ray-tracing – simulations – reflective optics – grazing incidence optics – x-ray optics

1. INTRODUCTION

The main motivation was to develop the quick algorithm and consequently the software for Schmidt (Schmidt, 1975) and Angel (Angel, 1979) lobster eye wide field of view reflective optics. These optics are intended mainly for X-rays, particuarly X-ray astronomy and astrophysics. Contrary to general ray-tracing algorithm (e.g. Spencer & Murty 1962), the usage is limited to some types of optics but the computational rate is extremely high. The software works on a common personal computer and the computing time is usually few seconds or less than one second.

The research resulted to simplified ray-tracing algorithm that was published in papers Tichý et al. (2016, 2011); Tichý (2013). Limitations for the optics come from this algorithm. The usage is generalised to any multi-foil optical system consisting of one or two orthogonally arranged stacks of flat mirrors. It is e.g. a case of optics that is similar to Schmidt lobster eye but spaces between mirrors are not equal.

Kirkpatrick-Baez reflective optical system (Kirkpatrick & Baez, 1948) can be simulated in an approximation when curved mirrors are replaced by set of flat surfaces. It is known that any continuous curve can be approximated by set of line segments. The approximation can be done with any given precision.

Users of the software are encourage to understand the algorithm presented in named papers to understand what the limitations for the optics are exactly and what LOPSIMUL does ”inside”.

This paper gives summary of the LOPSIMUL functionality in more details than the paper of Tichý & Hudec (2023) but none of these papers does not represent a user manual.

LOPSIMUL is intended for Microsoft® Windows™ 64-bit operating systems.

2. LOPSIMUL overview

LOPSIMUL consist of four windows, see Fig. 1.

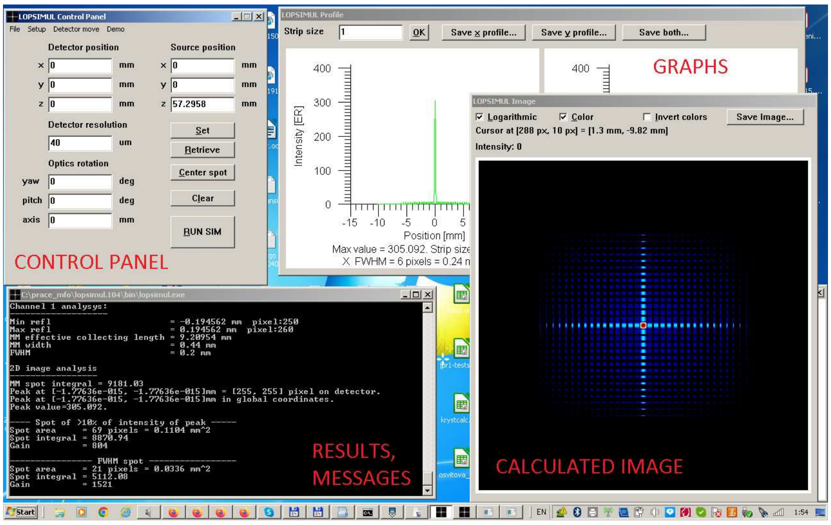

Figure 1. LOPSIMUL overview

The control panel represents the simulation input interface. The optics geometry, source type and all other parameters are entered through the control panel.

Other windows shows the simulation output. The console window shows simulation progress and numerical outputs. The image window shows the calculated image. The profile window shows graphs of profiles in x (horizontal) and y (vertical) axes.

2.1. Control panel

The control panel, see Fig. 2 is used for entering of all simulation inputs.

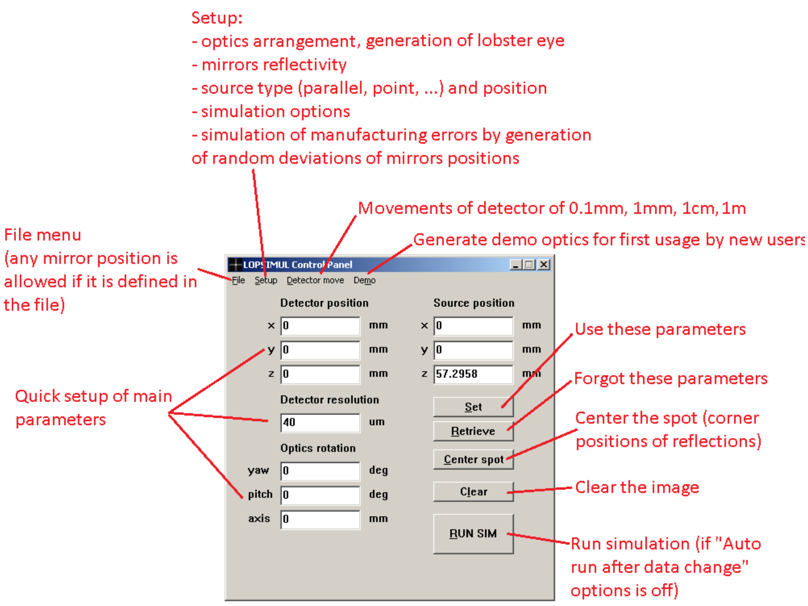

Figure 2. LOPSIMUL control panel

For the first usage, there are two built-in optics available in the "Demo" menu.

Main parameters are directly available in the control panel window. As default, the source is of parallel beam type and the coordinates in the control panel represent the source direction vector. For point source (and other sources that are available in the "Setup" menu), these coordinates represent the source position (or position of its center) in 3-D space.

Other parameters are clear to understand.

2.1.1. Optics set-up

For reasons explained in the Introduction, the optics set-up must be defined in terms of stacks. The term "stack" stands for set of mirrors. The stack must operate in one plane only and therefore it must be possible to simulate it in two-dimensional cross-section. The stacks are possible to generate in "Setup → Optical stacks list" submenu

The stacks are defined by following parameters: radius of the stack, pitch of mirrors, number of mirrors, mirror depth and thickness. Vertical or horizontal orientation of the stack can be set. Two stacks of different radii and different orientations form a Schmidt lobster eye system. Two stacks of the same radii and different orientation form an Angel lobster eye system.

More general system can be entered to the program via data-file. The data-file can be imported or exported via functions in "File" menu. In the input file, each mirror is defined as a set of four vertices of planar cross-section of the mirror. Mirrors are usually represented by rectangular cuboids (rectangles if the thickness is neglected). If opposite mirroring planes of mirrors are not parallel, mirrors can be represented by prisms of convex quadrilateral base.

2.1.2. Radiation source set-up

The radiation source can be set in "Setup → Source" submenu. Although LOP-SIMUL is intended mainly for X-ray optics, it can be used for other type of radiation if the proper model of reflectivity is set. LOPSIMUL can operate with parallel beam source, point source, line source and "flower 7" source. "Flower 7" source represents an approximation of disc source, where 7 point sources are used. One of point sources lays in the centre of the disc and 6 sources lays around the center. This arrangement looks like a flower. The source can be also defined in the input file.

2.1.3. Mirrors reflectivity set-up

Submenu "setup → material" allows to set-up reflectivity of mirrors.

LOPSIMUL contains few models of reflectivity: ideal mirror, constant reflectivity, linear model and two "trapezoid" models.

The linear model assumes that reflectivity $\mathbb{R}$ at grazing angle θ in radians equals

$$\mathbb{R}(\theta) = \begin{cases} Q\left(1 - \frac{\theta}{k}\right) & \forall 0 \leq \theta \leq k \\ 0 & \forall \theta \geq k \end{cases} \tag{1}$$

Constants Q and k are defined by the user.

The horizontal trapezoid model assumes that

$$\mathbb{R}(\theta) = \begin{cases} Q & \forall 0 \leq \theta \leq r \\ Q\frac{k-\theta}{k-r} & \forall r \leq \theta \leq k \\ 0 & \forall \theta \geq k \end{cases} \tag{2}$$

Constants Q, k and r are defined by the user.

The vertical trapezoid model assumes that

$$\mathbb{R}(\theta) = \begin{cases} Q\left(1 - \frac{\theta}{r}\right) & \forall 0 \leq \theta \leq k \\ 0 & \forall \theta \geq k \end{cases} \tag{3}$$

Constants Q, k and r are defined by the user.

Any model of reflectivity can be imported to the program in the form of table. Table generated at on-line calculator (Henke, 2023) can be directly imported to LOPSIMUL. Up to 10 of these tables can be imported to LOPSIMUL this way.

2.2. Image window

The image window shows the simulated resulting image, see Fig. 3. Black-and-white or false color view is available. Color scale can be inverted. Linear or logarithmic scale can be chosen. It is possible to save the image in .png or .bmp format. The image can be exported as text table for consequent processing in other software. If the mouse cursor is placed over the image, coordinates in image pixels and position in millimeters are shown together with intensity of the image at the corresponding point.

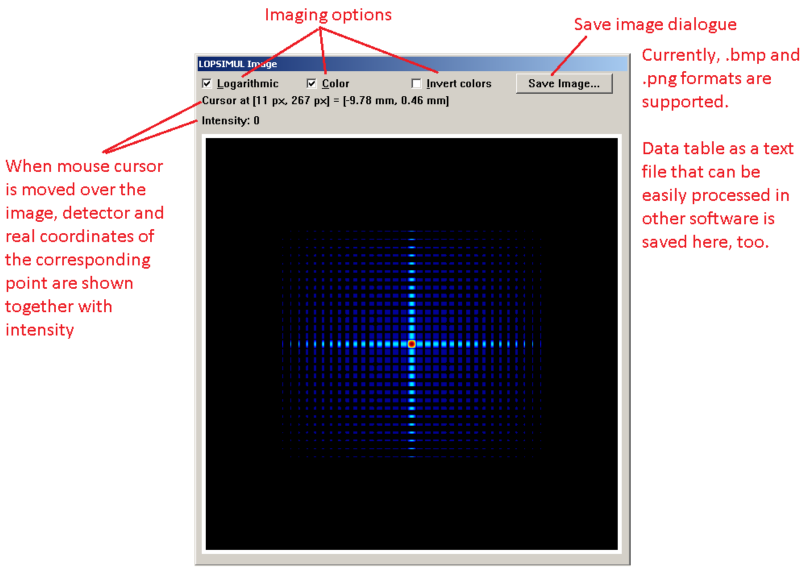

Figure 3. LOPSIMUL image window

2.3. Profiles window

Profiles window shows x and y cross-section graph of the image, see Fig. 4. The intensity is averaged over a strip of set size. The cross section is done through center of image that may not be the same as the spot position. If you would like to move the image to get the spot centered, use "Center spot" button of the Control Panel. Any of the profiles can be saved as image or both profiles can be saved in one image. Currently, .png and .bmp. image formats are available. Any of profiles can be exported as text table to be consequently processed in other software.

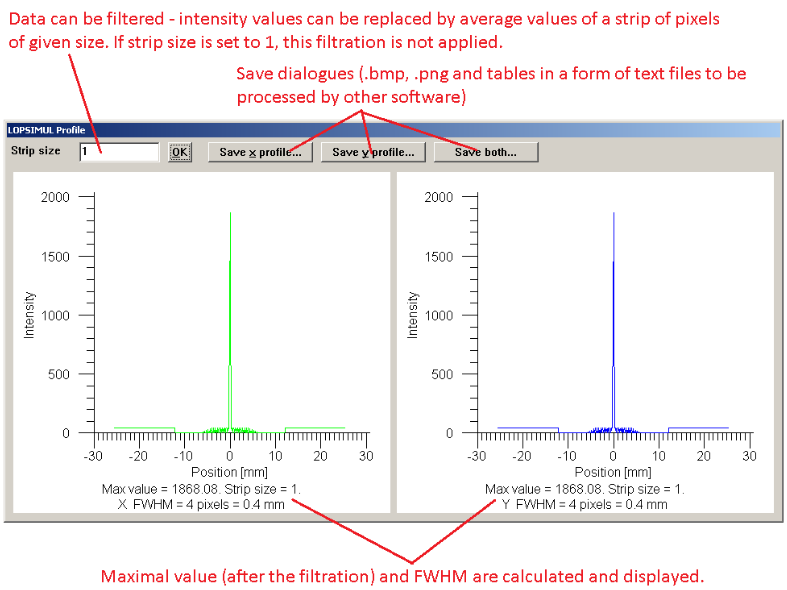

Figure 4. LOPSIMUL profiles window

If a simulation is finished but one or both graphs of profiles is (are) missing, the focal spot might not be centered. In this situation, try to press "Center spot" button in the control panel.

2.4. Console window

Console window shows progress of calculation during the simulations. When the simulation is finished, evaluation is listed in the console window, see Fig. 5.

For each of the channels (vertical and horizontal), the following values are calculated:

– Min refl, Max refl = border position of all reflections.

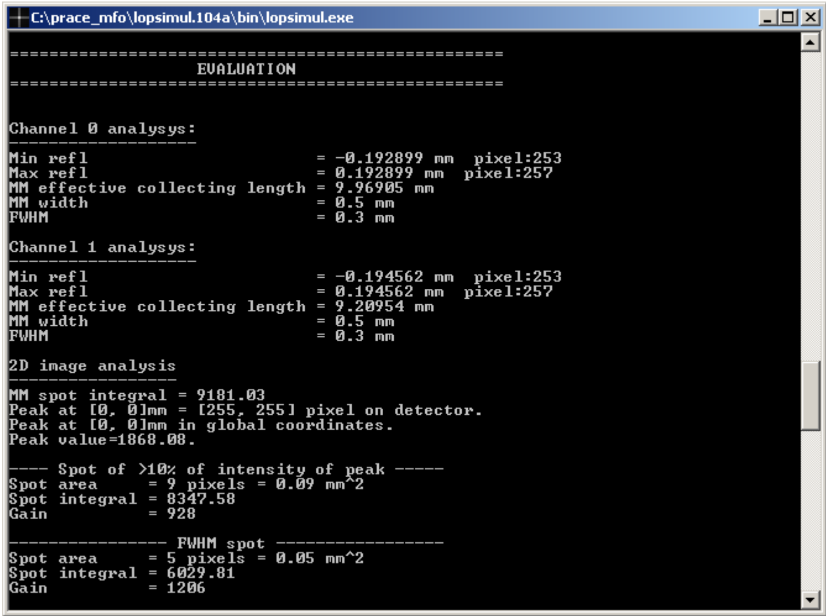

Figure 5. LOPSIMUL console window

- MM effective collecting length = effective collecting length related to the area bordered by Min rel and Max refl, i.e. by border rays that are reflected.
- MM width = width of focal image bordered by Min refl and max refl. It is not exactly equal to difference of Min refl and Max refl because of non-zero pixel size.
- FWHM = full width at half maximum of focal image.

The analysis of full 2-D image gives:

- MM spot integral = sum of intensities of all pixels laying within area bordered by Min refl and Max refl. I. e. it is total intensity in a rectangular box bordered by all double-reflected rays.
- Peak position in pixel coordinates.
- Peak position in milimeters related to global coodinate system.
- Intesity of the peak.

For area defined by FWHM and 10% rule, following values are calculated:

– Size of the area in pixels and square milimeters.

– Spot integral = sum of intensities of all pixels laying within this area.

– Gain

3. Conclusions

LOPSIMUL is optimized for some types of multi-foil reflective of optics, particularly for Schmidt and Angel lobster eye optics. These optics are used mainly for X-rays. LOPSIMUL offers extremely high computational rate but works only for particular optics types described above.

The code can be used e.g. for design and simulations of X-ray monitors based on Lobster Eye wide field optics.

LOPSIMUL can be downloaded and used by anybody for any purpose free of charge. LOPSIMUL is available for download (Tichý, 2023).

However, if results obtained by this program are published anywhere (e.g. in article, paper, thesis, report, etc.), users are asked to mention there that this program was used and cite at least one paper related to LOPSIMUL, e.g. this one or the paper that presents the simplified ray-tracing algorithm (Tichý et al., 2016). Citations of other papers are welcomed, too.

LOPSIMUL and any of its parts can be distributed by its author only. LOPSIMUL and any of its parts can be modified by the author only.

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