

CATS GUI Quick Start

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- **Log in** on a Sunray using your NetID or Guest ID, or log in on a Windows PC at CNF using your NetID@CIT.CORNELL.EDU, or your Guest ID.
- **Transfer your GDS file** to the W: drive on the PC , which is your home directory on the Andrew File System (AFS) server and also your home directory on minx, the Linux CATS server.
- **Start X Windows** on PC by double-clicking the **Xming** icon (Sunrays are already using X windows to display graphics on the screen).
- **Log in to minx.** On a PC, use the minx icon on the desktop. On a Sunray, use Applications -> minx
- **Start CATS** by typing cats2011 . If graphics windows don't pop up, start X Windows (see above) and start CATS again.
- **Turn on useful views** using View -> Views menu: pick **Commands, Fracture Setup and Active View**
- **Optional: To assign GDS layers to JEOL shot ranks (dose clocks)** – this is called Conditional Feature Assignment or **CFA**. In the **DataPrep** menu, pick **CFA**, then Browse (...) for Default File Name /home/CNFCommon/cnf_cfa_layers.ccfa.
- **Specify output file format** to be **JEOL30** using **Format** list in toolbar at top of screen.
- **In Fracture Setup View:**
 - **Widen the Property column** to make text visible.
 - **Set values of fracture parameters** by clicking in Value fields.
 - **1. Inputs and Output**
 - * **Assign GDS file to primary input** by clicking to right of **Primary** and opening it with the browse button (...) and Input... folder icon. CATS will automatically pick the root cell and determine pattern extents. *Note: Do not open the GDS file with the File menu; it does not put the file in the memory space for fracturing.*
 - * **Display the pattern** by clicking on the **Draw button (curved arrows)** in the toolbar, or by typing Ctrl-R.
 - * **Optional:** Browse cells with Structure value field, using the browse button (...).
 - * **Select layers to extract** with Layers value field, checking desired layers.
 - * **Optional:** Define **limits** if default limits are not OK, by typing lower-left and upper-right limits x_1, y_1, x_2, y_2 . For aligned exposures, these limits should be the same for all the layers. You can click the (...) button after clicking the Limits Value field and select Extent All for extent of all layers (usually the best choice), Extent for extent of extracted layers, Extent of Data, Symmetric Extent, or Pick, which allows you to select with the mouse on the pattern image.

- * **Set File Type** to **CATS Database** if you are doing CFA, otherwise switch it to **Native Machine Format**.
- * **Specify output file name starting with your initials and an underscore (.)** (because all pattern files go to the same folder on the e beam system) by clicking to the right of File Name. It will have a .jeol30 extension if writing Native Machine Format, or a .cref extension if doing CFA. Example: ab_demoLens4.jeol30 or ab_demoLens4.cref

– **2. Fracture Settings**

- * **Produce VSB_T** – fracturing algorithm that works to eliminate slivers; if you are doing CFA, **Produce FLATCREF**.
- * If you are doing CFA, set **Overlaps** to **Yes**, otherwise set **Overlaps** to **No**.
- * Optional: Reduce (**Bias**) size of written shapes by setting **Grow** to -0.005 or -0.010

– **4. Machine Parameters**

- * **Set Machine** to JBX-6300FS-EOS3 (lens 4/mode 3) or JBX-6300FS-EOS6 (lens 5/mode 6) or JBX-9300FS-100KV
- * **Set Field Size and Max. Field Size:**

Machine	Width	Height
JBX-6300FS-EOS3 (lens 4)	500	500
JBX-6300FS-EOS6 (lens 5)	62.5	62.5
JBX-9300FS-100KV	1000	1000

- **Press the Do button** at the top of the screen to fracture and produce JEOL .jeol30 file if not doing CFA, or CATS .cref file if doing CFA.
- **Display results** using two curved arrows icon or type **Ctrl-R**; then in **Active View**: uncheck the GDS file and check the output file above it. If you did CFA, right-click on display and pick **Draw Options -> Color by -> CFA**.
- **Quit CATS**.
- If you are doing CFA, at the minx command line change to the directory containing the GDS file, and type
 - `ls -t *.cref` to find the latest .cref file
 - `writfile2011` to start the program that converts .cref files to .jeol30 files. Enter the name of the .cref file, press enter to accept default output file name, type **Ctrl-D** to finish.
 - `ls -t *30` to find the latest output file; it may be a .jeol30 file or a .v30 file.
- **Use graphical file transfer program to transfer output file to JEOL 9300 or 6300** by typing

gftp

in the minx terminal window.

- The host name is `jeol` or `jeol6300`
 - User name: `ebtest` or `cnfuser`
 - Password: [ask tool manager]
 - Put the .jeol30 or .v30 file into `pattern/user`