MA6Gen3 – assisted alignment


1. Introduction

This document illustrates “assisted alignment” at CMi on Suss’ maskaligner MA6Gen3 using four sets of alignment marker provided in our template.

The alignment marks:

a) enable to align in x-axis, y-axis, and if used as a pair, also for theta,
b) their vernier structures covering four ranges (50, 100, 200, 500nm) allow to align independently of process linewidth bias, and indicate alignment at contact & after development,
c) fit within the field of vision of the microscope objective 10x (x=800µm y=1100µm).

The recognition software recognizes alignment mark patterns on the mask and on the substrate. Both patterns must beforehandly and separately be trained. Once this is done, upon aligning, the software simultaneously recognizes the marks, and shows in realtime the offsets between centers of the two markers in x-axis, y-axis, theta-rotation, for both the left and the right microscope. While aligning by moving the substrate via the joystick relative to the mask, the offset or misalignment reading is continuously updated, and thanks to this realtime feedback, allows to reach a highly accurate alignment, i.e. “assisted alignment”.

2. Alignment marker templates

CMi provides layout design templates at cmi.epfl.ch/photo/files/design/Template_CMi_*

The templates change as requirements, including yours, evolve. The current template has four sets of markers: classic cross inside of squares, and square/square, circle/circle and cross/cross structures, the latter three optimized for the image processing system, aimed at assisted alignment. Verniers/Nonius scales give additional subresolution alignment feedback.

If you design yourself alignment markers, consider that the recognition software works on contrast gradients, therefore put a gap between the two markers so that contrast curves don’t overlap.

Here the square inside square, with a gap maker:

Figure 1 inner square mrk2 aligned to outer square mrk1

The two layers shown separated in Figure 2 & fig Figure 3. The bigger square is patterned on the substrate during “first exposure”, the smaller square is on the mask during allowing for “alignment exposure.”

Figure 2 red outer square mark1, patterned on substrate
There are 8 Verniers, 4 for each axis, spanning four ranges, Vernier 50nm reaches up to 500nm in either direction, same 10x for 100, 200, 500nm.

On the mask aligner, the user interface presents itself as follows in Figure 5 MA6Gen3 full screen for square marks. Figure 5, here mask & substrate.

Figure 3 blue inner square marker2, mask to be aligned

NB: The “inner square marker2” of Figure 3Figure 3, must be boolean inverted, as shown in Figure 4, so that the substrate is visible through mask during alignment. Blue is the digitized data. When exposed in positive photoresist it develops away, and in Cr etch is removed from the mask and allows to peek through the glass onto the substrate. Find this layer by reading the layer explanations on the cmi website below the templates [layer not(53)->153].

Figure 4 blue square mark2 inverted, so that substrate is visible during alignment, blue = exposed = Cr etched away from mask. What is what remains in Cr.

A typical detail of what the microscope shows is in Figure 6, where the structured substrate appears as a dark big square, such as after pattern transfer into SiO2, and the mask appears as a bright small square, with its Chrome reflecting a lot of light.

Figure 5 MA6Gen3 full screen for square marks.

Figure 6 White zones with small square and dual Verniers (bottom half) are the markers of the mask of the 2nd layer lithography. They are to be superimposed / overlaid with the less bright marks of the pattern on mask1, with a bigger square and a single Vernier (top half).
The four types of alignment marks in the CMi supplied template are:

- concentric squares (Figure 6)
- concentric circles (Figure 7)
- wide gap cross & squares (Figure 8)
- classical cross & squares (Figure 9)

The latter three types work for various contrast situations, as their recognition features do not overlap. The classical cross & squares design may cause problems, as it is designed for "by eye" alignment, and in a machine environment, the touching cross features create overlapping contrast gradients, which are difficult to handle by the recognition algorithm.
3. Target training

Your first train your exposure recipe to use the alignment marks, then use them. As a starting point, you may get inspired by already available recipes ksu.tsa.assist.circle, ksu.tsa.assist.square, ksu.tsa.assist.cross, ksu.tsa.assist.classic.cross, but beware that you will get better control and therefore better results by teaching in your own images, as the contrast slightly differs for every design and material combination. In the recipe editor, tab Alignment, field AlignmentSetup. Mode “Assisted alignment”:

Load your mask, then start by positioning your mask features (e.g. small squares) near center of both microscopes (ocular/screen) as Figure 10.

Then insert the substrate, and move it also into the field of vision. This is not an alignment, this is getting them to be at arm’s length, see Figure 11.

As you train mask/substrate targets separately, move the substrate back out of the field of view with the joystick set to mode “Stage” as in Figure 10. Concentrate on alignment markers of layer 2 (mask), and put them in the centers, chose good focus and illumination.

Switch to “assisted alignment training mode” by clicking “AL Training” (bottom right corner Figure 11):

This switches to training buttons (in red square), and the current wrong targets (circles) Figure 12.

Figure 11 After loading substrate, trained targets are from recipe “circles”, therefore inadequate and to be retrained.

Figure 12 Target Training mode (AL Training)
The teaching task is to cycle through the four targets, and for each teach them to be squares, and define the “search area” and “define target” as given in these buttons.

Start with one of them:

**Target Mask Left ->Define Search Area**

Make the search area (pink rectangle) as big as possible. For this kind of structure this works best. One reason to make it smaller is if you have multiple identical markers in the field of vision, and you want to restrict the algorithm, alike a blinker for a horse.

Then specify what the target itself looks alike in this search area

**Target Mask Left ->Define Target**

Make the recognition area for the target snug but not touching with the target. Shapes (contrast gradients) outside of the target rectangle do not disturb the recognition, such as neighbouring features, dust, defocus, or the substrate related distractions. The recognition is done on contrast/illumination gradients, make those transitions be fully in the target defined area.

Then you get your training Result:

Save your work!!! Otherwise, you have to redo it over and over and over and over.
The interface comes back and happily reports:

![Selected Target Model and BMP file saved successfully!]

Note that the “target” image has been updated for the square (one square corner, and still three circles form the previous example.).

Advanced users may go and tweak the recognition algorithm, modify the scoring algorithm by changing contrast thresholds, and acceptance, but for this simple example here, this is sufficient.

Figure 15 Target Mask Left : trained

Once training of all targets is done, return to “alignment” mode by click on:

4. Alignment

The recognition algorithm is live and working and giving feedback about the alignment c.f. Figure 17, there are hundreds of micrometer of distance of misalignment, both dX & dY, we did not align yet.

Figure 17 Assist align feedback, detail of previous figure

Use the joystick (Stage) to align the substrate:

Do another time for right mask.

Then move the microscope to the substrate markers, and train left and right substrate.

Then move both targets one on top of each other. You see four targets trained (Figure 16):
In Figure 19 the misalignment has shrunk to submicrometer distances. The green fields are in very good agreement, $dX$ and $dY$, the rotation theta, $dT$ was not improved for this case.

The RO, the “thermal run-out”, meaning the difference between the distance of the markers on the mask and distance of the markers on the substrate, is RO=1.8um. This is due to different thermal expansion coefficients of the two materials, combined with different temperatures during patterning steps, resulting in differing dimensions.

See in Figure 19 the square indicative for displacement in X and Y, and the colored circle for displacement in Theta, green-CW, orange-CCW.
Another example using the traditional cross, right cross is too high, results in a rotation or theta misalignment:

After correcting with substrate movement, the three dX, dY and dT go into happy green. Thermal Runoff RO cannot be fixed but is premonitory of increasing misalignment towards edges of wafer.

Figure 20 assisted alignment with traditional cross

The detail of the feedback is:

It is up to the user to decide what precision is enough for an application.

Then the usual “Contact”, then “AL Check” and “exposure” sequences ensues.