

A new methodology for quantifying OPC recipe accuracy

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Abstract

An integrated methodology for developing recipes for optical proximity correction (OPC) is demonstrated. A complete implementation of software programs for generating the OPC corrections, determining mask and layout errors and automatically displaying contours of the worst violations has been accomplished. Integration of these elements facilitates recipe development by quantifying the effect of recipe changes on the overall critical dimension (CD) control. In this paper, a 65nm alternating aperture phase shift test mask is used for illustration of the method. The concept of a recipe comparison matrix is introduced to quantify the effect of recipe changes on across-chip metrics.

Keywords: lithography verification, optical proximity corrections, optical proximity correction recipes

1. Introduction

The continuing drive to reduce minimum geometries with optical methods forces IC makers to use low contrast processes with optical lithography to image sub $0.1\mu\text{m}$ geometries. Layout optimization to correct for optical proximity and etch effects is a routine lithography tool for increasing process windows with respect to final target dimensions. Methodologies for implementing full chip optical proximity correction have matured since the 1990's when first proposed for use to enhance i-line processing of $0.35\mu\text{m}$ technology.

The most common OPC correction methodology used to create reticles today divides the edges of the target pattern into segments. Each segment is allowed to deviate inwards or outwards in response to a modeled contour.

When applying a recipe approach as with Proteus™ (Synopsys, Mountain View CA), there are virtually an unlimited number of ways to correct layouts for optical and other process effects. There are many approaches to dissection, or the breaking up of edges into smaller edges so that each edge may be moved as needed. For example, Cork et al¹ and Cobb and Granik² discuss different ways of optimizing placement of the target point for measuring modeled intensity. Rieger et al³ introduced and Lugg et al⁴ extended the concept of feature specific tolerances in order to minimize mask complexity. This affects the size of the jogs generated by Proteus, the accuracy of the correction, and, potentially, mask rule violations. Fig. 1 illustrates two general methods for placing these target points which generally affects the accuracy of OPC results.

Recipe creation and generation is by nature an iterative process. In general, a recipe is chosen for a given technology and used to generate the OPC corrections for one or more layers. Certain sites are then reviewed for precision of the

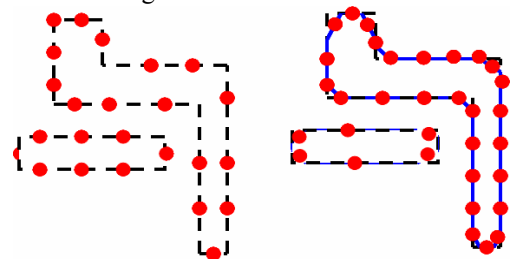


Fig. 1 Two possible choices for placing target points. In the left drawing, target points are distributed along the target perimeter. The right shows corner regions in which the target point is located slightly displaced from the design intent edge.

contour to the target and adjustments are made if needed. The recipe is then used to correct an entire mask. Often the OPC verification is done at this stage to identify unintentional fatal data errors such as pinching and bridging or mask rule violations (MRC), rather than improving CD distribution or process latitude.

In this paper, a new methodology is outlined which quantifies OPC correction accuracy by using the OPC verification tool SiVL™ (Silicon versus Layout) to rapidly quantify the effect of recipe changes over both test patterns and full chip layouts. The approach is to narrow allowable error tolerances so all measurements are reported as errors. Distributions for various error types are then compiled into a database and become useful for comparison of different OPC recipe

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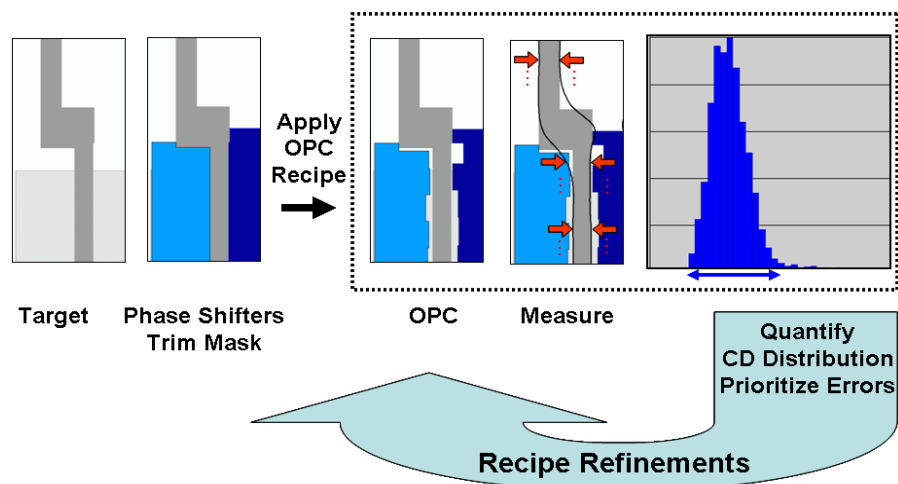


Fig. 2 Integrated recipe development

2. Theory

Perhaps the most significant challenge for developing a recipe for a technology is to construct optimizations that correct for specific deviations without increasing variations in other geometries. As stated in the introduction, the conventional approach is to develop specific recipes for a technology node. Key test patterns are characterized for deviation from target. Final OPC verification is done on full chip layouts generally to test for fatal pinching or bridging. An improved procedure discussed here is to develop recipes on small test cases and then use the OPC verification software to quantify deviation from target and aid in prioritizing regions of largest deviation from target. Recipes for correcting these high deviation regions are then modified until the resulting deviation is acceptable, at which time the full test chip undergoes another OPC verification cycle. This iterative process continues until fatal OPC and MRC errors are eliminated and CD distributions are within lithographic and mask making specification across the entire layout. Fig. 2 shows a schematic for recipe development using OPC verification tools.

An obvious method to compare the effect of multiple recipes on across-chip performance is to plot the measured distributions and compare ranges or standard deviations. While useful for passing or failing a recipe vs. specifications, looking at distributions lends no insight into how specific structures are affected by the application of a new recipe. Fig. 3 shows histograms of the measured CD by bin counts resulting from applying recipe “A” and “C”. Comparing the two distributions, it is obvious that Recipe “C” has a less pronounced high CD deviation tail but worse performance at low CD. In particular, there is a noticeable hump in the data not present for the Recipe “A” mask. It is not obvious which structures were adversely affected by Recipe “C” without inspecting a relatively large sample of sites in the -4 to -6 nm range. It is useful to have a method for easily finding such sites since the recipe developer would need to improve the OPC treatment in those regions.

A more complete approach is to also compute the site by site differences. Suppose we have 3 recipes. All three are used to generate a mask and their CD across chip uniformities are quantified using a verification program such as SiVL™ (Synopsys). The distribution of linewidths for each recipe can be measured with this tool. In addition, we can compute the distribution of the absolute deviations from targets: For example, suppose CD_{xy} is the linewidth measurement centered at coordinates x,y resulting from applying recipe j . Let’s define m_{ij} as the difference in absolute deviations resulting from applying the recipes at the same location:

$$m_{xy}|_{ij} = |CD_{xy} - CD_{xyTarget}|_{Recipe j} - |CD_{xy} - CD_{xyTarget}|_{Recipe i} \quad (1)$$

For any two recipes, we can compute the distribution of m_{xy} . Values of m_{xy} close to 0 are those locations whose accuracy to printed CD were the same between the two recipes. Negative values of m_{xy} represent locations where deviation from target was greater for recipe i than j . Conversely, large positive values represent locations that were

approaches. Outliers on measurement versus target plots are often clusters of similar geometries which require recipe modification.

This approach can be used on large mask layouts or smaller cutouts so various recipes can be compared prior to OPC verification. We will review the results of OPC recipe characterization using SiVL applied to a 65nm alternating phase shift (altPSM) test device.

significantly improved by i compared to recipe j . When comparing the performance of two recipes, the tails of m_{ij} can be inspected to determine which sites were most affected by changing from recipe i to j .

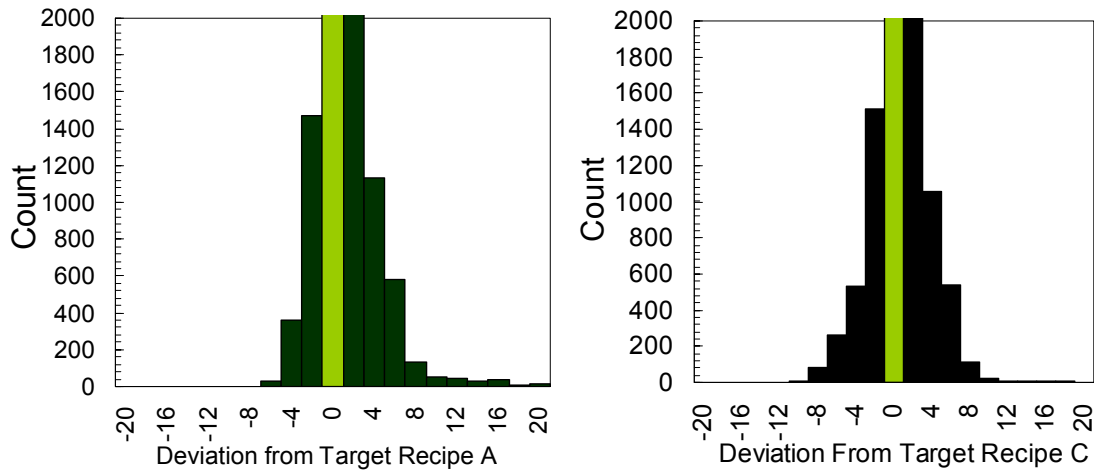


Fig. 3 Resulting histogram of gate CD results from a) Recipe “A” and b) Recipe “C”. The green bar represents all locations where the measured CD was target ± 1 nm.

Consequently, an obvious benefit of constructing tables of site by site recipe differences is that these differences can be sorted. Suppose recipe j is a modified version of recipe i . An inspection of the largest positive value of $m_{xy}|_{ij}$ quickly shows the locations at which the mask was most improved by using recipe j compared to recipe i . Conversely, large negative values show regions which were made worse by the recipe change.

We can better visualize recipe performance by constructing a triangular recipe performance matrix:

$CD_{xy} - CD_{xyTarget} _{Recipe\ i}$	
$m_{xy} _{ij}$	$CD_{xy} - CD_{xyTarget} _{Recipe\ j}$

Note that the diagonal elements represent a metric for the deviation from target of a particular recipe and the off diagonal elements a comparison of the effect of recipe i compared to recipe j . For a relatively small number of recipes, the elements of the matrix could be the histograms themselves (as will be shown in the next section), whereas a matrix of summary statistics is more useful for comparing larger numbers of recipes. This provides an excellent description of the effect for changing recipes.

The formalism shown above is useful for determining which locations have been altered the most by changing recipes. It is of course important to judge the merits of one recipe versus another for generating corrections. Constructing the following recipe comparison matrices is useful for this purpose:

1. "Average deviation" in which the diagonal elements are the average absolute deviation from target for each target. The off-diagonal elements are the difference between the absolute deviations from target of the row recipe minus the absolute deviation from target of the column recipe on a site by site basis.

2. "Standard deviation" in which the diagonal elements are the standard deviation of errors-from-target for each recipe and the off-diagonals are the ratio of the squares of the standard deviations (the variances) of the row recipe to the column recipe.
3. A "skew table". Skew is useful to quantify the symmetry of a distribution. It is given by:

$$skew = \frac{n}{(n-1)(n-2)} \sum \left(\frac{x_i - \bar{x}}{s} \right)^3 \quad (2)$$

Skew is zero for a balanced distribution, negative for a distribution with a left tail and positive for one with a high tail. A skew table shows the asymmetry of the deviation from target CD for each recipe along the diagonal. The off-diagonal elements would have the ratio of the skew for the row recipe. If the off-diagonal element is greater than 1, then the row recipe has more of its distribution in a tail than the column recipe. Whether the difference is due to a change in the low or high tail can be inferred from the sign of the skew for that recipe in the diagonal.

In the next section, we will show how histograms of site by site deviation from target can be used to understand recipe differences. Also, we will show how recipe comparison matrices can be used to infer differences among different recipes. Note that the standard deviation comparison matrix is unorthodox in one respect. Dimensions of diagonal elements are in linewidths such as nanometers. The off-diagonal elements are dimensionless.

3. Approach

The efficient use of OPC software to optimize recipe creation requires that these operations be linked with rapid feedback. To accomplish this, mask generation via Proteus and OPC characterization using SiVL were integrated using flexible scripts. Furthermore, an "Autorun" version of SiVL was developed in which detected errors are automatically loaded into an integrated MySQL™ database (MySQL AB, Uppsala, Sweden) and prioritized according to user specified criteria. Contours and error markers for a user selectable number of errors of each category are automatically

computed in IC WorkBench™ (ICWB, Synopsys). A macro is automatically created so engineers may quickly load SiVL results and the layout in ICWB as "working" document. Fig. 4 is a block diagram of the process.

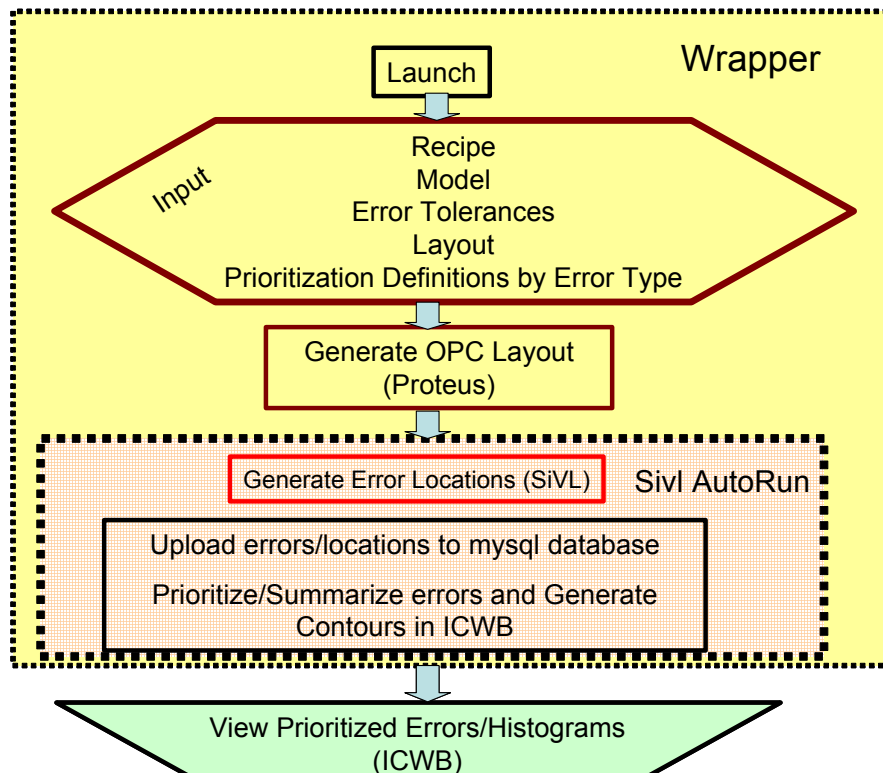


Fig. 4 Function block diagram used in this study.

Integration of Proteus output and the SiVL tool was key to accomplishing the above. A Perl script was written that generates a corrected mask and then launches SiVL. A SiVL flow (AutoRun) was developed to automate post-processing steps of loading the error data into a MySQL™ database, querying the error base for the most significant lithographic errors and generating contours of these prioritized errors. The output from SiVL is a database file and a layout with modeled contours showing the most important errors of user-defined categories. Fig. 5 shows

an example. The key feature of this output is that the most severe errors can be reviewed merely by clicking on a contour label. If desired, smaller test cases can be made from specific features to check the results of various recipe corrections.

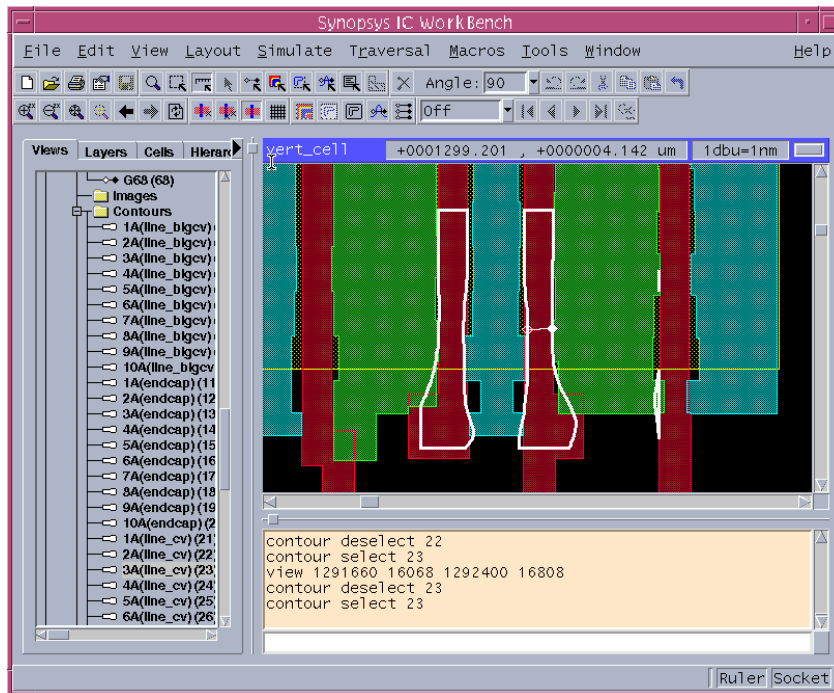


Fig. 5 SiVL AutoRun output showing prioritized errors for various error types.

The test case used for this paper was a 90nm internal test design which was scaled so that the minimum critical dimension on gate was reduced to 65nm. PSM-Create™ (Synopsys) was used to create 0, 180 shifters and the trim mask. An altPSM design was used for this study due to its added complexity for recipe development⁵. The recipes shown in this report were designed to demonstrate the process of recipe optimization and comparison of CD results. Note that the mask layout used was challenging due to “T” and corner structures placed within 50nm of the gate region. A general procedure was to evaluate a recipe by using Proteus to generate the OPC corrections and SiVL to check the layout. The CD from mean tolerance on gate was set to 0 so that all measurements were considered errors.

Proteus, SiVL and the analysis were integrated as described above. Recipe

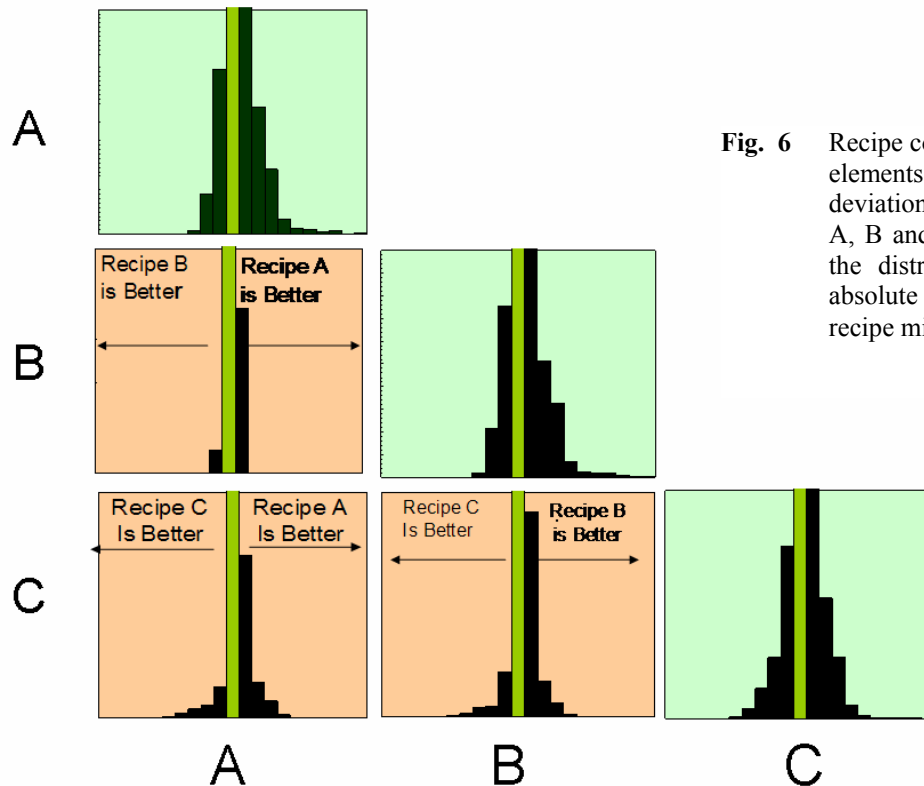


Fig. 6 Recipe comparison matrix. The diagonal elements are histograms of CD deviations resulting from using recipes A, B and C. Off-diagonal elements are the distributions of the differences in absolute deviations between the row recipe minus the column recipe.

modifications were then implemented in an effort to eliminate the tails of the CD distribution on active. The mask generation via Proteus and automatic verification processes were then repeated.

After several recipe iterations had been completed, a MySQL query program was written to combine errors at the same location for any two recipe combinations. Pair wise comparison tables were constructed and the relevant statistics were computed and summarized in tabular form shown in the next section.

4. Results

The method outlined above was used to analyze 3 OPC recipes for a 65nm alternative PSM target design. CD distributions for two of the recipes, A and C were already shown in Fig. 3. Fig. 6 shows the resulting recipe comparison histogram matrix. Along the diagonal are shown the distribution of $CD - CD_{\text{target}}$ for a particular recipe. The off-diagonal elements show histograms of $m_{xy}|_{ij}$, or the site-by-site differences in CD to target between recipes defining the row and column. Note that all axes are identical for all plots and that the lighter (green) bars indicate those sites at which there was no difference in printing accuracy between the two recipes. By looking along the diagonal at the histograms of $CD - \text{Target}$, it is clear that Recipe C has a smaller high end tail. No obvious difference between Recipe A and B is evident. However, the off diagonal histogram of $m_{xy}|_{AB}$, or the difference in CD to target between A and B shows that while most sites were unaffected by the recipe change, recipe A was closer to target by 2 nm at many locations. Additionally there were 6 sites that were closer to target by 6nm, though the scale hides these cases. This shows the value of examining site by site pair differences. More interesting are comparisons between Recipe C and Recipes A and B. The effect of clipping the high end tail is visible from the distribution to the left of the lighter green “No Difference” bar. However, there were many sites whose CD to target worsened with Recipe C as shown by the distribution to the right of the green bar. Fig. 7 shows a magnification of this histogram. An obvious advantage of tabulating m_{AB} in a database is that these differences can be easily sorted and displayed. For example, Fig. 8 shows a snapshot of a location that was most improved by Recipe C compared in Recipe A. Conversely, the lower left shows one of the locations that had larger deviation from target by using Recipe C compared to Recipe A. A key point is that this methodology allows the user to prioritize not only geometries that were improved by recipe changes, but also those that were worsened by the change.

A seven recipe comparison was also done in which three of the recipes were the same A, B and C mentioned above. One of the recipes (No OPC) had no OPC performed on it. Recipe comparison matrices were formulated to summarize CD to target (Table 1), CD to target standard deviation (Table 3) and skew (Table 2). By inspecting the diagonal in Table 1 we see that the deviation from target was greatest for the No OPC case, as expected. Recipe improvement is evident going down the diagonal in smaller increments with the exception of Recipe C and iii in which the standard deviations were the same. Negative off-diagonal elements less than 1 means that the absolute deviation from target on a site by site basis was smaller for the row recipe than for the column recipe. The off-diagonal value of Recipe C and iii indicate that there was no difference in the variation in CD to target, assuming normal distributions.

Table 2 tabulates the estimated 3-sigma variation of $CD - CD_{\text{Target}}$ for each recipe along matrix diagonals,

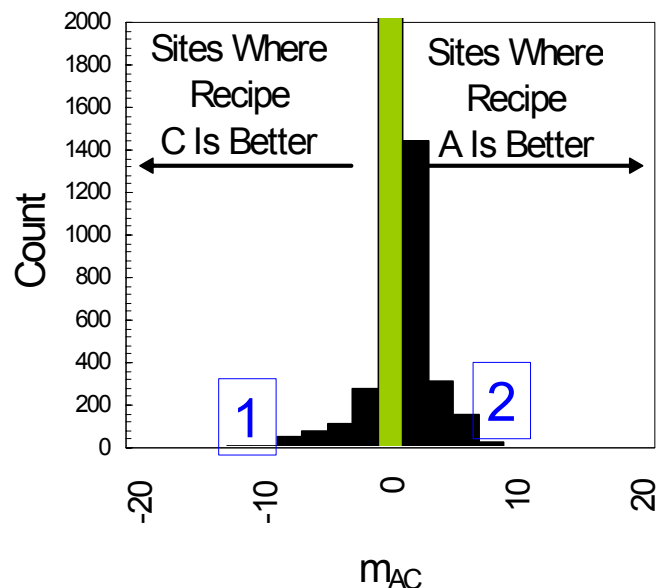


Fig. 7 Histogram of the difference in absolute deviation from target for Recipe C – Recipe A. The point marked 1 is the site at which Recipe C improved CD the most. Point 2 is a location at which Recipe

and the ratio [row recipe variance / column recipe variance] on the off-diagonals. Note that the off diagonal elements in Table 2 are closely related to the F ratio described in standard statistics texts.⁶

Table 3 summarizes skew of the various recipes along the diagonal and the ratio of skew for off-diagonal elements. For example, the skew without OPC is rather small. Since the standard deviation is large, this implies that without OPC the data are relatively balance around the average $CD - CD_{target}$. On the other hand, recipes I, ii, A, B show very large high end tails. Recipe C and iii have fewer measurement sites on the high tail end. Note that Recipe C has a ratio less than unity for all combinations except the No OPC case. In practice, a high skew may lead us to a class of features showing a similar problem to address.

The best overall recipe choice is derived by considering all metrics. The No OPC case is dismissed immediately due to its large variance from target. Recipes C and iii show no difference in their standard deviations or ratio of variances. However, there is a small difference in the ratio of the skews (see Table 3). Consequently, Recipe C appears to be the best recipe of the seven test recipes considered.

4. Conclusions

An integrated approach to recipe development has been demonstrated using commercially available OPC design, OPC verification and layout visualization tools. Once a recipe is created, it is used to design a OPC corrected mask. An OPC verification is automatically run. Any errors are automatically prioritized and contours generated for a user-selectable number of errors. This allows a recipe development team to rapidly prioritize which structures to optimize.

A new method was developed to quantify the accuracy to target between recipes. It is based on pair wise differences to target for the same sites of all two recipe combinations. Based on the distribution of pair wise differences to target, a recipe comparison matrix is shown to quantify relative differences between recipes. Using this approach, differences between recipes can be quantified. Site by site pair wise comparisons allow developers to repair structures made worse by recipes that generally show improved performance.

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- ⁶The F ratio is typically tabulated as the larger variance divided by the smaller variance. See for example G. Box, W. Hunter, S. Hunter, "Statistics for Experimenters", Wiley and Sons, New York (1978)

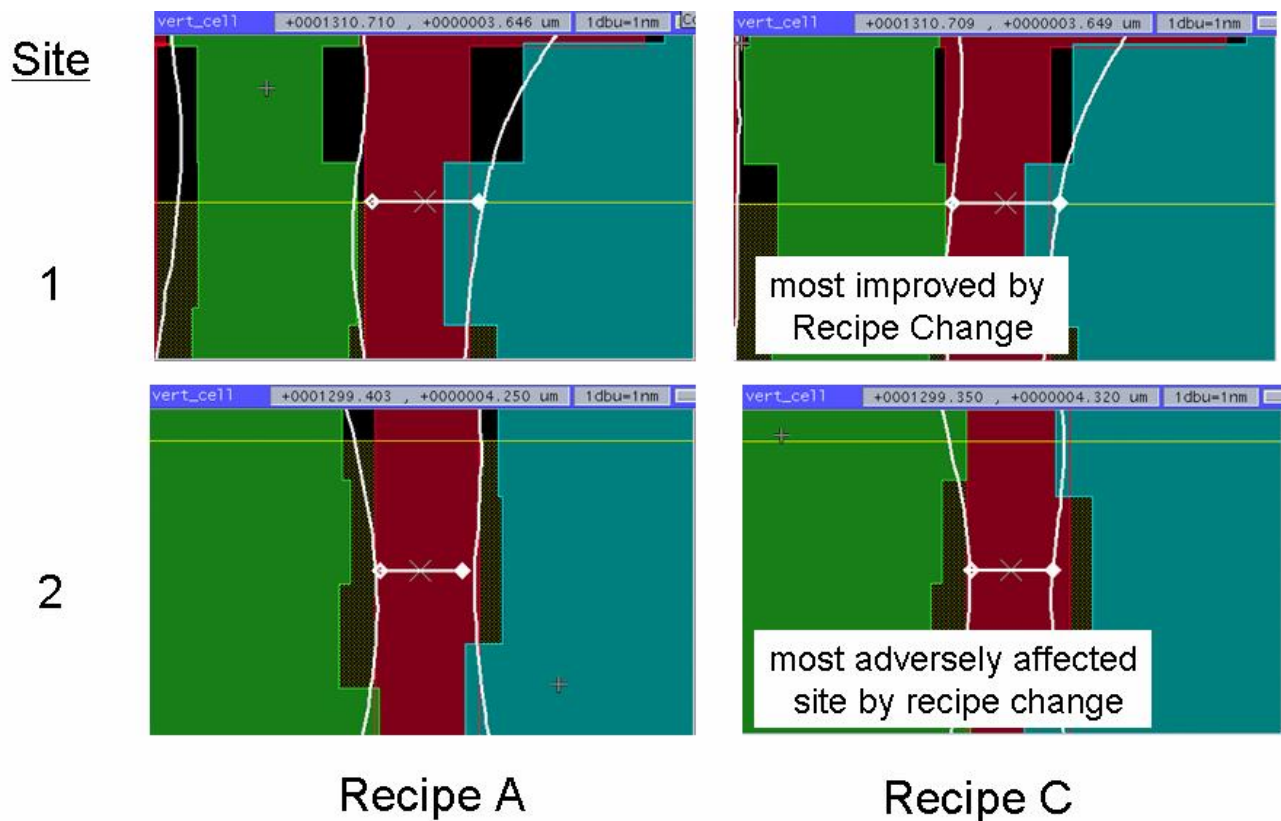


Fig. 8 Two sites that were most affected by changing from Recipe A to Recipe C. Site A was significantly improved by Recipe C while site 2 had an unintended interaction leading to worse CD to target deviation than Recipe A.

Table 1 A recipe comparison matrix for 7 different recipes, including A, B, C shown pictorially in Fig. 5. Along the diagonal are the average deviations from target of the individual recipes. Off-diagonal elements are the average deviations from target between the row and column recipe combination. All elements have units of nm.

		Recipe						
Averages	No OPC	-10.6	8.5	8.5	8.7	8.7	8.6	8.6
	i	-8.5	1.1	0.0	0.2	0.2	0.1	0.1
	ii	-8.5	0.0	1.1	0.2	0.1	0.1	0.1
	A	-8.7	-0.2	-0.2	0.8	0.0	-0.1	-0.1
	B	-8.7	-0.2	-0.1	0.0	0.8	-0.1	0.0
	C	-8.6	-0.1	-0.1	0.1	0.1	0.2	0.0
	iii	-8.6	-0.1	-0.1	0.1	0.0	0.0	0.2
	iii	-8.6	-0.1	-0.1	0.1	0.0	0.0	0.2

Table 2 Recipe comparison matrix for standard deviation. The diagonal elements are 3 standard deviations from target for each recipe. The off diagonal elements are the ratio of the squares of the row and column standard deviations. Off diagonal elements are closely related to standard statistical F ratio. Off diagonal elements of 1.00 indicate no difference in distribution spread

		Recipe						
		No OPC	i	ii	A	B	C	iii
$3 \sigma_{\text{Est}}^2 \sigma_R^2 / \sigma_C^2 \text{ Ratio}$	No OPC	25.05	5.24	5.92	6.93	6.85	7.10	7.10
	i	0.19	10.96	1.13	1.33	1.31	1.36	1.36
	ii	0.17	0.89	10.31	1.17	1.16	1.20	1.20
	A	0.14	0.75	0.85	9.50	0.99	1.02	1.03
	B	0.15	0.76	0.86	1.01	9.55	1.04	1.04
	C	0.14	0.74	0.83	0.98	0.97	9.39	1.00
	iii	0.14	0.74	0.83	0.98	0.96	1.00	9.39

Table 3 Recipe comparison matrix for skew. Diagonal elements are those of the indicated recipe. Off-diagonal elements are the ratio of the row to the column skews. A skew greater than unity indicates that the row recipe has a larger tail than the column recipe.

		Recipe						
		No OPC	i	ii	A	B	C	iii
Skew	No OPC	-0.11	-0.03	-0.07	-0.08	-0.09	-0.85	-0.81
	i	-29.04	3.41	2.04	2.43	2.69	25.00	23.92
	ii	-14.18	0.49	1.67	1.19	1.32	12.26	11.73
	A	-12.14	0.41	0.84	1.41	1.11	10.31	9.87
	B	-10.94	0.37	0.76	0.90	1.27	9.28	8.89
	C	-1.18	0.04	0.08	0.10	0.11	0.14	0.96
	iii	-1.23	0.04	0.09	0.10	0.11	1.05	0.14