Standard Cell Partition Size Variance and its Effect on Physical Design

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Abstract

In order to address the challenges of future integrated circuit design, both logic synthesis and physical design will need to be tightly integrated. This includes integrating the circuit structure information produced by logic synthesis with the placement stage of physical design. The first step is to determine the effects of partitioning decisions on placement performance. This paper describes the development of statistical methods to analyze these effects, and experimental results on preliminary data.

1. Introduction

The integrated circuit design problem will be affected by challenges of deep submicron processes as feature sizes continue to shrink. In order to address these challenges, both logic synthesis and physical design will need to be tightly integrated using a controlled design style [1]. Our proposed research concentrates on integrating the circuit structure information produced by logic synthesis with the placement stage of physical design. The first step is to determine the effects of partitioning decisions on placement performance. This paper describes preliminary work on developing methods to analyze these effects.

Physical design starts with a *placement* process to determine the *layout*, or arrangement of the cells on the chip. The placement objectives are to minimize the resultant layout area and the resultant signal propagation delays, and to minimize the time required to complete the placement process. In a typical design, there are usually many more standard cells than macro cells. Thus, before the placement procedure is performed, the standard cells are partitioned into groups, or *domains*, to reduce the total number of components to be initially placed. Because netlists can be modeled by a hypergraph [2], domains are created by applying hypergraph partitioning. The criteria for hypergraph partitioning are to minimize the number of edges between partitions and to have groups of equal sizes (same number of vertices). There appears to be no criteria for number of domains, thus this quantity is often arbitrarily selected. However, the resultant grouping of the standard cells may not be the best arrangement for a given design. Thus, our first area of exploration was the effect of the number of standard cell groupings (domains) on the resultant layout. The hypothesis for our experiment is that the number of domains will affect the resultant layout area and delay, as well as program execution time, for a mixed macro and standard cell placement solution.

2. Method

The hMetis multilevel hypergraph partitioning tool [3] was selected to create domains, while the GAP mixed macro and standard cell placement tool [4] was selected to perform the layout for the resultant netlist partitioning. GAP uses a genetic algorithm to optimize placement. Genetic algorithms are *stochastic*: there are a number of random events that occur during the algorithm operation. Therefore, for a given input, separate runs of the genetic algorithm will produce different outputs for the same input parameters. This implies that one run of GAP for each partitioning result would not produce sufficient data for analysis. Thus, several runs are needed for each group, with statistical tests applied to analyze each data set.

For our experiment, we wanted to determine the effect of varying the number of domains (d) on the resultant placement layout area (A), layout delay (D), and placement execution time (T). Therefore, after generating data (A,D,T) for different values of d, we needed to determine the specific statistical tests that would allow us to test our hypothesis.

2.1. ANOVA

The first task is to determine if variations in the number of domains affected the performance of the placement tool. Thus, the first statistical test that we selected to analyze our data was ANOVA (*ANalysis Of VAriance*). ANOVA models are used to study the relation between a dependent variable and one or more

independent variables [5] - the objective is to determine how differences in the independent variables affect the dependent variable. For our experiment, there is one independent variable (the number of domains *d*) and three dependent variables (area *A*, delay *D*, time *T*). Each independent variable is termed a *factor*, while each value of the variable is called a *level*.

A statistical test has a *null hypothesis* H_0 - this hypothesis is either accepted or rejected, depending on the results of the test. In ANOVA, the null hypothesis H_0 is that the mean responses of a dependent variable are equal for all factor levels of the independent variables.

During the ANOVA procedure, an *F test* is performed which produces a *P-value*. If the P-value is less than or equal to the selected *level of significance* α, then the null hypothesis H_0 is rejected. This indicates that there is strong evidence that a significant relation exists between the dependent variable and at least one independent variable. Otherwise, if the P-value is greater than α, then a significant relation cannot be identified.

2.2. Bonferroni t-test

The F test of ANOVA can identify if there are significant differences between at least two means. However, when comparing more than two means, the F test does not identify the specific means that are significantly different. In order to obtain more detailed information about the differences among the means, multiple comparison tests must be run.

The simplest approach to multiple comparisons is to perform a *t-test* on every pair of means. For a t-test, the null hypothesis is that the means are equal [6]. As with ANOVA, the t-test produces a P-value. If the P-value is less than or equal to the selected level of significance, then there is strong evidence that a significant difference exists between the two means.

However, there is a problem with repeated t-tests. Suppose there are *m* means and each t-test is performed at the level of significance α. Then, there are *m(m-1)/2* pairs to compare, each with a probability α of a *type 1 error* (a false rejection of the null hypothesis). An upper bound on the probability of making at least one type 1 error during the multiple comparisons is shown in Eq. (1).

$$\Pr\{\} = 1 - (1-\alpha)^{\frac{m(m-1)}{2}} \qquad (1)$$

As the number of means increases, this bound approaches 1. The Bonferroni inequality [7] is often used to address this problem. In the *Bonferroni t-test*, the level of significance is divided by the number of means. This ensures that the probability of a type 1 error is no greater than the original level of significance. Therefore, we selected the Bonferroni t-test as our second statistical test.

2.3. Multiple Regression

After the significant relations have been identified, the next step is to identify how variances in the independent variables influence the mean responses of the affected dependent variables. A *multiple regression* model [5] is applied to each dependent variable Y as shown in Eq. (2).

$$Y = b_0 + b_1 X_1 + b_2 X_2 + \cdots + b_n X_n \qquad (2)$$

Each *b* is a regression coefficient, and indicates the change in the mean of the probability distribution of *Y* per unit increase in the associated independent variable *X*. A positive value for *b* indicates a direct relation between *Y* and the independent variable, while a negative value for *b* indicates an inverse relation. Thus, we selected regression analysis as our third statistical test.

3. Experimental results

The mixed macro and standard cell benchmark netlist g2 was used [8] - this netlist contains 17 macro cells, 113 standard cells, and 295 nets. The circuit is very small by contemporary standards, but allowed us to quickly generate data to test our analysis method. A range of values was selected for the number of domains. Since netlist g2 has 113 standard cells, the selected range was *d* = {5,10,15,20} domains. The SAS® program was used to perform the statistical tests [9, 10].

3.1. ANOVA

The ANOVA procedure was run in SAS, with level of significance $\alpha = 0.05$. This is a standard value that is used in many statistical studies and is the default level of significance in SAS. The results are shown in Table 1. Note each P-value is less than the level of significance α=0.05. Thus there is strong evidence that values A, *D*, and *T* are affected by variances in number of domains d.

3.2. Bonferroni t-test

The results of ANOVA showed that the differences between the means for the domain data were shown to be significant, thus a t-test was run in SAS for each pair of means using the Bonferroni correction. Tables 2, 3, and 4 show the results for comparisons of factor levels of number of domains *d*. There is an upper and lower confidence limit for each comparison. If the confidence limits do not include zero, then there is strong evidence that the difference between the means is significant.

For area *A* (Table 2), the confidence limits include zero for all comparisons except *d*=5 and *d*=15. Thus, there is

insufficient evidence that the differences between mean area results for different values of *d* are significant.

For delay *D* (Table 3), the confidence limits include zero for all comparisons except the pairs 5-15 and 5-20. Therefore, there is also insufficient evidence that the differences between mean delay results for different values of *d* are significant.

For time *T* (Table 4), none of the confidence limits include zero for any comparison. In this case, there is strong evidence that differences between mean time results for different values of *d* are significant.

Based on the Bonferroni t-test results, there is insufficient evidence to relate the difference in number of domains to either layout area *A* or layout delay *D*. However, there is strong evidence that the differences in number of domains affect placement time *T*.

3.3. Multiple regression

The results of the Bonferroni t-test indicated that a statistically significant relation existed between time *T* and number of domains *d*. Thus, multiple regression was run in SAS using the regression model for *T* shown in Eq. 3. Regression analysis on the data yielded the values b_0 = 113.802 and b_1 = 5.68599. Since b_1 is positive, there is a direct relation between execution time and number of domains. This means that increasing the number of domains will increase the average program execution time.

$$T = b_0 + b_1 d \qquad (3)$$

4. Discussion

Recall that the hypothesis for our experiment was that the number of domains will affect the resultant layout area and delay, as well as program execution time, for a mixed macro and standard cell placement solution. Our results indicated a direct relationship between number of domains and placement time. This result can be inferred without statistical analysis, since one can assume that a placement tool will take more time to process a large number of domains. However, this result seems to indicate that our statistical approach is valid.

The area and delay results were inconclusive, which is likely due to the small size of netlist g2. Thus, we need to generated data from larger netlists in order to fully test our hypothesis. Hopefully, this will result in conclusive results for layout area and delay with respect to number of domains, and provide the necessary background for further research in determining the effects of partitioning decisions on placement performance.

5. References

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Dependent variable	P-value
A	0.0434
D	0.0099
T	0.0001

Table 1. ANOVA results for number of domains.

Comparison of factor levels for d	Confidence limits	
	Lower	Upper
5 - 10	-3469918	355528
5 - 15	-3836206	-10760
5 - 20	-2945375	1100242
10 - 15	-2227996	1495420
10 - 20	-1340011	2609268
15 - 20	-973723	2975556

Table 2. Bonferroni t-test results for area A.

Comparison of factor levels for d	Confidence limits	
	Lower	Upper
5 - 10	-96283	30936
5 - 15	-136668	-9449
5 - 20	-129974	-2755
10 - 15	-105648	24876
10 - 20	-98954	31570
15 - 20	-58568	71956

Table 3. Bonferroni t-test results for delay D.

Comparison of factor levels for d	Confidence limits	
	Lower	Upper
5 - 10	-26.7864	-23.0136
5 - 15	-59.0864	-55.3136
5 - 20	-85.8258	-81.8242
10 - 15	-34.1864	-30.4136
10 - 20	-60.9258	-56.9242
15 - 20	-28.6258	-24.6242

Table 4. Bonferroni t-test results for time T.