June 1, 1982

TO: Dick Scotson

cc: T. Trumbull
J. Cummins
T. Markwood
T. McDonald

FROM: Paul Cousino

SUBJECT: Selective Paring and Reduction Program

The Selective Paring and Reduction Program which will be a part of the total effort to eliminate weighting is proposed to work as follows.

Sample requested:

300 Salem FF85
300 FFM85 Females 18-34 (Excluding Salem FF85)

Requested returned sample would thus look as follows:

	Male				Female			
Brand	18-24	25-34	35-49	50+	18-24	25-34	35-49	50+
Salem	28	48	55	52	18	29	29	41
Kool					74	79		
Newport					81	34		
Marlboro Menthol					20	11		
All Other Menthol					1	0		

An outgoing sample would be designed using return rates available based on previous experience with switching and return behavior. Using Steve Tucholski's memo and figures which he and I calculated, a suggested sample would be:

	Male				Female			
Brand	18-24	25-34	35-49	50+	18-24	25-34	35-49	50+
Salem	58	75	93	74	42	42	40	52
Kool					171	114		
Newport					187	48		
Marlboro Menthol					47	15		
All Other Menthol					3	0		

Actual Returned Sample

	Male				Female			
Brand	18-24	25-34	35-49	50+	18-24	25-34	35-49	50+
Salem	40	48	55	52	20	30	29	41
Kool					84	109		
Newport					77	34		
Marlboro Menthol					20	11		
All Other Menthol					0	0		

As you can see in this example, the returned sample is not exactly the same as the requested sample. Due to the choosing on Status Code 01 and weighting by expected return/switching rates, no cell is appreciably short. We note, however, that some cells are much larger than expected. For example, Salem 18- to 24-year-old males are 43% higher than expected. When using the returned sample in its current form, shortages (as in Newport 18- to 24-year-old females) are exacerbated by the overages ocurring in other cells (such as Kool 18- to 24-year-old females). The program which I am requesting can be designed in one of two ways. All cells will be reduced or paired to the level of the requested sample or only those cells which are significantly different would be paired. The second method would result in less loss of completed interviews but greater accuracy. The first method may be easier to carry out. Some discussion on this topic may be indicated.

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The returned sample after being passed through the Selective Paring and Reduction Program would look like one of the following two samples:

Sample 1

Brand	Male 18-24	Male 25-34	Male 35-49	Male 50+	Female 18-24	Female 25-34	Female 35-49	Female 50+
Salem	28	48	55	52	18	29	29	41
Kool					74	79		
Newport					78	34		
Marlboro Menthol					20	11		
All Other Menthol					0	0		

Sample 2

Brand	Male 18-24	Male 25-34	Male 35-49	Male 50+	Female 18-24	Female 25-34	Female 35-49	Female 50+
Salem	28	48	55	52	18	30	29	41
Kool					74	79		
Newport					78	34		
Marlboro Menthol					20	11		
All Other Menthol					0	0		

Sample 1 above would be derived by paring the returned sample to the extent that it exactly matches the desired quotas. In Sample 2, however, the program pares only cells that are significantly different. In this example, only one cell is unaffected (females 25-34).

In cases where a cell comes up short of its desired quota, the following procedures will be implemented.

1. If the ratio of desired completes to actual completes is either less than 1.2 ~~1.5~~ or greater than 2.5, the cell will stand short as it is and will not be weighted.
2. If the ratio of desired completes to actual completes is between ~~1.5~~ 1.2 and 2.5 inclusive, and the actual cell is greater than or equal to the sample size divided by the total number of cells in the sample, standard weighting procedures will then be implemented for that cell.
3. In the case of Number 2, but where the actual completes cell is less than ~~the sample divided by total cells~~, the cell will stand as is. (37)

Dick, if you have any questions about this particular program or need to discuss it further (I hope more discussion will be forthcoming), please give me a call.

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National Family Opinion, Inc.

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