Reproducing p-values for sequential designs using SAS

In the Wikipedia the following table for e.g. Pocock boundaries is mentioned:

|  |  |  |
| --- | --- | --- |
| List of *p*-values used at each interim analysis, assuming the overall *p*-value for the trial is 0.05 | | |
| **Number of planned analyses** | **Interim analysis** | ***p*-value threshold** |
| 2 | 1 | 0.0294 |
|  | 2 (final) | 0.0294 |
| 3 | 1 | 0.0221 |
|  | 2 | 0.0221 |
|  | 3 (final) | 0.0221 |
| 4 | 1 | 0.0182 |
|  | 2 | 0.0182 |
|  | 3 | 0.0182 |
|  | 4 (final) | 0.0182 |
| 5 | 1 | 0.0158 |
|  | 2 | 0.0158 |
|  | 3 | 0.0158 |
|  | 4 | 0.0158 |
|  | 5 (final) | 0.0158 |

These can be reproduced as follows:

First observe that the p-values above are for two-sided hypothesis and the p-values are two-sided:

Then in SAS

**proc** **seqdesign** altref=**10**

boundaryscale=pvalue

;

TwoSidedPocock: design method=poc

alt=twosided stop=reject

nstages=**5**

alpha=**0.05** beta=**0.10**

;

**run**;

give a table

| **Boundary Information (p-Value Scale) Null Reference = 0** | | | | | | |
| --- | --- | --- | --- | --- | --- | --- |
| **\_Stage\_** |  | | **Alternative** | | **Boundary Values** | |
| **Information Level** | | **Reference** | | **Lower** | **Upper** |
| **Proportion** | **Actual** | **Lower** | **Upper** | **Alpha** | **Alpha** |
| **1** | 0.2000 | 0.025356 | -1.59237 | 1.59237 | 0.00791 | 0.99209 |
| **2** | 0.4000 | 0.050713 | -2.25195 | 2.25195 | 0.00791 | 0.99209 |
| **3** | 0.6000 | 0.076069 | -2.75807 | 2.75807 | 0.00791 | 0.99209 |
| **4** | 0.8000 | 0.101426 | -3.18474 | 3.18474 | 0.00791 | 0.99209 |
| **5** | 1.0000 | 0.126782 | -3.56065 | 3.56065 | 0.00791 | 0.99209 |

Note that this a one-sided p-value, so this has to be doubled:

2\*0.00791=0.01582