

*Program Name:* **po\_pbibe**

*Language:* SAS

*Objective:* Computation of the Bayesian posterior probability of the hypothesis of individual bioequivalence

*Input:*

N	sample size
EPS	positive constant determining the equivalence range $((1+\varepsilon)^{-1}, 1+\varepsilon)$ specified for individual bioavailability ratios
PI0	minimum value specified under the alternative hypothesis for the probability of observing an individual bioavailability ratio to fall in the range $((1+\varepsilon)^{-1}, 1+\varepsilon)$
ZQ	arithmetic mean of the log-individual bioavailability ratios obtained in the sample
S	sample mean of the log-bioavailability ratios
TOL	tolerance for the numerical error entailed in determining the solution to equation (9.32) for any value of $\sigma$ used as an abscissa in the integration formula
SW	width of the search grid used for finding an interval which contains the exact value of the solution to (9.32)
IHMAX	maximum number of interval-halving steps carried out for improving the accuracy of the solution to (9.32)

*Output:*

N	cf. input list
EPS	" " " "
PI0	" " " "
ZQ	" " " "
S	" " " "
TOL	" " " "
SW	" " " "
IHMAX	" " " "
PO_PBIBE	posterior probability of the alternative hypotheses of individual bioequivalence as computed by means of 96-point Gauss-Legendre quadrature