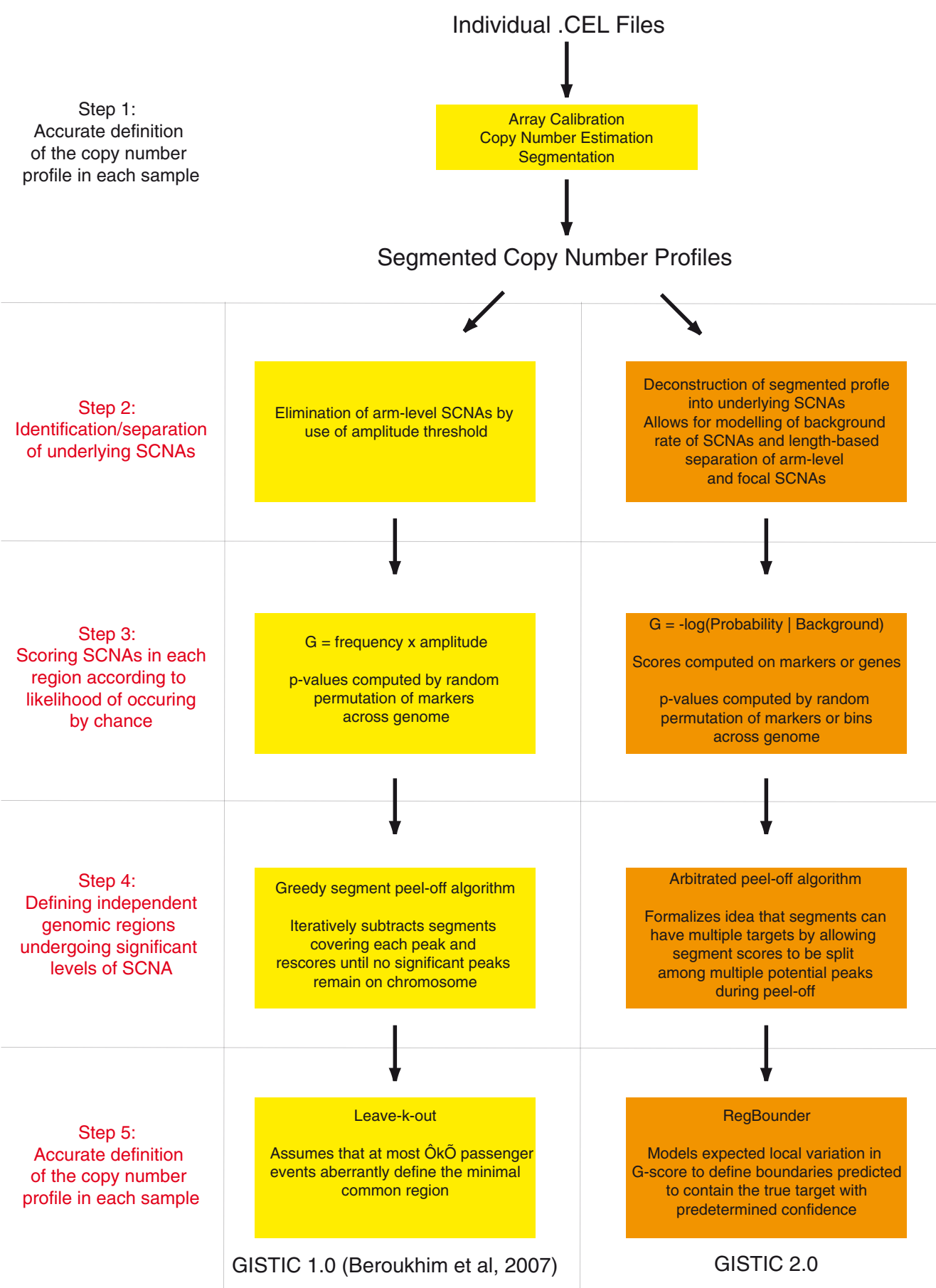
Individual .CEL Files
Step 1:
Accurate definition
of the copy number
profile in each sample
Array Calibration
Copy Number Estimation
Segmentation
Segmented Copy Number Profiles
Step 2:
Identification/separation
of underlying SCNAs
Elimination of arm-level SCNAs by
use of amplitude threshold
Deconstruction of segmented profle
into underlying SCNAs
Allows for modelling of background
rate of SCNAs and length-based
separation of arm-level
and focal SCNAs
Step 3:
Scoring SCNAs in each
region according to
likelihood of occuring
by chance
G = frequency x amplitude
p-values computed by random
permutation of markers
across genome
G = -log(Probability | Background)
Scores computed on markers or genes
p-values computed by random
permutation of markers or bins
across genome
Step 4:
Defining independent
genomic regions
undergoing significant
levels of SCNA
Greedy segment peel-off algorithm
Iteratively subtracts segments
covering each peak and
rescores until no significant peaks
remain on chromosome
Arbitrated peel-off algorithm
Formalizes idea that segments can
have multiple targets by allowing
segment scores to be split
among multiple potential peaks
during peel-off
Step 5:
Accurate definition
of the copy number
profile in each sample
Leave-k-out
Assumes that at most ÔkÕ passenger
events aberrantly define the minimal
common region
RegBounder
Models expected local variation in
G-score to define boundaries predicted
to contain the true target with
predetermined confidence
GISTIC 1.0 (Beroukhim et al, 2007)
GISTIC 2.0