

表 3 每个 peak calling 算法的重要参数

Table 3 Important parameters for each peak calling algorithm

| 算法 | 重要参数 |
|-----------|---|
| Algorithm | Important parameters |
| CCAT | <p>最小得分: 归一化差的最小值 Minimum score: minimum score of normalized difference</p> <p>最小计数: 峰值读取计数的最小值 Minimum count: minimum number of read counts at the peak</p> <p>移动步: 窗口滑动的一步 Moving Step: step of window sliding</p> <p>SlidingWinSize: 滑动窗口的大小 SlidingWinSize: size of sliding window</p> <p>自助通: 在引导过程中传球次数 Bootstrap pass: number of passes in the bootstrapping process</p> |
| MACS | <p>NoLambda: 如果属实, MACS 将使用固定的背景 λ 作为每个峰区本地 λ NoLambda: if True, MACS will use fixed background lambda as local lambda for every peak region</p> <p>NoModel: 是否建立移动模型 NoModel: whether or not to build the shifting model</p> <p>MFold: 在可信度高的富集率 MFOLD 范围内的区域而不是背景区域进行建模 MFold: regions within MFOLD range of high-confidence enrichment ratio against background to build model</p> <p>PValue: P 值的截止峰值检测 PValue: p-value cutoff for peak detection</p> |
| SICER | <p>WindowSize: 扫描基因组宽度的窗口大小 WindowSize: size of the windows to scan the genome width</p> <p>GapSize: islands 间的碱基对的允许间隙 GapSize: allowed gap in base pairs between islands</p> <p>FDR: 错误发现率控制意义 FDR: false discovery rate controlling significance</p> |
| ZINBA | <p>Select model: 指定选择模型 = 假跳过模型选择过程完全可以节省大量时间 Specifying select model = FALSE skips the model selection process altogether and may save a significant amount of time</p> <p>扩展: 平均片段库长度 (选择大小) Extension: average fragment library length (size selected)</p> <p>Win Size: 选择一个更大的窗口大小增加的分析速度, 但降低分辨率和灵敏度来检测丰度 Win Size: Selecting a larger window size increases speed of analysis but decreases resolution and sensitivity to detect enrichment</p> <p>offset: 较小的非零偏移距离的增加的敏感性也增加了计算 burden offset: Smaller non-zero offset distances increase sensitivity but also increase computational burden</p> <p>FDR: FDR = 真正的指定模型使用 FDR 阈值而不是后验概率。这通常会导致更自由的 peak calls。如果为假, 然后利用后验概率通过 1-阈值接近峰。 FDR: FDR = TRUE specifies the model to use the FDR threshold rather than posterior probabilities. This typically results in more liberal peak calls. If false, then uses posterior probability to threshold peaks using 1-threshold.</p> |
| F-seq | <p>特征: 特征长度的长度 Feature Length: feature length</p> <p>阈值: 标准偏差 Threshold: standard deviations</p> |