|  |  |  |  |
| --- | --- | --- | --- |
| Parameter | **DesEq2** | **edgeR** | **Voom/Limma-trend** |
| **Loi** | NB | Poisson (NB) | Normal Distribution |
| **Utilise** | Read Counts² (RC), pas FPKM | RC and FPKM | RC and FPKM |
| **Modèle** | **Generalized Linear Model** | NB models (BCV)  GLM models | Local linear models |
| **Erreur 1 Type** | FP+++ | Type 1 existe (FDR>0.1) | Contrôlée (FDR<0.1) |
| **Tests** | Wald Test  Likelihood ratio Test |  |  |
| **Performance** | + | +++ | ++ |
| **Rapidité** | + | ++ | +++ |
| **Niveau** | Gènes only | Gènes | Gènes end Exons |
| **Défauts** | -Difficult SD estimate  -Shrinkage (different precision for high/low var genes) |  |  |
| **Avantages** | - Contrôle des données aberrantes  - Independent Hypothesis Weighting | -accounts for both biological and technical variability  -can be used with 1 or 2 replicate samples | - Best performance in unequal quantity samples  -Robust to outliers and hypervariable genes  -Can analyse RNA-seq and Microarrays |
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²(only the count values allow assessing the measurement precision correctly)