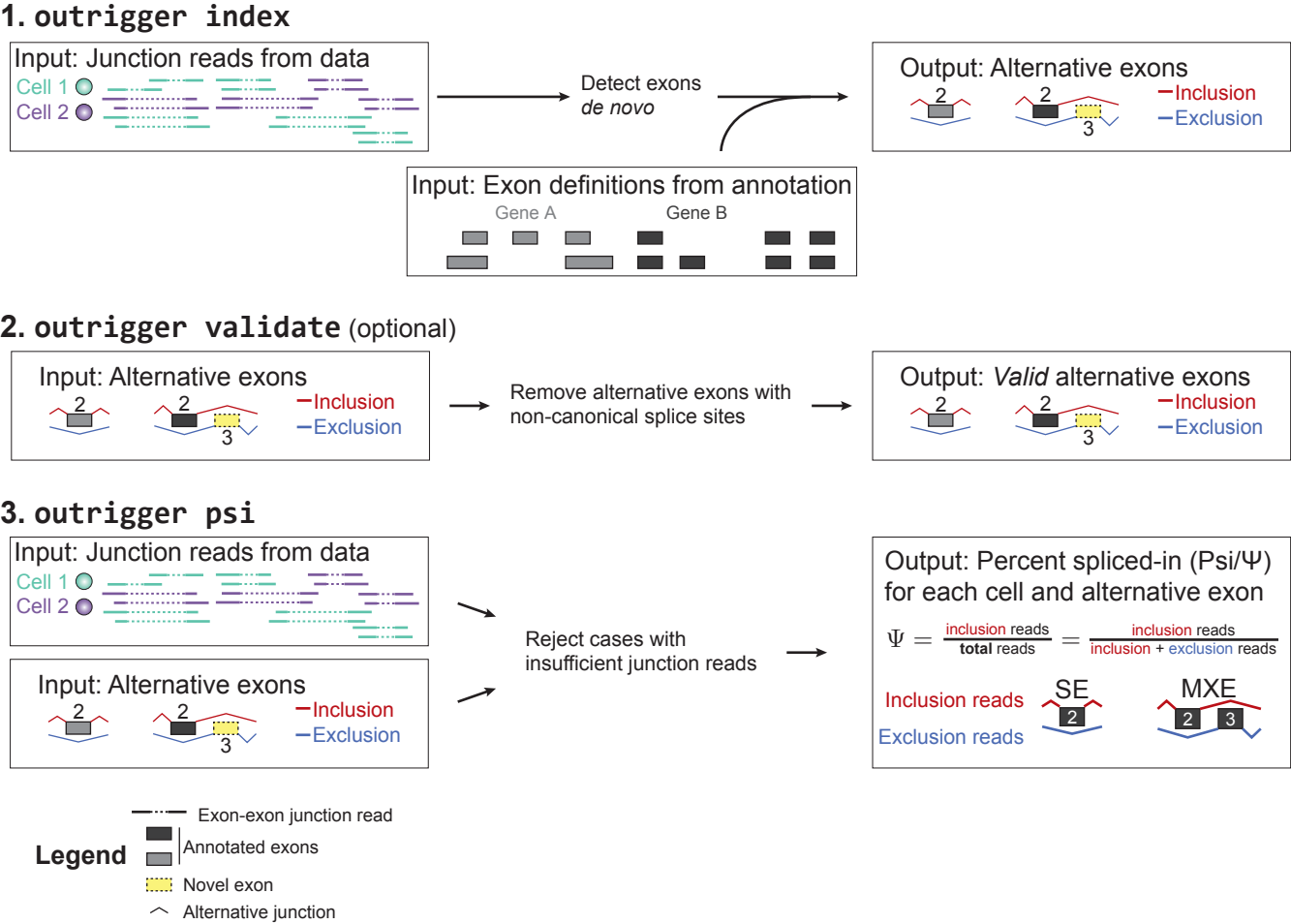
1. outrigger index
Input: Junction reads from data
Cell 1
Cell 2
Detect exons
de novo
Output: Alternative exons
2
2
3
Inclusion
Exclusion
Input: Exon definitions from annotation
Gene A
Gene B
2. outrigger validate (optional)
Input: Alternative exons
2
2
3
Inclusion
Exclusion
Remove alternative exons with
non-canonical splice sites
Output: Valid alternative exons
2
2
3
Inclusion
Exclusion
3. outrigger psi
Input: Junction reads from data
Cell 1
Cell 2
Input: Alternative exons
2
2
3
Inclusion
Exclusion
Reject cases with
insufficient junction reads
Output: Percent spliced-in (Psi/Ψ)
for each cell and alternative exon
Ψ = inclusion reads / total reads = inclusion reads / inclusion + exclusion reads
Inclusion reads
Exclusion reads
SE
2
MXE
2
3
Legend
Exon-exon junction read
Annotated exons
Novel exon
Alternative junction