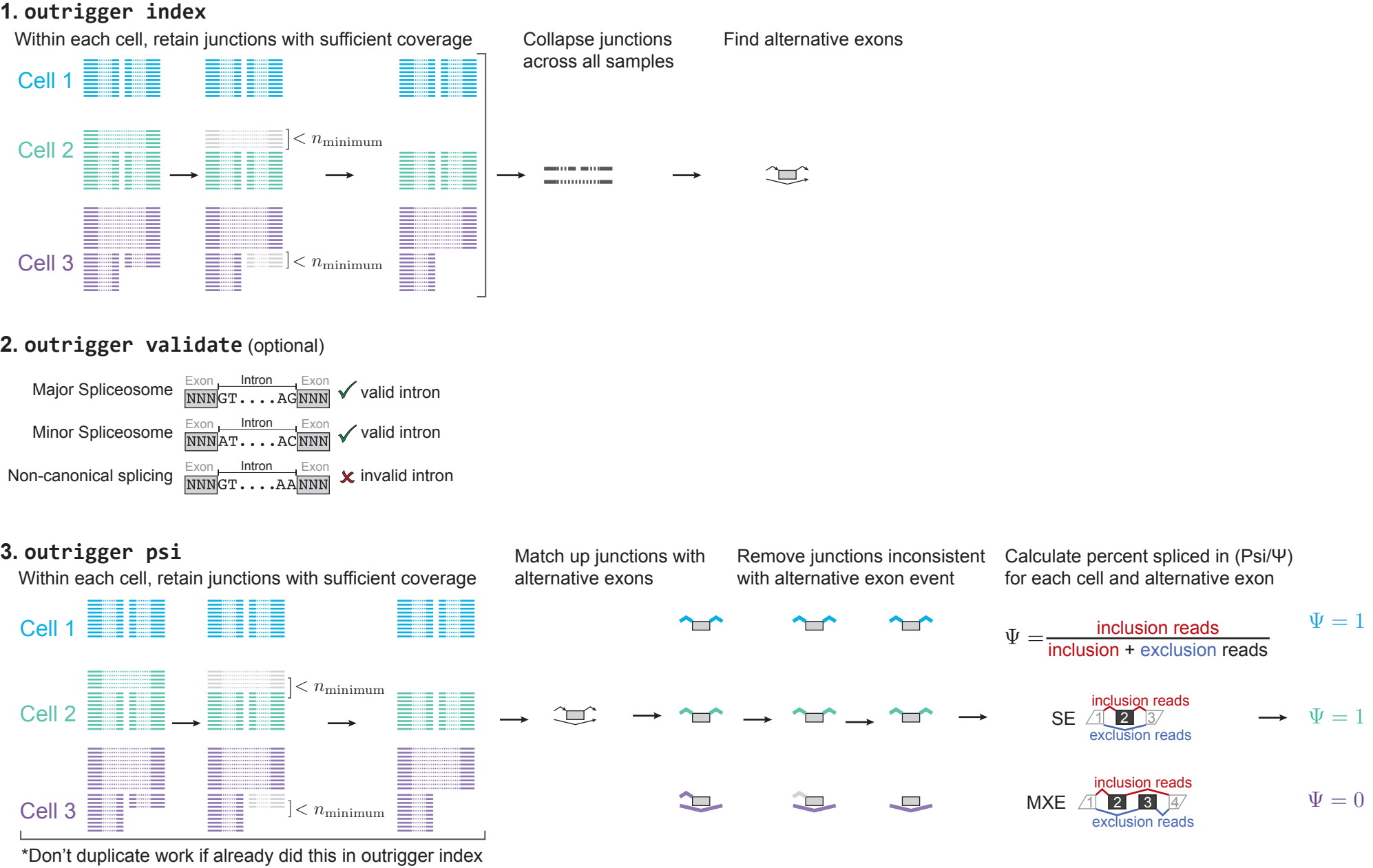
1. outrigger index
Within each cell, retain junctions with sufficient coverage
Collapse junctions across all samples
Find alternative exons
Cell 1
Cell 2
Cell 3
< $n_{minimum}$
< $n_{minimum}$
2. outrigger validate (optional)
Major Spliceosome
Exon
Intron
Exon
NNNGT....AGNNN
valid intron
Minor Spliceosome
NNNAT....ACNNN
valid intron
Non-canonical splicing
NNNGT....AANNN
invalid intron
3. outrigger psi
Within each cell, retain junctions with sufficient coverage
Match up junctions with alternative exons
Remove junctions inconsistent with alternative exon event
Calculate percent spliced in (Psi/Ψ) for each cell and alternative exon
Cell 1
Cell 2
Cell 3
< $n_{minimum}$
< $n_{minimum}$
$\Psi = \frac{\text{inclusion reads}}{\text{inclusion + exclusion reads}}$
$\Psi = 1$
SE
inclusion reads
exclusion reads
$\Psi = 1$
MXE
inclusion reads
exclusion reads
$\Psi = 0$
*Don't duplicate work if already did this in outrigger index