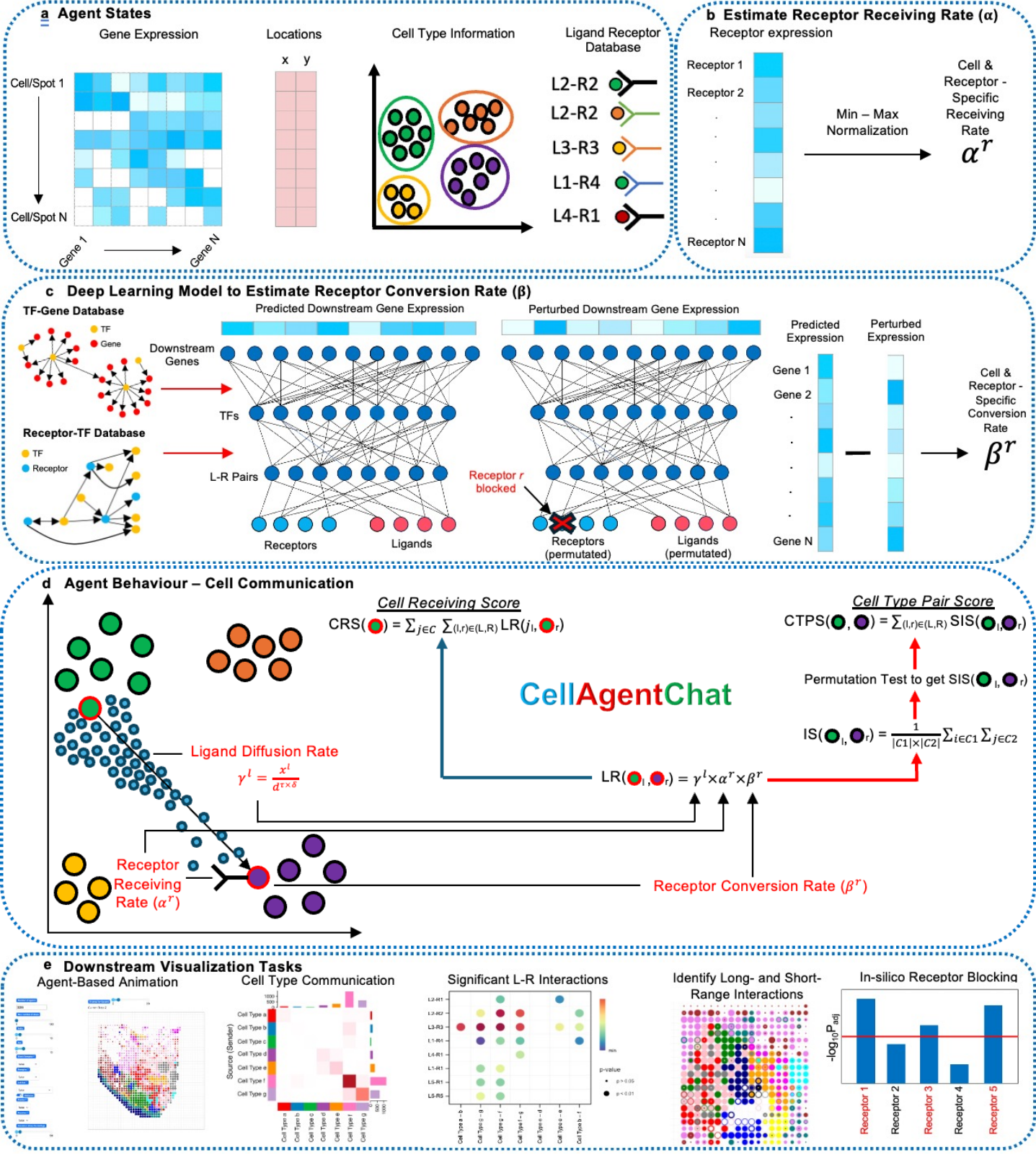
a Agent States
Gene Expression
Locations
Cell Type Information
Ligand Receptor Database
Cell/Spot 1
Cell/Spot N
Gene 1
Gene N
x y
L2-R2
L2-R2
L3-R3
L1-R4
L4-R1
b Estimate Receptor Receiving Rate (α)
Receptor expression
Receptor 1
Receptor 2
Receptor N
Min – Max Normalization
Cell & Receptor - Specific Receiving Rate
$\alpha^r$
c Deep Learning Model to Estimate Receptor Conversion Rate (β)
TF-Gene Database
TF
Gene
Receptor-TF Database
TF
Receptor
Downstream Genes
TFs
L-R Pairs
Receptors
Ligands
Predicted Downstream Gene Expression
Perturbed Downstream Gene Expression
Receptor r blocked
Receptors (permutated)
Ligands (permutated)
Predicted Expression
Perturbed Expression
Gene 1
Gene 2
Gene N
Cell & Receptor - Specific Conversion Rate
$\beta^r$
d Agent Behaviour – Cell Communication
Cell Receiving Score
$CRS(\bullet) = \sum_{j \in C} \sum_{(l,r) \in (L,R)} LR(j_l, \bullet_r)$
CellAgentChat
Cell Type Pair Score
$CTPS(\bullet, \bullet) = \sum_{(l,r) \in (L,R)} SIS(\bullet_l, \bullet_r)$
Permutation Test to get $SIS(\bullet_l, \bullet_r)$
$IS(\bullet_l, \bullet_r) = \frac{1}{|C1| \times |C2|} \sum_{i \in C1} \sum_{j \in C2}$
$LR(\bullet_l, \bullet_r) = \gamma^l \times \alpha^r \times \beta^r$
Ligand Diffusion Rate
$\gamma^l = \frac{x^l}{d^{\tau \times \delta}}$
Receptor Receiving Rate ($\alpha^r$)
Receptor Conversion Rate ($\beta^r$)
e Downstream Visualization Tasks
Agent-Based Animation
Cell Type Communication
Source (Sender)
Cell Type a
Cell Type b
Cell Type c
Cell Type d
Cell Type e
Cell Type f
Cell Type g
Significant L-R Interactions
L2-R1
L2-R2
L3-R3
L1-R4
L4-R1
L1-R1
L5-R1
L5-R5
p-value
Identify Long- and Short-Range Interactions
In-silico Receptor Blocking
$-\log_{10} P_{adj}$
Receptor 1
Receptor 2
Receptor 3
Receptor 4
Receptor 5