Supplemental Video Legends

Supplemental Video 1: The accompanying animation to Fig. 3.

The binding of (green) 150,000 $19x10^{-9}$ m receptors to (red) 150,000 $21x10^{-9}$ m ligands was simulated in 0.1 s increments under different conditions. Cells were represented by spheres with $5x10^{-6}$ m radii and the flat contact area had a radius of $4x10^{-6}$ m. The on-rate was $2.0x10^{5}$ M^{-1} s^{-1}, the off-rate was 0.1 s^{-1}, and the confinement distance was $2x10^{-9}$ m. **(TOP LEFT)** Binding to an immobile receptor was simulated. Membranes were spaced $40x10^{-9}$ m apart. The receptors and their complexes with ligands were immobile while free ligands had diffusion coefficients of $3.0x10^{-14}$ m^2 s^{-1}. **(TOP MIDDLE)** Binding to a mobile receptor was simulated. The receptors now also had diffusion coefficients of $3.0x10^{-14}$ m^2 s^{-1} while complexes had diffusion coefficients of $1.5x10^{-14}$ m^2 s^{-1}. **(TOP RIGHT)** Binding-induced receptor arrest was simulated. Free receptors and ligands had diffusion coefficients of $3.0x10^{-14}$ m^2 s^{-1} while complexes had diffusion coefficients of $0.5x10^{-15}$ m^2 s^{-1}. **(BOTTOM LEFT)** The effects of suboptimal membrane separation were simulated. 100,000 virtual molecules led to a $20x10^{-9}$ instead of $40x10^{-9}$ m starting membrane separation. The σ for the normal curve penalizing the on-rate was $10x10^{-9}$ m. The σ for the normal curve penalizing movement between regions was $10x10^{-9}$ m for the $40x10^{-9}$ m complexes and $5.25x10^{-9}$ m for the $21x10^{-9}$ m ligands. **(BOTTOM MIDDLE)** The effects of a decreased σ on the movement of complexes were simulated. The σ for the normal curve penalizing the movement of complexes between regions was reduced to $5x10^{-9}$ m. **(BOTTOM RIGHT)** The effects of increasing the contribution of receptor/ligand complexes to the membrane separation were simulated. The numbers of virtual molecules were reduced to 20,000.

Supplemental Video 2: The accompanying animation to Fig. 4.

150,000 molecules that moved towards the contact area with a velocity of $0.05x10^{-6}$ m s^{-1} and had diffusion coefficients of $1.0x10^{-15}$ m^2 s^{-1} were simulated for 600 s in 0.1 s increments. Cells were represented by spheres with $5x10^{-6}$ m radii and contact areas were either curved or flat with radii of $4x10^{-6}$ m. The curved contact area was divided into 10 rings of 20 sectors. The flat contact areas were divided into 20x20 grids of square regions. Each region was allowed to contain up to 6250 molecules. The locations of molecules are shown when there was directed movement towards a **(LEFT)** curved or **(MIDDLE)** flat contact area where the targets were centered at the middle of the contact area and normally distributed with a σ of $0.1x10^{-6}$ m. **(RIGHT)** The locations of molecules are shown when there was directed movement towards a flat contact area where the targets were centered $3.5x10^{-6}$ m away from the middle of the $4x10^{-6}$ m contact area and were normally distributed with a σ of $0.5x10^{-6}$ m.

Supplemental Video 3: The accompanying animation to Fig. 5.

The same conditions used in Fig. 5 were used. The locations of **(TOP RED)** MHC complexes with off-rates of 0.02 s^{-1}, **(TOP GREEN)** MHC complexes with off-rates of 0.2 s^{-1}, **(TOP BLUE)** MHC complexes with off-rates of 2.0 s^{-1}, **(LEFT RED)** ICAM-1, **(LEFT BLUE)** CD48, **(RIGHT RED)** LFA-1, **(RIGHT GREEN)** TCRs and **(RIGHT BLUE)** CD2 are shown.