Note: anything with "" isn't a full variable name, but just part of the variable name.

Variable Name in Code	Definition
Common	
mu	Viscosity of fluid
a	Cell/Sphere radius
d	Critical distance
L	Length of flow chamber
b	Height of flow chamber
w	Width of flow chamber
CCD_FPS	Frames per second (FPS) of camera used to record videos for Trackmate
y	Distance from center of cell/sphere to chamber floor
speed_const	Ratio for calculating relative surface velocity of cells, interpolated/extrapolated from Goldman and Brenner part II, Table 3
stop_dist	Stopping criteria distance (µm)
Q_nc	User-inputted flow rate (µL/hr)
Q	User-inputted flow rate (pm^3/s)
Module 0	
spec_site_density	User-inputted site density or densities (sites/$µm^2$) for a specific receptor-ligand bond
nonspec_site_density	User-inputted site density or densities (sites/$µm^2$) for a non-specific receptor-ligand bond
spec_force	List of force(s) (pN) used in experiments for specific bond
nonspec_force	Force(s) (pN) used in experiments for non-specific bond, calculated from user-inputted flow rates (Q)
nonspec_spots_files	User-named "spots in track statistics" csv files obtained from Trackmate for non-specific bond

nonspec_track_files	User-named "track statistics" csv files obtained from Trackmate for non-specific bond
spec_spots_files	User-named "spots in track statistics" csv files obtained from Trackmate for non-specific bond
spec_track_files	User-named "track statistics" csv files obtained from Trackmate for non-specific bond
nonspec_bond_times	Average bond lifetimes, for each pair of "track statistics" and "spots in track statistics" files, of cells in nonspecific bonds
nonspec_tmin	Average bond lifetime for all non-specific bonds recorded
spec_bond_times	Average bond lifetimes, for each pair of "track statistics" and "spots in track statistics" files, of cells in nonspecific bonds
spec_tmin	Average bond lifetime for all specific bonds recorded, to be used as the stopping criteria time if it is greater than nonspec_tmin
files	User-inputted "spots in track statistics" files
m_l_list	User-inputted site densities (if applicable)
C_l_list	User-inputted coating concentrations (if applicable)
bond_times	Average bond lifetimes for each set of flow rate and coating concentration (C_l) or site density (m_l)
lifetime_bin_vals	Normalized bond lifetimes, used for comparing the lifetime distributions for 2 different C_l or m_l
Modules 1/2	
track_data	User-inputted "track statistics" file(s)
spots_data	User-inputted "spots in track statistics" file(s)
coating_concs	User-inputted C_l values
shear_rates	Newtonian shear rate of fluid for input flow rates (1/s)

forces	Applied tensile force(s) (pN) used in experiments
tmin_input	Non-specific bond lifetime
koff_avg_vals	k_{off} values, averaged across all trials for one flow rate and C_l or m_l
koff_vals_each_trial	Average k_{off} values for each trial
"error"	Standard error of the mean
NbNT_vals	N_b/N_T values when there is only one trial
k_b	Boltzmann constant, defaulted at 0.0138 units (energy/time)
T	Temperature, defaulted at 310.15 K
"s"	Parameters for slip model fitting
"cs"	Parameters for catch-slip model fitting
U_hd_vals	Hydrodynamic velocities (U_{hd}) for each bound cell
U_cell_vals	Rolling velocities (U_{cell}) for each bound cell
u_f_vals	Critical velocities for each flow rate
m_r	Cell/sphere receptor site density (sites/μm^2)
N_T_vals	Optimized values for N_T for each flow rate
kplus_vals	k_+ for all flow rates and site densities
D	User-inputted sum of surface diffusivities
alpha	User-inputted reactive radius around receptor
Pe_vals	Peclet number for each condition
Nu_vals	Nusselt number for each condition
lambda_vals	Dimensionless duration time for each condition
kin_vals	k_{in} for each m_l
kin_avg	k_{in} averaged across all site densities
kplus_star_vals	k_+^* for all flow rates and site densities,

	averaged across all trials under each condition
kplus_star_avg	k_+^* for each trial under each condition
"fit_vals"	Values obtained from nonlinear curve fitting
P	Probability of binding event between receptor and ligand (curve fitting parameter)
A_c	Contact area between receptor and ligand (curve fitting parameter)