Requirement of An Allosteric Kinetics of NMDA Receptors for
Spike-Timing-Dependent Plasticity
Hidetoshi Urakubo, Minoru Honda, Robert C Froemke, and Shinya Kuroda
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# Supplementary Information

**Contents**

## Preface

The STDP model consists of the postsynaptic membrane potential model (**Part A**), the postsynaptic signaling cascades model (**Part B**) and the AMPAR trafficking model (**Part C**). The postsynaptic membrane potential model consists of a postsynaptic neuron model and pre- and postsynaptic stimulation models, and the postsynaptic signaling cascades model consists of $Ca^{2+}$ influx/removal model and the intracellular signaling cascades model. All simulations were executed on the GENESIS simulator with kinetikit interface (Bhalla and Iyengar, 1999), and stimulations were run after 500 s-pre-run to reach an equilibrium state. Throughout the simulations, the exponential Euler method with inhomogeneous and adaptive integration time step was used for stable and precise computation. The constructed programs are available for download at http://www.kurodalab.org/info/STDP/index.html. All details of the model are stated in the following sections.

## Part A: Modeling of Postsynaptic Membrane Potential   (Figure 1A)
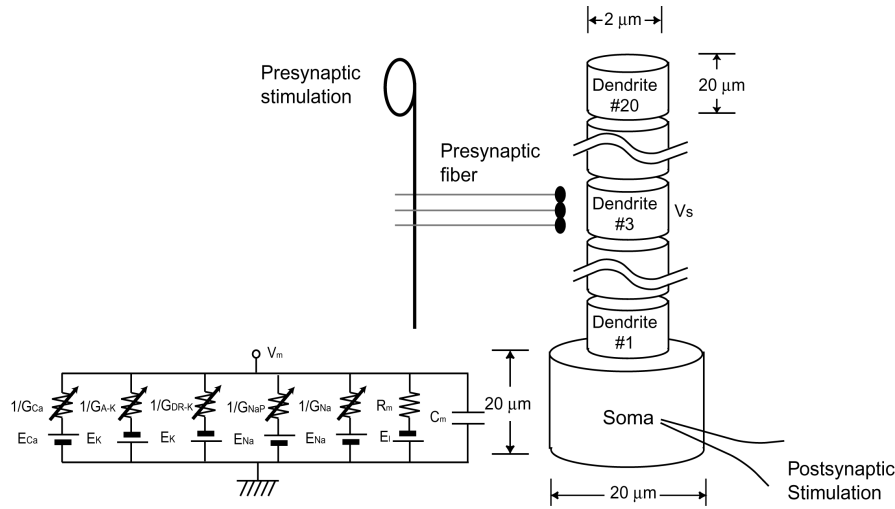
## 1. Postsynaptic Neuron



**Figure SI1**

We constructed a multi-compartment model of a postsynaptic neuron with Hodgkin-Huxley like channel kinetics, and estimated membrane potential in responses to pre- and postsynaptic stimulation on the basis of rat hippocampal CA1 neurons (**Figure SI1**) (Migliore et al., 1999; Poirazi et al., 2003).   In experiments, a presynaptic stimulus depolarizes a postsynaptic site, whereas a postsynaptic spike, triggered by current injection to soma, backwardly propagates into dendrites and depolarizes the postsynaptic site.   NMDARs and VGCCs at the synaptic site detect the depolarization $V_s$ and determine the postsynaptic $Ca^{2+}$ influx.   To model these phenomena, one somatic and 20 dendritic compartments were sequentially connected with the indicated lengths and diameters (**Figure SI1**).   Then spike-generating $Na^+$, persistent $Na^+$, delayed rectifier $K^+$, A-type $K^+$ and L-type voltage gated $Ca^{2+}$ channels were inserted with a variety of densities (see sections 1.1 – 1.4). The synaptic site was assumed to be 60 $\mu$m apart from the soma (3$^{rd}$ dendritic compartment from the soma).   We omitted a compartment representing the postsynaptic spine in the present study, because membrane potentials of the postsynaptic spine and the parent dendrite were almost the same in our preliminary simulation.

The passive properties of the model neuron were as follows.   Intracellular resistivity $R_i$ was 0.15 k$\Omega$cm, membrane resistivity $R_m$ was 28 k$\Omega$cm$^2$ for axon and soma (14 k$\Omega$cm$^2$, for dendrites), and membrane capacitance $C_m$ was $1 \times 10^3$ nF/cm$^2$ for axon and soma ($2 \times 10^3$ nF/cm$^2$ for dendrites).   These parameters gave a

membrane potential decay constant of 28 × 10$^{-3}$ s.   The equilibrium potential of leak channels $E_m$ was adjusted to maintain a –65-mV resting membrane potential for each compartment.   All data were taken from the published literature (Migliore et al., 1999; Golding et al., 2001; Poirazi et al., 2003).

Kinetics and distributions of spike-generating Na$^+$, persistent Na$^+$, delayed rectifier K$^+$, A-type K$^+$, and L-type voltage gated Ca$^{2+}$ channels, as well as kinetics of pre- and postsynaptic stimulation, are described in the following subsections.   The equilibrium potentials of Na$^+$ channels $E_{Na}$, K$^+$ channels $E_K$, AMPAR channels $E_{AMPAR}$, and NMDAR channels $E_{NMDAR}$ were 55 mV, –90 mV, 0mV and 0mV, respectively. Time, voltage, conductance and current units in the subsections are 's', 'mV', 'mS/cm$^2$' and 'μA/cm$^2$', respectively.

## 1.1 Spike-Generating Na$^+$ Current $I_{Na}$
Spike-generating Na$^+$ channel kinetics for $I_{Na}$ are given by

$$I_{Na}(t,V) = \bar{g}_{Na} m^2 h i (E_{Na} - V),$$

$$\frac{dm}{dt} = \frac{1}{5 \times 10^{-5}} \left[ \frac{1}{1 + \exp(-(V+40)/3)} - m \right],$$

$$\frac{dh}{dt} = \frac{1}{5 \times 10^{-4}} \left[ \frac{1}{1 + \exp((V+45)/3)} - h \right],$$

$$\frac{di}{dt} = \frac{1}{\tau_i} \left[ \frac{1 + Na_{att} \cdot \exp((V+60)/2)}{1 + \exp((V+60)/2)} - i \right],$$

$$\tau_i = \max \left[ \frac{\exp(0.08897(V+60))}{0.3 \left[ 1 + \exp(0.4448(V+60)) \right]}, 3 \times 10^{-3} \right],$$

where $\bar{g}_{Na}$ is the peak conductance density, $m, h$ and $i$ are the gate functions of activation, inactivation and slow inactivation, respectively, and $Na_{att}$ is the dendritic inactivation factor in repetitive spiking.   The gate function $i$ represents attenuation of spike amplitudes in high frequency bursts, which has been experimentally shown to be small at the soma and high in distal dendrites (Migliore, 1996).   Here, $\bar{g}_{Na}$ = 7 mS/cm$^2$ for soma and dendrites, and $Na_{att}$ is defined by

$$Na_{att} = \begin{cases} 0.95 & (0 \leq d < 50) \\ -2.6 \times 10^{-3} d + 1.08 & (50 < d \leq 300) \\ 0.30 & (300 < d) \end{cases},$$

where $d$ (μm) is the dendritic distance from the soma. The kinetics and distributions were taken from the literature (Migliore et al., 1999; Poirazi et al., 2003).

## 1.2 Delayed-Rectifier K$^+$ Current $I_{DR-K}$
Delayed-rectifier K$^+$ channel kinetics for $I_{DR-K}$ are given by

$$I_{\text{DR-K}}(t,V) = \overline{g}_{\text{DR-K}} m^2 (E_{\text{K}} - V),$$

$$\frac{dm}{dt} = \begin{cases} \dfrac{1}{3.5 \times 10^{-3}} \left[ \dfrac{1}{1 + \exp(-(V + 46.3)/3)} - m \right] & \text{for soma} \\[3ex] \dfrac{1}{2.2 \times 10^{-3}} \left[ \dfrac{1}{1 + \exp(-(V + 42)/2)} - m \right] & \text{for dendrite} \end{cases},$$

where $\overline{g}_{\text{DR-K}}$ is the peak conductance density. Here, $\overline{g}_{\text{DR-K}}$ were 1.4 mS/cm$^2$ and 0.867 mS/cm$^2$ for soma and dendrites, respectively (Poirazi et al., 2003).


## 1.3 A-Type K$^+$ Current $I_{\text{A-K}}$

A-type K$^+$ channel kinetics of proximal dendrites (under 100 μm from soma) for $I_{\text{A-Kprox}}$ is given by

$$I_{\text{A-Kprox}}(t,V) = \overline{g}_{\text{A-K}} m h (E_{\text{K}} - V),$$

$$\frac{dm}{dt} = \frac{0.25(1+\alpha)}{\beta \times 10^{-3}} \left[ \frac{1}{1+\alpha} - m \right],$$

$$\alpha = \exp\left[0.03707 k (V - 11)\right],$$

$$\beta = \exp\left[0.02039 k (V - 11)\right],$$

$$k = -1.5 - 1\big/\left(1 + \exp\left[(V + 40)/5\right]\right),$$

$$\frac{dh}{dt} = \frac{1}{\tau_h} \left[ \frac{1}{1 + \exp\left[0.1112(V + 56)\right]} - h \right],$$

$$\tau_h = \max\left[ 2.6(V + 50) \times 10^{-4}, 2 \times 10^{-3} \right],$$

where $\overline{g}_{\text{A-K}}$ is the peak conductance density. Also, A-type K$^+$ channel kinetics of distal dendrites (over 100 μm from soma) for $I_{\text{A-Kdist}}$ is given by

$$I_{\text{A-Kdist}}(t,V) = \overline{g}_{\text{A-K}} m h (E_{\text{K}} - V),$$

$$\frac{dm}{dt} = \frac{0.5(1+\alpha)}{\beta \times 10^{-3}} \left[ \frac{1}{1+\alpha} - m \right],$$

$$\alpha = \exp\left[0.03707 k (V + 1)\right],$$

$$\beta = \exp\left[0.01446 k (V + 1)\right],$$

$$k = -1.8 - 1\big/\left(1 + \exp\left[(V + 40)/5\right]\right),$$

$$\frac{dh}{dt} = \frac{1}{\tau_h} \left[ \frac{1}{1 + \exp\left[0.1133(V + 56)\right]} - h \right],$$

$$\tau_h = \max\left[ 2.6(V + 50) \times 10^{-4}, 2 \times 10^{-3} \right].$$

Here, $\overline{g}_{\text{A-K}}$ is given by

$$\overline{g}_{A\text{-}K} = \begin{cases} 7.5 & (0 \le d < 100) \\ 48.67 \cdot d/350 & (100 < d \le 350) \\ 48.67 & (350 < d) \end{cases},$$

where $d$ (μm) is the dendritic distance from the soma.    A-type $K^+$ channels suppress backpropagating APs in distal dendrites, and conversely amplify the APs via inactivation of the $h$ gate when APs and EPSPs are coincided at pre- $\rightarrow$ post-spiking (Hoffman et al., 1997). The kinetics and distributions were taken from the literature (Migliore et al., 1999; Poirazi et al., 2003).

1.4 L-type Voltage-Gated $Ca^{2+}$ Channel $I_{\text{L-Ca}}$

L-type $Ca^{2+}$ channel kinetics $I_{\text{L-Ca}}$ is given by

$$I_{\text{L-Ca}}(t,V) = \overline{g}_{\text{L-Ca}} m^3 h \frac{V}{1-\exp(\phi V)},$$

$$\frac{dm}{dt} = \frac{1}{3.6\times10^{-3}} \left[ \frac{1}{1+\exp(-(V+37))} - m \right],$$

$$\frac{dh}{dt} = \frac{1}{2.9\times10^{-2}} \left[ \frac{1}{1+\exp((V+41)/0.5)} - h \right],$$

where $\phi = 0.0756$ mV$^{-1}$, and $\overline{g}_{\text{L-Ca}}$ is the peak conductance density.    $\overline{g}_{\text{L-Ca}}$ is given by

$$\overline{g}_{\text{L-Ca}} = \begin{cases} 93 & (\text{soma}) \\ 146 & (0 < d \le 50) \\ 3.2 & (50 < d) \end{cases},$$

where $d$ (μm) is the dendritic distance from the soma.    L-type $Ca^{2+}$ channels enlarge the half-width of backpropagating APs as observed in experiments (Golding et al., 2001), and contribute to the possible occurrence of $Ca^{2+}$-channel mediated dendritic spikes (Golding et al., 1999).    Prolonged APs are important for sufficient $Ca^{2+}$ influx via NMDARs with $Mg^{2+}$-unblock at pre- $\rightarrow$ post-spiking (Neville and Lytton, 1999). The derivation of voltage dependence for $Ca^{2+}$ current is described in the section about "$Ca^{2+}$ influx and removal."

## 2. Pre- and Postsynaptic Stimulation

2.1 Neurotransmitter Release by Presynaptic Stimulation

Presynaptic stimulation stimulates postsynaptic receptors via probabilistic release of neurotransmitter (glutamate) from presynaptic terminal. The probability of glutamate release depends on preceding glutamate releases, and STDP depends on the probabilistic release (Tsodyks and Markram, 1997; Froemke et al., 2006).    Here, we formulated the probabilistic glutamate release at a synapse, $P(t)$, to estimate $Ca^{2+}$

influx via NMDARs, as follows (Matveev and Wang, 2000) :

$$P(t) = 1 - \exp\left[-\alpha N(t)\right],$$

$$N(t) = \max\left[0, N_0 - \sum_{t>t_j^{syn}} v(t-t_j^{syn})\right],$$

$$v(t') = \exp(-t'/\tau_D) \cdot H(t'),$$

where $N_o$ is the maximum vesicle number, $\alpha$ is the fusion rate constant, $\tau_D$ is the recovery time constant, $t_j^{syn}$ is the time of $j^{th}$ glutamate release event, and $H(t)$ is the Heaviside step function.   Here, $N_o$ = 1.1, $\alpha$ = 4, and $\tau_D$ = 0.25 s.   $P(t)$ is approximated to be 1 If no-presynaptic stimulation occurs over 0.5 s.   When a presynaptic neuron fires at $t_i^{pre}$, glutamate release event occurs with the probability $P(t_i^{pre})$, and the event is count as $j^{th}$ glutamate release ($t_j^{syn} \leftarrow t_i^{pre}$ ).

   The probabilistic release was prepared in two ways.   One is the absolute release profile at a single synapse to estimate $Ca^{2+}$ influx via NMDARs.   The other is the trial average (or ensemble mean) of release profiles to estimate AMPAR- and NMDAR-EPSPs, since multiple synaptic inputs are given to a postsynaptic neuron by a single stimulation of as axon bundle. The trial average is represented by $P_{rel}(t_i^{pre})$.

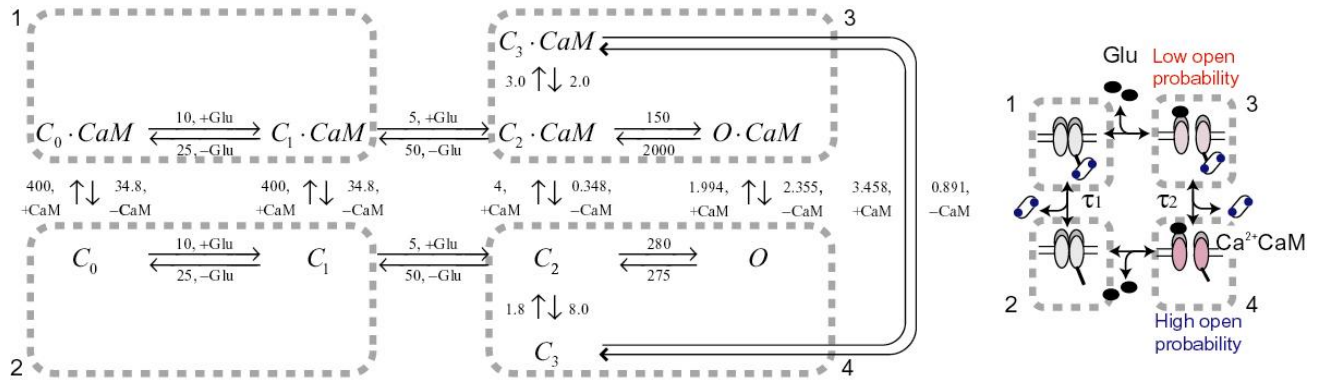2.2 Response of Postsynaptic Receptors and the Allosteric Kinetics of NMDARs

Synaptic current is composed of AMPAR-mediated current $I_{AMPAR}$ and NMDAR-mediated current $I_{NMDAR}$.   First, $I_{AMPAR}$ was modeled by using α-function as follows:

$$I_{AMPAR}(t,V_s) = \bar{g}_{AMPAR} \sum_j P_{rel}(t_j^{Pre}) g_{AMPAR}(t-t_j^{Pre})(E_{AMPAR} - V_s)$$

$$g_{AMPAR}(t') = \frac{t'}{3 \times 10^{-3}} \exp\left[1 - \frac{t'}{3 \times 10^{-3}}\right] \cdot H(t'),$$

where $\bar{g}_{AMPAR}$ is the peak conductance, $P_{rel}(t_i^{pre})$ is the trial average of release profiles, $t_j^{Pre}$ is time at $j^{th}$ presynaptic stimulus (s), $E_{AMPAR}$ is the equilibrium potential, and $H(t)$ is the Heaviside step function.   Here $\bar{g}_{AMPAR}$ = 0.3 nS, and $E_{AMPAR}$ = 0 mV. $I_{AMPAR}$ is the ensemble of multiple synaptic inputs from stimulated axon bundles.

   Next, $I_{NMDAR}$ was modeled in consideration of extracellular $Mg^{2+}$-block (Castellani et al., 2001) and channel open kinetics of CaM-bound and CaM-unbound NMDARs (Ehlers et al., 1996; Rycroft and Gibb, 2002) as follows:

$$I_{NMDAR}(t,V_s) = \bar{g}_{NMDAR} \cdot (O + O \cdot CaM) \cdot \frac{E_{NMDAR} - V_s}{1 + ([Mg^{2+}]/3.57)\exp(-0.062V_s)}$$

Figure (NMDAR allosteric kinetics diagram):

Top row states:
$C_3 \cdot CaM$      (box 3)

$C_0 \cdot CaM$ $\underset{25,-Glu}{\overset{10,+Glu}{\rightleftharpoons}}$ $C_1 \cdot CaM$ $\underset{50,-Glu}{\overset{5,+Glu}{\rightleftharpoons}}$ $C_2 \cdot CaM$ $\underset{2000}{\overset{150}{\rightleftharpoons}}$ $O \cdot CaM$

$C_3 \cdot CaM$: $3.0 \uparrow\downarrow 2.0$

Vertical transitions (±CaM):
$400, +CaM \uparrow\downarrow 34.8, -CaM$    $400, +CaM \uparrow\downarrow 34.8, -CaM$    $4, +CaM \uparrow\downarrow 0.348, -CaM$    $1.994, +CaM \uparrow\downarrow 2.355, -CaM$    $3.458, +CaM \quad 0.891, -CaM$

Bottom row states:
$C_0$ $\underset{25,-Glu}{\overset{10,+Glu}{\rightleftharpoons}}$ $C_1$ $\underset{50,-Glu}{\overset{5,+Glu}{\rightleftharpoons}}$ $C_2$ $\underset{275}{\overset{280}{\rightleftharpoons}}$ $O$

$C_2$: $1.8 \uparrow\downarrow 8.0$ to $C_3$

Right panel (Figure 4A): boxes 1, 2, 3, 4; Glu; Low open probability; High open probability; $\tau 1$; $\tau 2$; $Ca^{2+}\cdot CaM$

where $\bar{g}_{NMDAR}$ is the peak conductance, $E_{NMDAR}$ is the equilibrium potential, $[Mg^{2+}]$ is the concentration of extracellular $Mg^{2+}$, $C_0$, $C_1$, $C_2$, $C_3$, $C_0 \cdot CaM$, $C_1 \cdot CaM$, $C_2 \cdot CaM$, $C_3 \cdot CaM$ are the concentration of closed-state NMDAR channels, and $O$ and $O \cdot CaM$ are the concentration of open-state channels. $CaM$ represents $2Ca^{2+}\cdot CaM$ or $3Ca^{2+}CaM$, and the numeric on arrows are rate constants in $\mu M^{-1}s^{-1}$ or $s^{-1}$, which were set on the basis of the experimental kinetics of NMDARs (Ehlers et al., 1996; Rycroft and Gibb, 2002) except that the affinity of Glu to NMDARs for C0 regions (87 nM) was used because the affinity to the C1 region of NMDARs was too high (4 nM) and the binding of $Ca^{2+}\cdot CaM$ to NMDARs was saturated even at the basal $Ca^{2+}$ level. Here $\bar{g}_{NMDAR}$ = 50 nS$\mu M^{-1}$, $E_{NMDAR}$ = 0 mV, $[Mg^{2+}]$ = 1.5 mM (Froemke and Dan, 2002), and the total NMDAR concentration was 1 $\mu M$. The right panel in the description of NMDAR kinetics shows the schematic representation of the allosteric kinetics of NMDARs (**Figure 4A**), where the indicated numbered bashed boxes denote corresponding components in the left panel. NMDAR binds to both $2Ca^{2+}\cdot CaM$ and $3Ca^{2+}\cdot CaM$ (James et al., 1995; Akyol et al., 2004), and the kinetics constants for "NMDAR$\cdot 2Ca^{2+}\cdot CaM$ + $Ca^{2+}$ $\leftrightarrow$ NMDAR$\cdot 3Ca^{2+}\cdot CaM$" is the same as those for "$2Ca^{2+}\cdot CaM$ + $Ca^{2+}$ $\leftrightarrow$ $3Ca^{2+}\cdot CaM$." Decrease of free $nCa^{2+}\cdot CaM$ concentration by binding to NMDARs was omitted for simplicity. Here, the time constants of the transition of $Ca^{2+}\cdot CaM$ -unbound and –bound NMDARs were set at 230 and 2.3 ms, respectively, under the condition where CaM was 1 $\mu M$. All the kinetic constants were set to satisfy the principle of detailed balance in thermodynamics equilibrium.

States of NMDAR channels are discontinuously changed at the time of presynaptic stimulation ($t_i^{pre}$), because the glutamate release by presynatic stimulation is a flash event ($\sim$ 100 $\mu s$) (Clements, 1996). The update equation is given by:

$$C_0 \leftarrow C_0 \cdot e^{-10 \cdot \mathrm{Glu}_{tot}}$$

$$C_1 \leftarrow 2C_0 \left\{ e^{-5 \cdot \mathrm{Glu}_{tot}} - e^{-10 \cdot \mathrm{Glu}_{tot}} \right\} + C_1 \cdot e^{-5 \cdot \mathrm{Glu}_{tot}}$$

$$C_2 \leftarrow C_0 \left\{ 1 + e^{-10 \cdot \mathrm{Glu}_{tot}} - 2e^{-5 \cdot \mathrm{Glu}_{tot}} \right\} + C_1 \left\{ 1 - e^{-5 \cdot \mathrm{Glu}_{tot}} \right\} + C_2$$

$$C_0 \cdot CaM \leftarrow C_0 \cdot CaM \cdot e^{-10 \cdot \mathrm{Glu}_{tot}}$$

$$C_1 \cdot CaM \leftarrow 2C_0 \cdot CaM \left\{ e^{-5 \cdot \mathrm{Glu}_{tot}} - e^{-10 \cdot \mathrm{Glu}_{tot}} \right\} + C_1 \cdot CaM \cdot e^{-5 \cdot \mathrm{Glu}_{tot}}$$

$$C_2 \cdot CaM \leftarrow C_0 \cdot CaM \left\{ 1 + e^{-10 \cdot \mathrm{Glu}_{tot}} - 2e^{-5 \cdot \mathrm{Glu}_{tot}} \right\} + C_1 \cdot CaM \left\{ 1 - e^{-5 \cdot \mathrm{Glu}_{tot}} \right\} + C_2 \cdot CaM$$

where $\mathrm{Glu}_{tot}$ is the total intensity of released glutamate. Here $\mathrm{Glu}_{tot} = 0.4 \times P_{rel}(t_i^{pre})$ μM·s. The discontinuous update is calculated from the second order glu-binding reactions and the temporal pattern of glutamate release $Glu(t)$:

$$C_0 \xrightarrow{10 Glu(t)} C_1 \xrightarrow{5 Glu(t)} C_2 ,$$

$$C_0 \cdot CaM \xrightarrow{10 Glu(t)} C_1 \cdot CaM \xrightarrow{5 Glu(t)} C_2 \cdot CaM ,$$

$$\frac{dC_0}{dt} = -10 Glu(t) C_0, \quad \frac{dC_1}{dt} = 10 Glu(t) C_0 - 5 Glu(t) C_1, \quad \frac{dC_2}{dt} = 5 Glu(t) C_1,$$

$$\frac{dC_0 \cdot CaM}{dt} = -10 Glu(t) C_0 \cdot CaM,$$

$$\frac{dC_1 \cdot CaM}{dt} = 10 Glu(t) C_0 \cdot CaM - 5 Glu(t) C_1 \cdot CaM,$$

$$\frac{dC_2 \cdot CaM}{dt} = 5 Glu(t) C_1 \cdot CaM,$$

where $Glu(t) = \mathrm{Glu}_{tot} \lim_{\Delta t \to 0} f(\Delta t)$,

$$f(\Delta t) = \begin{cases} 0 & (t < 0) \\ 1/\Delta t & (0 \le t < \Delta t) \\ 0 & (\Delta t \le t) \end{cases} .$$

## 2.3 Postsynaptic Stimulation

Postsynaptic stimulation, a brief current injection to soma $I_{current}$, was modeled using α-function as follows:

$$I_{current}(t) = \bar{I}_{peak} \sum_j \frac{t - t_j^{Post}}{5 \times 10^{-4}} \exp \left[ 1 - \frac{t - t_j^{Post}}{5 \times 10^{-4}} \right] \cdot H(t - t_j^{Post}),$$

where $\bar{I}_{peak}$ is the peak current, and $t_j^{Post}$ is time at $j^{th}$ postsynaptic stimulus (s). Here $\bar{I}_{peak}$ = 0.5 nA, which was sufficient to induce an action potential.

## Part B: Modeling of Postsynaptic Signaling Cascades    (Figure 1B)

## 3. $Ca^{2+}$ Influx and Removal

We modeled $Ca^{2+}$ influx to a spine via NMDARs and VGCCs as well as $Ca^{2+}$ removal from the spine, and estimated postsynaptic $Ca^{2+}$ concentration $[Ca^{2+}]_i$ in responses to pre- and postsynaptic stimulation (**Figure SI2**).   Presynaptic stimulation activates AMPARs and NMDARs, and leads to $Ca^{2+}$ influx mainly via NMDARs including the effect of $Mg^{2+}$ unblock by EPSPs.   Postsynaptic stimulation induces an AP, and the depolarization signal leads to $Ca^{2+}$ influx via VGCCs.   Increased $[Ca^{2+}]_i$ is removed by $Ca^{2+}$ pump, and returns to the basal level (Sabatini et al., 2001).

        We set NMDARs, VGCCs, and $Ca^{2+}$ pump distributed in the membrane of a postsynaptic spine (Sabatini et al., 2002).   Generally, $Ca^{2+}$ influx $j^{Ca}_X$ ($nmol \cdot s^{-1} \cdot cm^{-2}$) through channel $X$ is obtained from the Goldman-Hodgkin-Katz current equation $i^{Ca}_X$, which is dependent on postsynaptic membrane potential $V_s$, $[Ca^{2+}]_i$ and extracellular $Ca^{2+}$ concentration $[Ca^{2+}]_o$, as follows:

$$j^{Ca}_X = \frac{i^{Ca}_X}{2F}$$
$$= -\frac{p^{Ca}_X \phi V_S \left\{ [Ca^{2+}]_o - [Ca^{2+}]_i \exp(\phi V_S) \right\}}{1 - \exp(\phi V_S)}$$
$$\sim -\frac{P^{Ca}_X V_S}{1 - \exp(\phi V_S)}$$

where $p^{Ca}_X$ is the permeability of channel $X$, $P^{Ca}_X = 2\phi\, p^{Ca}_X\, [Ca^{2+}]_o$ ($nmol \cdot s^{-1} \cdot mV^{-1} \cdot cm^{-2}$), and $\phi$ is $2F/RT$, where $F$ is Faraday's constant, $R$ is the gas constant, and $T$ is the absolute temperature.   Here $\phi$ = 0.0756 $mV^{-1}$, and the component $[Ca^{2+}]_i/[Ca^{2+}]_o$ $\exp(-2\phi V_s)$ was omitted in consideration of $[Ca^{2+}]_o >> [Ca^{2+}]_i$.   Because we focused on NMDAR-dependent LTP and LTD, we omitted metabotropic glutamate receptor-dependent intracellular $Ca^{2+}$ release to avoid unnecessary complexity.

3.1 $Ca^{2+}$ Influx via NMDARs
$Ca^{2+}$ permeability of NMDARs with voltage-dependent $Mg^{2+}$ block (Castellani et al., 2001), $P^{Ca}_{NMDAR}$, is given by

$$P^{Ca}_{NMDAR}(V,t) = \overline{P}_{NMDAR}\left(O + O \cdot CaM\right)\frac{1}{1 + ([Mg^{2+}]/3.57)\exp(-0.062V_S)}$$

where $[Mg^{2+}]$ is the concentration of extracellular $Mg^{2+}$, $\overline{P}_{NMDAR}$ is the maximum channel permeability of NMDARs, and $O$ and $O \cdot CaM$ are the concentrations of open-state NMDAR channels where the discontinuous update by glutamate release occurs at $t_j^{syn}$ with $Glu_{tot}$ = 0.4 $\mu M \cdot s$ (see above).   Here, $[Mg^{2+}]$ = 1.5 mM (Froemke and Dan, 2002).   We set $\overline{P}_{NMDAR}$ = 0.5, 1, 2.5, and 2.5 $nmol \cdot s^{-1} \cdot mV^{-1} \cdot cm^{-2}$ in the

allosteric model, the no-allosteric model with slow suppression, the no-allosteric model with rapid suppression, and the allosteric model with opposite time constants ($\tau_1$ = 230 ms, $\tau_2$ = 2.3 ms), respectively, not to induce potentiation nor depression by uncorrelated pre- and post-spiking. NMDARs were distributed in the membrane of the PSD compartment (shown below), and the maximum permeability produces 1 $\mu$M-peak $Ca^{2+}$ at the cytosolic compartment by a single presynaptic stimulation (Sabatini et al., 2002).

## 3.2 $Ca^{2+}$ Influx via VGCCs

The permeability of high voltage activated L-type VGCCs, $P^{Ca}_{VGCC}$, is given by

$$P^{Ca}_{VGCC}(V,t) = \bar{P}_{VGCC} m^3 h \frac{V}{1 - \exp(\phi V)} ,$$

$$\frac{dm}{dt} = \frac{1}{0.0036}\left[\frac{1}{1 + \exp(-(V + 37))} - m\right] ,$$

$$\frac{dh}{dt} = \frac{1}{0.029}\left[\frac{1}{1 + \exp((V + 41)/0.5)} - m\right] ,$$

where $\bar{P}_{VGCC}$ is the maximum channel permeability of VGCCs ( $\bar{P}_{VGCC}$ = 0.04 nmol$\cdot$s$^{-1}$$\cdot$mV$^{-1}$$\cdot$cm$^{-2}$). L-type $Ca^{2+}$ channels in spines play specific roles in inducing STDP (Bi and Poo, 1998; Peng et al., 2004; Froemke et al., 2005).

## 3.3 $Ca^{2+}$ Removal

Removal of free $Ca^{2+}$ by $Ca^{2+}$ pump in the membrane $j^{Ca}_{pump}$ (nmol$\cdot$s$^{-1}$$\cdot$cm$^{-2}$) is simply given by

$$j^{Ca}_{pump} = 0.8\left([Ca^{2+}]_{rest} - [Ca^{2+}]_i\right)$$

where $[Ca^{2+}]_{rest}$ is the basal $Ca^{2+}$ concentration. Here, $[Ca^{2+}]_{rest}$ = 0.05 $\mu$M. The $Ca^{2+}$ pump decreases elevating $[Ca^{2+}]_i$ in a double exponential manner, consisting of a 3-ms fast component for free $Ca^{2+}$ and a 30-ms slow component for CaM-interacting $Ca^{2+}$ (Sabatini et al., 2002).
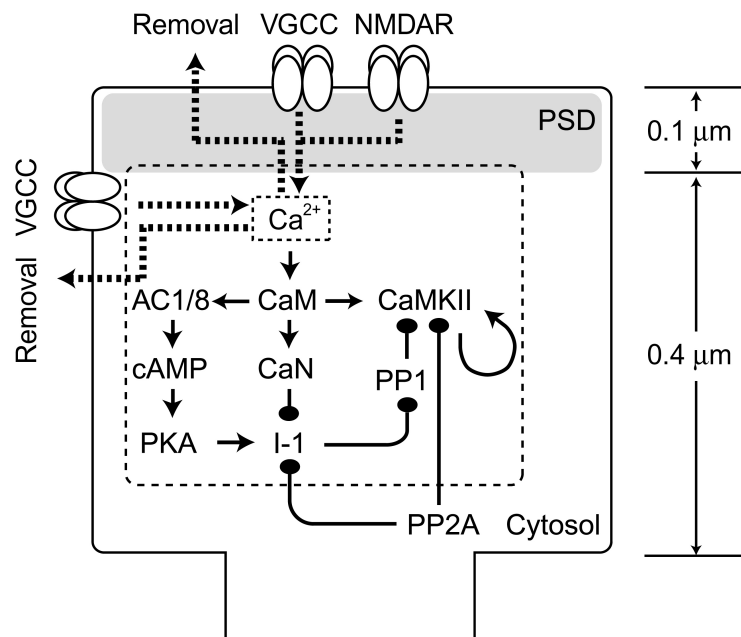
## 4. Intracellular Signaling Cascades
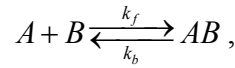


**Figure SI2**

We set the framework of biochemical intracellular signaling cascades within a spine on the basis of the earlier models (Bhalla and Iyengar, 1999; Kuroda et al., 2001; Doi et al., 2005) and observations (**Figure SI2**) (Winder and Sweatt, 2001; Lisman et al., 2002). We tried to make an essential and rather simple model of intracellular signaling cascades to avoid redundancy and unnecessary complexity. The intracellular signaling cascades involves the $Ca^{2+}$-dependent activation of CaMKII (see sections 4.3.1, 4.3.2), PKA via AC1/8 (4.3.4) and CaN (4.3.3). CaMKII activation also involves its autophosphorylation by itself or neighboring subunits. PP1 and PP2A dephosphorylates CaMKII. PKA phosphorylates I-1, and CaN and PP2A dephosphorylates it (4.3.5). Phosphorylated I-1 binds PP1 and inactivates it (4.3.5). Therefore, PP1 activation and inactivation depend on CaN and PP2A, and on PKA, respectively. CaMKII, and PP1 and PP2A phosphorylates and dephosphorylates AMPARs, respectively, whose trafficking depends (see below; 5. Modeling of AMPAR trafficking).

We set a spine as a cylinder, which is 0.5 $\mu$m long and has a 0.2-$\mu$m$^2$ section area (Stuart et al., 1999). The spine was divided into the PSD and cytosol compartments with 0.1-$\mu$m and 0.4-$\mu$m lengths, respectively (**Table SIa**). We assumed that all molecules as indicated by the dashed box (except PP2A that exists only in the cytosol) diffuse between PSD and cytosol (see below), because PP2A is reportedly not enriched in the PSD fraction (Strack et al., 1997). The localization of these
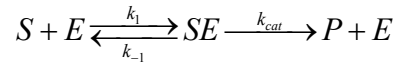
molecules at PSD fraction implicitly represents their bindings to scaffold proteins such as PSD95, SAP97 and AKAP (Halpain et al., 1998; Wang et al., 2002; Petersen et al., 2003; Bauman et al., 2004; Bordelon et al., 2005).   We assumed that the molecules within each compartment were well mixed, and that they deterministically interacted on the basis of mass assumption.   The detailed interactions are described below.

## 4.1 Formalization of Molecular Interaction

All interactions in the signal transduction pathways were represented by binding and enzymatic reactions (Bhalla and Iyengar, 1999; Doi et al., 2005).   For example, a binding reaction in which A binds to B to form AB is expressed by the following equation:

$$A + B \underset{k_b}{\overset{k_f}{\rightleftarrows}} AB \, ,$$

where $k_f$ and $k_b$ are the rate constants for the forward and backward reactions.   The rates $k_f$ and $k_b$ are generally determined by two experimentally observable constants, the dissociation constant $K_d$ and the time constant $\tau$.   $K_d$ is defined as $K_d = k_b / k_f$.   In turn, enzymatic reactions were modeled by the Michaelis-Menten formulation:

$$S + E \underset{k_{-1}}{\overset{k_1}{\rightleftarrows}} SE \xrightarrow{k_{cat}} P + E$$

where S, E and P denote substrates, enzymes and products, respectively.   The kinetic parameters $k_1$, $k_{-1}$, and $k_{cat}$ are determined by two observable constants: the Michaelis constant $K_m$ and the maximum enzyme velocity $V_{max}$.   $K_m$ is defined as $K_m = (k_{-1} + k_{cat}) / k_1$, and $V_{max}$ is defined as $V_{max} = k_{cat}[E]_{total}$, where $[E]_{total}$ is the total concentration of the enzyme.   We assumed $k_{-1} / k_{cat} = 4$ for all enzymatic reactions (Bhalla and Iyengar, 1999).

## 4.2 Formalization of Molecular Diffusion

Diffusion of the signal transduction molecules was represented by the following reaction-diffusion equations:

$$\frac{\partial [X]_{cytosol}}{\partial t} = D_X \frac{\partial^2}{\partial x^2}[X]_{cytosol} + \sum_i R^i_{X,cytosol} + \frac{S_{cytosol}}{V_{cytosol}} \sum_i j^i_{X,cytosol}$$

$$\sim \frac{D_X}{(\Delta x)^2} \left\{ [X]_{PSD} - [X]_{cytosol} \right\} + \sum_i R^i_{X,cytosol} + \frac{S_{cytosol}}{V_{cytosol}} \sum_i j^i_{X,cytosol}$$

where $[X]_{cytosol}$ and $[X]_{PSD}$ are the concentration of molecule $X$ in cytosolic and PSD compartments, respectively, $D_X$ is the diffusion coefficient, $R_{X,cytosol}$ is the reaction components, $J_{X,cytosol}$ is the influx or removal components, and $\Delta x$ is the effective distance between cytosolic and PSD compartments.   Here, we set $\Delta x = 0.15$ $\mu$m.

Diffusion coefficients $D_x$ of $Ca^{2+}$, cAMP, CaM, CaMKII, PKA, CaN and PDE were obtained from the literature, and those of I-1 and PP1 were estimated from the relationship between $D_x$ and molecular weight $M_x$ (**Table SIb**). The diffusion coefficients of complexes were assumed to take the smallest value in those of constituents for simplicity. The diffusion between a spine and a parent dendrite was not modeled, because the diffusion of fast molecular dynamics such as $Ca^{2+}$ is negligible (Sabatini et al., 2002).

## 4.3 Overview of Molecular Interactions

Notations of **Figures SI3** and **SI4**: Circles and boxes with arrows denote molecule-molecule interactions and enzymatic reactions, respectively. Rate constants (Numbered circles or boxes) and concentrations of molecules are shown in **Tables SIa–SIj**.

### 4.3.1 $Ca^{2+}$·CaM Interaction

$Ca^{2+}$ binding kinetics of CaM has extensively been analyzed (Linse et al., 1991; Holmes, 2000). CaM binds to four $Ca^{2+}$ ions, but two or three $Ca^{2+}$-binding is enough to activate CaM (James et al., 1995; Chin and Means, 2000). For simplicity, $3Ca^{2+}$·CaM is assumed to be an active form, and reactions for $4Ca^{2+}$·CaM are omitted. The description of kinetic constants is shown in **Figure SI3** and **Tables SIc and SId**.

### 4.3.2 $Ca^{2+}$·CaM·CaMKII System

$Ca^{2+}$·CaM binds to each subunit of a holoenzyme of CaMKII, and $Ca^{2+}$·CaM-bound subunits are phosphorylated at Thr286 by active neighboring subunits, which are $Ca^{2+}$·CaM-bound and/or Thr286 phosphorylated subunits. $Ca^{2+}$·CaM induced successive autophosphorylation of CaMKII subunits (De Koninck and Schulman, 1998), leading to the persistent activation of CaMKII (Fukunaga et al., 1993; Shen et al., 2000). On the basis of the previous CaMKII model (Dupont et al., 2003), we expanded the model for treatment of $Ca^{2+}$·CaM-, $2Ca^{2+}$·CaM-, and $3Ca^{2+}$·CaM-bound states (**Figure SI3**), and further modified the binding constants between bare CaM and the inactive subunit in consideration of experimentally observed basal activity (Fukunaga et al., 1993; Kawaguchi and Hirano, 2002). This modification also implicitly represents CaMKII by binding to NMDARs (Bayer et al., 2001; Leonard et al., 2002). The modified CaMKII shows bistable activity as a balance with PP1 activity. The present CaMKII model calculated the phosphorylation rate by active neighbors from the fraction of active subunits approximately (Dupont et al., 2003). The diffusion of active form of CaMKII from the PSD fraction is set lower than that of inactive form, because the active form of CaMKII accumulates at the PSD fraction (Strack et al., 1997; Shen et al., 2000).

The CaMKII activation inhibited by PP1 and PP2A activities, which dephosphorylate the Thr286 site of CaMKII (**Figure SI3**; **Table SIe**).   PP2A exist only in the cytosol compartment (Strack et al., 1997).   The description of kinetic constants is shown in **Figure SI3** and **Tables SIc–SIe**.

### 4.3.3   CaN System

A regulatory subunit of CaN binds $4Ca^{2+}$, and a catalytic subunit of CaN binds $Ca^{2+} \cdot CaM$. CaN activation depends on both $Ca^{2+}$ and $Ca^{2+} \cdot CaM$ (Hubbard and Klee, 1987; Kakalis et al., 1995; Klee et al., 1998; Groth et al., 2003).   Because one of the $Ca^{2+}$ sites is always saturated and the other has no functional role in CaN activation, we assumed that both the rest of the $2Ca^{2+}$-binding and $Ca^{2+}CaM$-binding are responsible for the CaN activation (Feng and Stemmer, 2001; Gallagher et al., 2001). The description of kinetic constants is shown in **Figure SI4** and **Tables SIc and SIh**.

### 4.3.4   AC1·cAMP·PKA System

AC1/8 is activated by $3Ca^{2+} \cdot CaM$, and catalyses ATP into cAMP, which is converted into 5'-AMP by an active form of PDE (Xia and Storm, 1997; Cooper, 2003).   PKA consists of two regulatory subunits, R (RII), and two catalytic subunits, C.   A regulatory subunit of PKA has two cAMP-binding sites, A and B.   Binding of cAMP at the site A requires the prior binding of cAMP to the site B.   Conjunctive binding of 4 cAMP to 2R leads to successive dissociation of C, which is an active form (Taylor et al., 1990; Nguyen and Woo, 2003).   The description of kinetic constants is shown in **Figure SI4** and **Tables SIc,SIf and SIg**.

### 4.3.5   CaN, PKA, PP2A·I-1·PP1 System

I-1 is phosphorylated by active form of PKA, and phosphorylated I-1 is dephosphorylated by active forms of PP2A and CaN (Price and Mumby, 1999). Phosphorylated I-1 binds to PP1 and inactivates it (Huang et al., 1999; Huang and Paudel, 2000).   The description of kinetic constants is shown in **Figure SI4** and **Tables SIi and SIj**.

$$0.75\ [CaMKII\text{-}n_1Ca^{2+}CaM]\ +\ [CaMKII^*\text{-}3Ca^{2+}CaM]$$
$$+\ 0.8\ [CaMKII^*\text{-}n_2Ca^{2+}CaM]\ +\ 0.8\ [CaMKII^*\text{-}n_2Ca^{2+}CaM]\ =\ _{active}CaMKII\quad (n_1 = 1,2,3,\ n_2 = 1,2)$$

**Figure SI3.** $Ca^{2+}\cdot CaM\cdot CaMKII$ system

Circles and boxes with arrows denote molecule-molecule interactions and enzymatic reactions, respectively.   Concentrations of molecules are shown in **Table SIc**, and rate constants (Numbered circles or boxes) are shown in **Tables SId and SIe**.

**Figure SI4.** AC1·cAMP·PKA system (left), CaN system (top right) and I-1 system (bottom right)
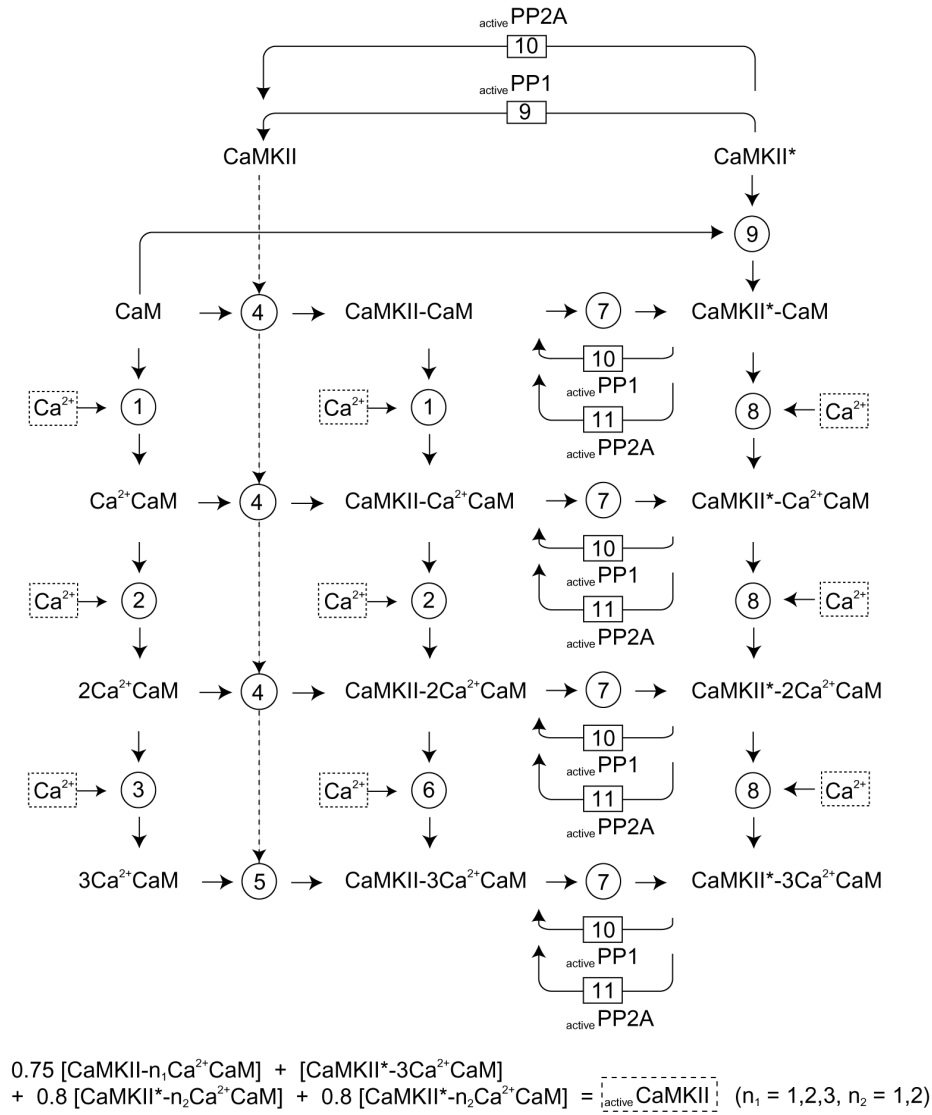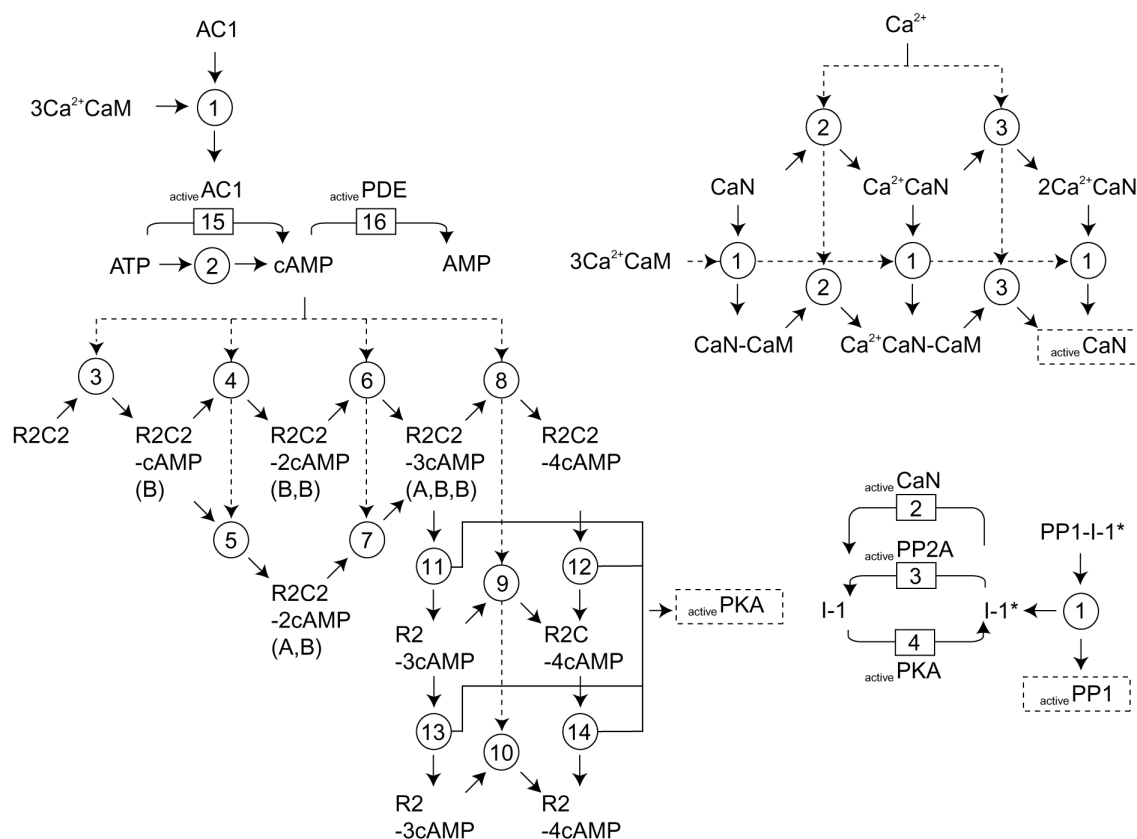
Circles and boxes with arrows denote molecule-molecule interactions and enzymatic reactions, respectively. Concentrations of molecules are shown in **Table SIc**, and rate constants (Numbered circles or boxes) are shown in **Tables SIf–SIj**.

## Part C: Modeling of AMPAR Trafficking  (Figure 1C)
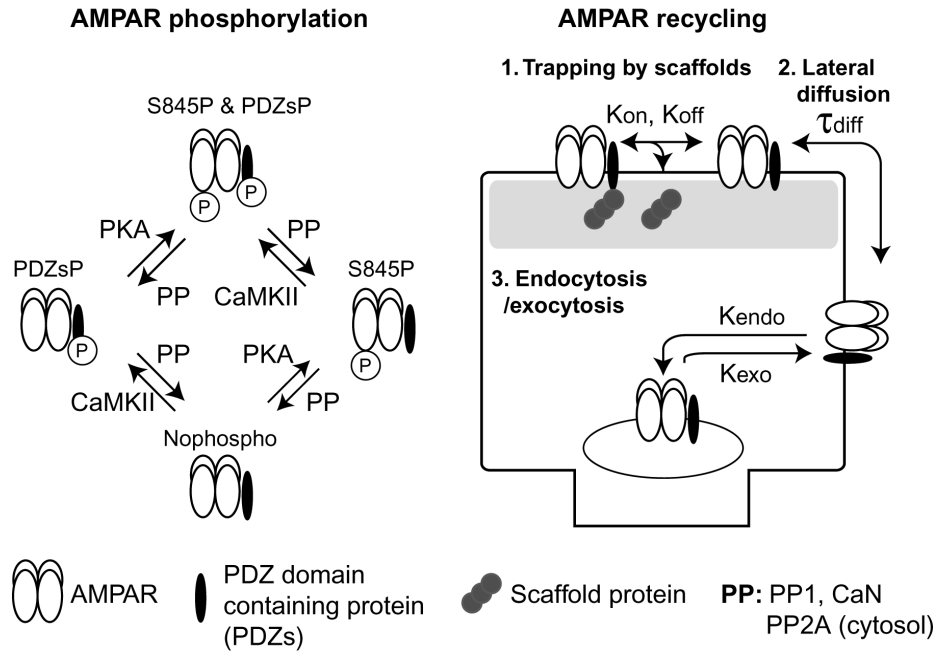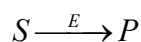
## 5. AMPAR Trafficking



**Figure SI5**

On the basis of the recent progress in AMPARs trafficking (Malinow and Malenka, 2002; Collingridge et al., 2004), we constructed a simplified model of phosphorylation-dependent AMPAR trafficking because the detailed mechanism remains unknown (**Figure SI5**).   The AMPAR trafficking model consists of AMPAR phosphorylation and recycling models.   We represented GluR1, rather than GluR2/3, as AMPARs in the STDP model because LTP and LTD can be elicited in GluR2 (-/-) and GluR3 (-/-) mice (Meng et al., 2003).

### 5.1    AMPAR Phosphorylation

AMPAR is complexed with PDZ-containing scaffold proteins (PDZs), such as SAP97 and stargazin (Sans et al., 2001; Vandenberghe et al., 2005).   PDZs are phosphorylated by CaMKII (Mauceri et al., 2004; Tomita et al., 2005).   AMPARs are phosphorylated by PKA at Ser845.   Phosphorylated AMPARs and PDZs are dephosphorylated by PP1 and CaN (Lee et al., 2000; Snyder et al., 2003).   Because rate constants regarding these phosphorylation and dephosphorylation have yet to be determined, we here redefined the enzymatic reactions with the simple formulation as follows:

$$S \xrightarrow{E} P$$

$$\frac{d[S]}{dt} = -K_{\mathrm{f}}[E][S]$$

$$\frac{d[P]}{dt} = K_{\mathrm{f}}[E][S]$$

where $K_{\mathrm{f}}$ is the reaction rate constant, and S, E and P denote substrates, enzymes, and products, respectively.   This formulation implicitly assumes the relatively low concentration of enzyme·substrate complex, or high $K_{\mathrm{m}}$ in the standard formulation of enzymatic reactions (Sasagawa et al., 2005).   The unique constants, $K_{\mathrm{f}}$, were determined to reproduce the ratio of the phosphorylated and unphosphorylated AMPARs in the naïve state and the phosphorylation/dephosphorylation rate of AMPARs in experimental observation. The description of kinetic constants are shown in **Figure SI5** and **Table SIk**.

## 5.2    AMPAR Recycling

AMPAR recycling contains three processes; trapping by scaffold, lateral diffusion and endocytosis/exocytosis (Malinow and Malenka, 2002; Collingridge et al., 2004). The phosphorylated PDZs associated with AMPARs and the non-phosphorylated one strongly and weakly interact with scaffold proteins at PSD, respectively, which were here assumed as cytoskeletal anchors such as PSD-95 attached with F-actin and Myosin VI (Kim and Sheng, 2004).   Therefore, phosphorylation of PDZs results in stabilization of AMPARs at PSD, and the dephosphorylation results in the dissociation from PSD (Shi et al., 1999; Hayashi et al., 2000; Triller and Choquet, 2005).   Any form of AMPARs laterally diffuses between the PSD membrane and the plasma membrane (Triller and Choquet, 2005).   The dephosphorylated AMPARs (GluR1s at Ser845) are rapidly internalized into endosome, whereas the phosphorylated AMPARs are slowly internalized (Carroll et al., 2001; Cousin and Robinson, 2001; Blanpied et al., 2002; Kittler et al., 2005; Tigaret et al., 2006).   In addition, the phosphorylated AMPARs, but not dephosphorylated form, are reinserted into the plasma membrane (Ehlers, 2000; Esteban et al., 2003).

Here, the phosphorylation-dependent increase of AMPAR numbers trapping by scaffold at PSD corresponds to the increase of synaptic conductance (LTP), whereas the dephosphorylation-dependent decrease corresponds to the decrease of synaptic conductance (LTD).   The phosphorylation-dependent processes implicitly involve the phosphorylation-dependent changes of AMPAR conductance (Derkach et al., 1999; Banke et al., 2000).   The description of kinetic constants is shown in **Figure SI5** and **Table SIl**.

**Table SIa.** Geometry of a Spine

| | $V_x$ (μm³) | $S_x$ (μm²) | SVR (μm⁻¹) |
|---|---|---|---|
| PSD compartment | 0.02 | 0.3585 | 17.927 |
| Cytosol compartment | 0.08 | 0.8341 | 10.425 |
| Total | 0.1 | 1.1926 | 11.926 |

**Table SIb.** Diffusion Coefficients

| | $Ca^{2+}$ | cAMP (ATP) | CaM | CaMKII | PKA |
|---|---|---|---|---|---|
| $M_x$ (kDa) | 0.04 | 0.329 (Woolf and Greer, 1994) | 16.8 (Bradshaw et al., 2002) | 649 (Bradshaw et al., 2002) | 40.5 (Woolf and Greer, 1994) |
| $D_x$ (μm²s⁻¹) | 600 (Stuart et al., 1999) | 500 (Stuart et al., 1999) | 250 (Luby-Phelps et al., 1995) | 6 (Woolf and Greer, 1994; Stuart et al., 1999) [†††] | 32 (Woolf and Greer, 1994; Stuart et al., 1999) |

| | AC1/8 | CaN | I-1 | PP1 | PP2A | PDE |
|---|---|---|---|---|---|---|
| $M_x$ (kDa) | | 77 (Winder and Sweatt, 2001) | 28 (Winder and Sweatt, 2001) | 37 (Winder and Sweatt, 2001) | 156 (Winder and Sweatt, 2001) | 120 (Woolf and Greer, 1994) |
| $D_x$ (μm²s⁻¹) | 0[*] | 20 (Woolf and Greer, 1994) | 35.9[†] | 31.4[†, ††] | 0[**] | 7.2 (Woolf and Greer, 1994) |

(*) AC1/8 is a transmembrane protein.

(**) PP2A was assumed to be exclusively localized at cytosol, but not at PSD (Strack et al., 1997; Lisman and Zhabotinsky, 2001).

(†) $D_x$ were calculated from $D_x = 152M_x^{-1/3}-14.2$ as a relation between $M_x$ and $D_x$ (Woolf and Greer, 1994).

(††) PP1 is trapped and co-localized at PSD; therefore, $D_{PP1}$ for PSD → cytosol were assumed to take the six times smaller value (Strack et al., 1997; Bordelon et al., 2005).

(†††) Active CaMKII is trapped and co-localized at PSD; therefore, $D_{CaMKII}$ for PSD → cytosol in CaM-bound and/or phosphorylated CaMKII were assumed to take the 10 times smaller value (Strack et al., 1997; Shen et al., 2000).

**Table SIc.** Molecular Concentrations

| Molecule | Concentration ($\mu$M) | Notes |
|---|---|---|
| $Ca^{2+}$ | 0.05 | Basal $Ca^{2+}$ concentration ranges from 0.05 $\mu$M to 0.1 $\mu$M (Sabatini et al., 2002). |
| CaM | 80 | (Holmes, 2000). |
| CaMKII | 20 | CaMKII is highly abundant in PSD, where it constitutes 1-2% of the total protein (Lisman et al., 2002), and the concentration is predicted to be up to 50 $\mu$M (Erondu and Kennedy, 1985; Bradshaw et al., 2002; Petersen et al., 2003). |
| CaN | 3 | CaN is localized at PSD (Halpain et al., 1998; Gomez et al., 2002). |
| AC1/8 | 2 | Electron microscopy has revealed that AC1 is highly co-localized at PSD with weak diffusion in the spine head (Mons and Cooper, 1995; Mons et al., 1995; Wang et al., 2002). |
| ATP | 10000 | (Bhalla and Iyengar, 1999). |
| cAMP | 0.1 | Basal cAMP concentration is about 0.1 $\mu$M (Alberts et al., 2002). |
| 5'-AMP | 1000 | (Bhalla and Iyengar, 1999). |
| PDE | 1 (Buffered) | Assumption. |
| PKA | 2 (R2C2 complex), 0.05 (Free C) | PKA is highly co-localized at PSD by an anchor protein, AKAP (Carr et al., 1992; Colledge et al., 2000). |
| I-1 | 4 | Assumption. |
| PP1 | 2 | PP1 is trapped and co-localized at PSD (Strack et al., 1997; Bordelon et al., 2005). |
| PP2A | 0.03 | PP2A concentration is set lower than PP1 (Peng et al., 2004). |

**Table SId.** Molecular-Molecular Interactions in $Ca^{2+} \cdot CaM \cdot CaMKII$ System

| No. | Kf | Kb | Notes |
|---|---|---|---|

| 1 | 51.2 $\mu M^{-1}s^{-1}$ | 200 $s^{-1}$ | (Linse et al., 1991; Brown et al., 1997; Holmes, 2000; Gaertner et al., 2004). |
|---|---|---|---|
| 2 | 133.3 $\mu M^{-1}s^{-1}$ | 1000 $s^{-1}$ | (Linse et al., 1991; Brown et al., 1997; Holmes, 2000; Gaertner et al., 2004). |
| 3 | 25.6 $\mu M^{-1}s^{-1}$ | 400 $s^{-1}$ | (Linse et al., 1991; Brown et al., 1997; Holmes, 2000; Gaertner et al., 2004). |
| 4 | 0.0004 $\mu M^{-1}s^{-1}$ | 1 $s^{-1}$ | (Bayer et al., 2001; Dupont et al., 2003). |
| 5 | 8 $\mu M^{-1}s^{-1}$ | 1 $s^{-1}$ | (Bradshaw et al., 2003; Dupont et al., 2003) |
| 6 | 25.6 $\mu M^{-1}s^{-1}$ | 0.02 $s^{-1}$ | (Bayer et al., 2001; Dupont et al., 2003). |
| 7 | *func* $(s^{-1})$ | 0 | *func* = 0.29 $(-0.220\ [CaMKII] + 1.826\ [CaMKII]^2 - 0.800\ [CaMKII]^3) \times [CaMKII]$ , where [CaMKII] = [$_{active}$CaMKII] / [total CaMKII conc] (Dupont et al., 2003). |
| 8 | 1 $\mu M^{-1}s^{-1}$ | 1 $s^{-1}$ | (Dupont et al., 2003). |
| 9 | 8 $\mu M^{-1}s^{-1}$ | 0.001 $s^{-1}$ | (Dupont et al., 2003). |

**Table SIe.** Enzymatic Reactions in $Ca^{2+} \cdot CaM \cdot CaMKII$ System

| No. | Km ($\mu M$) | Kcat ($s^{-1}$) | Notes |
|---|---|---|---|
| 10 | 11 | 0.335 | (Bradshaw et al., 2002; Bradshaw et al., 2003) |
| 11 | 11 | 0.335 | Assumption. |

**Table SIf.** Molecular-Molecular Interactions in $AC1 \cdot cAMP \cdot PKA$ System

| No. | Kf | Kb | Notes |
|---|---|---|---|
| 1 | 5 $\mu M^{-1}s^{-1}$ | 1 $s^{-1}$ | (Taylor et al., 1990; Guillou et al., 1999; Cooper, 2003; Nguyen and Woo, 2003). |
| 2 | $4 \times 10^{-7}\ s^{-1}$ | 0 | Representation of basal AC activity (Guillou et al., 1999; Cooper, 2003). |
| 3 | 0.2 $\mu M^{-1}s^{-1}$ | 0.1 $s^{-1}$ | Cyclic AMP (0.5 $\mu M$) gives the half maximal kinase activity (Viste et al., 2005), and the affinity of the site A is doubly lower than that of the site B (Herberg et al., 1996), and the site B has slow binding kinetics (Taylor et al., 1990; Saucerman et al., 2003). |
| 4 | 0.1 $\mu M^{-1}s^{-1}$ | 0.2 $s^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 5 | 2 $\mu M^{-1}s^{-1}$ | 5 $s^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 6 | 4 $\mu M^{-1}s^{-1}$ | 5 $s^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |

| 7 | 0.1 $\mu$M$^{-1}$s$^{-1}$ | 0.1 s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 8 | 2 $\mu$M$^{-1}$s$^{-1}$ | 10 s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 9 | 20 $\mu$M$^{-1}$s$^{-1}$ | 1 s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 10 | 200 $\mu$M$^{-1}$s$^{-1}$ | 0.1 s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 11 | 2 s$^{-1}$ | 10 $\mu$M$^{-1}$s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 12 | 20 s$^{-1}$ | 1 $\mu$M$^{-1}$s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 13 | 1 s$^{-1}$ | 20 $\mu$M$^{-1}$s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |
| 14 | 10 s$^{-1}$ | 2 $\mu$M$^{-1}$s$^{-1}$ | (Taylor et al., 1990; Herberg et al., 1996; Saucerman et al., 2003; Viste et al., 2005). |

**Table SIg.** Enzymatic Reactions in AC1·cAMP·PKA System

| No. | Km ($\mu$M) | kcat (s$^{-1}$) | Notes |
|---|---|---|---|
| 9 | 40 | 10 | (Bhalla and Iyengar, 1999; Guillou et al., 1999; Cooper, 2003). |
| 10 | 10 | 20 | (Bhalla and Iyengar, 1999; Guillou et al., 1999; Cooper, 2003). |

**Table SIh.** Molecular-Molecular Interactions in CaN System

| No. | Kf | Kb | Notes |
|---|---|---|---|
| 1 | 40 $\mu$M$^{-1}$s$^{-1}$ | 0.04 s$^{-1}$ | The Hill coefficient of Ca$^{2+}$-binding to CaN in the presence of excess amount of CaM is 2.5–3 (Stemmer and Klee, 1994; Klee et al., 1998). |
| 2 | 20 $\mu$M$^{-1}$s$^{-1}$ | 1 s$^{-1}$ | (Stemmer and Klee, 1994; Klee et al., 1998). |
| 3 | 10 $\mu$M$^{-1}$s$^{-1}$ | 2 s$^{-1}$ | (Stemmer and Klee, 1994; Klee et al., 1998). |

**Table SIi.** Molecular-Molecular Interactions in PP1·I-1 System

| No. | Kf ($\mu$M$^{-1}$s$^{-1}$) | Kb (s$^{-1}$) | Notes |
|---|---|---|---|
| 1 | 1 | 100 | (Huang et al., 1999; Huang and Paudel, 2000). |

**Table SIj.** Enzymatic Reactions in PP1·I-1 System

| No. | Km ($\mu$M) | kcat (s$^{-1}$) | Notes |
|---|---|---|---|
| 2 | 8.1 | 5.3 | (Hemmings et al., 1984; Huang et al., 1999; Huang |

| | | | |
|---|---|---|---|
| | | | and Paudel, 2000). |
| 3 | 3 | 2.8 | Assumption. |
| 4 | 3 | 2.8 | (Klee et al., 1998). |

**Table SIk.** Time Constants of AMPAR Recycling System

| AMPAR-State | Nophos | S845P | PDZsP | S845P/ PDZsP | Notes |
|---|---|---|---|---|---|
| $K_{on}$ (uM$^{-1}$s$^{-1}$) | 0.03 | 0.03 | 0.5 | 0.5 | AMPAR punctates exist at PSD, and AMPARs are accumulated at PSD by LTP inducing stimulation (Shi et al., 1999; Hayashi et al., 2000; Andrasfalvy and Magee, 2004). |
| $K_{off}$ (s$^{-1}$) | 0.0333 | 0.0333 | 0.0333 | 0.0333 | Mean trapping time of AMPARs by scaffold is 30–60 s (Borgdorff and Choquet, 2002). |
| $\tau_{diff}$ (s) | 0.313 | 0.313 | 0.313 | 0.313 | Calculated from 0.4 $\mu$m$^2$s$^{-1}$ diffusion coefficient and 0.2–0.6 $\mu$m distance between PSD and cytosol (Tardin et al., 2003; Racz et al., 2004; Adesnik et al., 2005). |
| $K_{exo}$ (s$^{-1}$) | 0 | 5.55× 10$^{-4}$ | 0 | 5.55× 10$^{-4}$ | Time constant of S845-P GluR1 exocytosis is 30 min (Ehlers, 2000; Passafaro et al., 2001; Esteban et al., 2003). |
| $K_{endo}$ (s$^{-1}$) | 1 | 1.85× 10$^{-3}$ | 1 | 1.85× 10$^{-3}$ | The time constant of GluR1 endocytosis at the basal level is 9 min (Ehlers, 2000; Lin et al., 2000), and that of S845-P GluR1 was assumed to be accelerated (Kittler et al., 2005; Tigaret et al., 2006). |

**Table SII.** AMPAR Phosphorylation/Dephosphorylation

| No. | Kf ($\mu$M$^{-1}$s$^{-1}$) | Notes |
|---|---|---|
| S845 phospho by PKA | 20 | Ser845 of GluR1 is phosphorylated at the naïve state (Lee et al., 2000). Phosphorylation time constant were based on (Heynen et al., 2000; Snyder et al., 2003). |

| PDZs phospho by CaMKII | 1 | PDZs should be dephosphorylated at the naïve state for LTP. The phosphorylation time constant was assumed to be similar to that of Ser831 of GluR1 (Lee et al., 2000). |
|---|---|---|
| S845 dephospho by PP1 and PP2A | 4 | GluR1 is phosphorylated at Ser845 in the naïve state (Lee et al., 2000). The Phosphorylation time constant was based on (Heynen et al., 2000; Snyder et al., 2003). |
| PDZs dephospho by PP1 and PP2A | 100 | PDZs should be dephosphorylated at the naïve state for LTP. The phosphorylation time constant was assumed to be similar to that of Ser831 of GluR1 (Lee et al., 2000). |
| S845 dephospho by CaN | 1.5 | GluR1 is phosphorylated at Ser845 in the naïve state (Lee et al., 2000). The phosphorylation time constant was based on (Heynen et al., 2000; Snyder et al., 2003). |
| PDZs dephospho by CaN | 1 | PDZs should be dephosphorylated at the naïve state for LTP. The phosphorylation time constant was assumed to be similar to that of Ser831 of GluR1 (Lee et al., 2000). |

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