

# Instructions for kuzumoto\_et\_al\_2007

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## 1. Instructions for kuzumoto\_et\_al\_2007

This document describes how to regenerate figures in [Kuzumoto et al. 2007](#).

1. Run Table1-0Hz.make.xml at xml/takeuchi\_et\_al\_2006, which makes Table1-0Hz.xml at target/takeuchi\_et\_al\_2006 and GUI will open it. Then click [Model] - [Start] and save the result xml after calculation.

Right click Table1-0Hz.make.xml and select [simBio] - [Run Protocol] on Package Explorer of Eclipse. Then the simBio GUI will appear, so click [Model] - [Start], and wait until the calculation is over. It will take hours depends on your machine power. If you run on a single core CPU and want to stop during calculation, please use Task Manager with [Ctrl] + [Alt] + [Del] key combination on Windows.

After calculation, please save the result with simBio menu [File] - [Save].

2. Run kuzumoto\_et\_al\_2007\_0.0Hz.make.xml at xml/kuzumoto\_et\_al\_2007, which makes kuzumoto\_et\_al\_2007\_0.0Hz.xml at target/kuzumoto\_et\_al\_2007 from target/takeuchi\_et\_al\_2006/Table1-0Hz.xml, and GUI will appear. Then [Model] - [Start] and save the result xml after calculation.

The calculated file is stored as src/xml/kuzumoto\_et\_al\_2007/kuzumoto\_et\_al\_2007\_0.0Hz.xml, which you can use as the result instead of waiting time consuming calculation. To do so, please copy the xml to target/kuzumoto\_et\_al\_2007, or alternatively edit the "basemodel" path in the following make xml.

3. Run kuzumoto\_et\_al\_2007\_2.5Hz.make.xml at xml/kuzumoto\_et\_al\_2007, which makes kuzumoto\_et\_al\_2007\_2.5Hz.xml at target/kuzumoto\_et\_al\_2007 from 0.0Hz. Then execute and save the result.

For your convenience, the calculated file is stored at src/xml/kuzumoto\_et\_al\_2007/kuzumoto\_et\_al\_2007\_2.5Hz.xml. You can move this file to target/kuzumoto\_et\_al\_2007 before proceeding, instead of waiting for the calculation to finish.

4. Now, Fig.2\_3\_4.make.xml, Fig.5.protocol.xml, Fig.6.protocol.xml, Fig.7\_8.protocol.xml can be executed by right click and select [simBio] - [Run Protocol]. Those xmls make data at target/kuzumoto\_et\_al\_2007 folder for Figures.

## 2. Errata

### 2.1. Manuscript

- p. 5, l. 46, "Matsuoka et al, 2003" should be "Matsuoka et al, 2004".
- p. 12, l. 26, "(Fig. 8B, right)" should be "(Fig. 8, right)".

### 2.2. Supplementary data

#### 2.2.1. Table S5

The last character like a rectangle # following "Rmc" can be omitted in the equation of [Ptotal]i.

Add equation,  $d[\text{ATPCaPump}] = d[\text{ATPSERCA}] + d[\text{ATPPMCA}]$

### 2.2.2. Table S7

Equation of I<sub>CaL</sub> was expressed considering fPKA changes between 0 and 1.

In org.simBio.bio.kuzumoto\_et\_al\_2007.current.cf.ICaL, PKA\_factor changes between 1 and about 3.87.

In equation of rate (C#CCa) =  $k_{C,CCa} \cdot ([Ca^{2+}]_{cm} \cdot p(AP)) \cdot p(U)$ , p(U) should be p(C).

### 2.2.3. Table S8

Equation was expressed considering fPKA changes between 0 and 1.

In org.simBio.bio.kuzumoto\_et\_al\_2007.current.potassium.IKs, fPKA changes between 1 and 2.3.

### 2.2.4. Table S14

In source code, field names are similar to the paper Negroni and Lascano, 1996.

To correct half sarcomere length at rest, bias1 (r1 in source) and bias2 (r2) was introduced, because  $[Ca^{2+}]_i$  at rest is increased compared to the previous models.

The equation "#5 =  $0.027 \times \text{ATPfactor}$ " should be "#5 =  $8000 \times \text{ATPfactor}$ ".

### 2.2.5. Table S16

The sum of cation #Na+K+2×Ca# doesn't equal to the sum of anion (Cl+LA) under 2.5 Hz stimulation. Because of the Ca handling through SR as discussed in Takeuchi et al., 2006.