**Circulation model (Windkessel, Body Fluid Dynamic, CV with hemodialysis)**

**Simulation Parameter{**

Input: Simulation Mode— Type: ComboBox

simulation\_mode = Hemodialysis {Hemodialysis, Cardiovascular, Hemodialysis-Cardiovascular}

Input: Time Step — Type: TextBox

time\_step = 0.1667 // seconds

Input: Outflow — Type: ComboBox

is\_outflow = true

Input: Inflow — Type: ComboBox

is\_inflow = true

**}**

**3D organ model (Electro, Mechanical)**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Multi-Dimensional Stimulus Protocol{**

Input: Computation Time — Type: TextBox

maximum\_time: 5000000

Input: Stimulus Mode — Type: ComboBox

stimulus\_mode : S1 Stimulus {S1 Stimulus, S1S2 Stimulus}

Input: GNa — Type: Slider

gna\_scale :1.5

**}**

**Mesh Profile{**

Input: Mesh File (INP) — Type: FileBrowse

mesh\_file: ./mesh\_elect/vent/human\_hf\_214319/heart\_het.inp

Input: Fiber Mesh File (INP) — Type: FileBrowse

fiber\_mesh: fiber.inp

Input: Surface Mesh File — Type: FileBrowse

surface\_file:./mesh\_elect/vent/human\_hf\_214319/surface.inp

Input: Mesh Type — Type: ComboBox

mesh\_type: tet {tet,tetfiber,square,triangle}

Input: Dimension — Type: ComboBox

mesh\_dimension: 3 {2,3}

Input: VTK Output — Type: ComboBox

vtk\_output: solid {solid, surface}

Input: S1 Stimulus Nodes — Type: FileBrowse

pace\_s1\_file: ./mesh\_elect/vent/human\_hf\_214319/heart\_apex.dat

Input: S2 Stimulus Nodes — Type: FileBrowse

pace\_s2\_file: ./mesh\_elect/vent/human\_hf\_214319/heart\_L.dat

**}**

**Diffusion Profile{**

Input: Diffusion Scale — Type: TextBox

diffusion\_scale : 3.0

Input: Diffusion Scale Fiber — Type: TextBox

diffusion\_scale\_fiber : 0.1

Input: Diffusion Mode — Type: ComboBox

diffusion\_mode: normal {normal, fibrosis}

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Bootstrap**

**Drug Option{**

Input: Dose Response Data — Type: FileBrowse

experimental\_file = hill\_experiment\_data/drug\_block\_4channels.csv

Input: Drug Name — Type: TextBox

drug\_name = quinidine

Input: Number of Samples — Type: TextBox

sample\_size = 20

Input: Fitting Type — Type: ComboBox

fitting\_type = Hill {Hill, hERG Dynamic}

**}**

**Cardiac Muscle**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Ionic Conductance Scaling{**

Input: GKs — Type: Slider — Min: 0.1 — Max: 100.0

gks\_scale :1.0

Input: GKr — Type: Slider — Min: 0.1 — Max: 100.0

gkr\_scale :1.0

Input: GK1 — Type: Slider — Min: 0.1 — Max: 100.0

gk1\_scale :1.0

Input: PCa —Type: Slider — Min: 0.1 — Max: 100.0

gcal\_scale :1.0

Input: GNa — Type: Slider — Min: 0.1 — Max: 100.0

gna\_scale :1.0

Input: GNaL — Type: Slider — Min: 0.1 — Max: 100.0

gnal\_scale :1.0

Input: GNab — Type: Slider — Min: 0.1 — Max: 100.0

gnab\_scale :1.0

Input: Gcab — Type: Slider — Min: 0.1 — Max: 100.0

gcab\_scale :1.0

Input: Gncx — Type: Slider — Min: 0.1 — Max: 100.0

gncx\_scale :1.0

**}**

**in silico simulation**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Simulation Settings{**

Input: Cores — Type: ComboBox

simulation\_type: CPU {CPU, GPU}

Input: Number of Cores — Type: TextBox

number\_of\_cpu: 10

**}**

**Postprocessing**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: FALSE

numbers\_pacing: 1

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: FALSE

numbers\_pacing\_write : 1

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Simulation Settings{**

Input: Cores — Type: ComboBox

simulation\_type: CPU {CPU, GPU}

Input: Number of Cores — Type: TextBox

number\_of\_cpu: 10

**}**

**Restitution**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Restitution{**

Input: Cycle Length End— Type: TextBox

cycle\_length\_end : 200

Input: Cycle Length Step — Type: TextBox

cycle\_length\_step : 100

**}**

**Simulation Settings{**

Input: Cores — Type: ComboBox

simulation\_type: CPU {CPU, GPU}

Input: Number of Cores — Type: TextBox

number\_of\_cpu: 10

**}**

**Population**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: FALSE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Population{**

Input: Using Population — Type: ComboBox —- Enabled: FALSE

is\_population : true

Input: Population Data File — Type: FileBrowse

Population\_file : population.dat

**}**

**Simulation Settings{**

Input: Cores — Type: ComboBox

simulation\_type: CPU {CPU, GPU}

Input: Number of Cores — Type: TextBox

number\_of\_cpu: 10

**}**

**Genetic Variation**

**Cell Profile{**

Input: Cell Model — Type: ComboBox

cell\_model : ORdv1.0\_epi {ORdv1.0\_epi, ORdstatic, Margara}

Input: Solver — Type: ComboBox

solver : Euler {Euler, CVODE}

Input: Time Step — Type: TextBox

time\_step\_min : 0.5

Input: Time Step Maximum — Type: TextBox

time\_step\_max : 2.0

Input: Writing Time Step — Type: TextBox

writing\_step : 2.0

Input: Genetic Variation — Type: ComboBox —- Enabled: TRUE

mutation: Normal {Normal,A385,G504,A385+G504}

**}**

**Stimulus Protocol{**

Input: Number of Pacing — Type: TextBox —- Enabled: TRUE

numbers\_pacing: 100

Input: Number of Paces to Write Count — Type: TextBox —- Enabled: TRUE

numbers\_pacing\_write : 10

Input: Cycle Length — Type: TextBox

cycle\_length : 2000

Input: Stimulus Duration — Type: TextBox

stimulus\_duration : 0.5

Input: Stimulus Amplitude Scale — Type: TextBox

stimulus\_amplitude scale : 1.0

**}**

**Drug Profile{**

Input: Drug Name — Type: TextBox

drug\_name: bepridil

Input: Drug Concentrations — Type: TextBox

drug\_concentrations: 33.0,66.0,99.0,132.0

Input: Hill File — Type: FileBrowse

hill\_file: bepridil/IC50\_samples.csv

Input: hERG Dynamic File — Type: FileBrowse

hERG\_file: bepridil/boot\_pars.csv

**}**

**Simulation Settings{**

Input: Cores — Type: ComboBox

simulation\_type: CPU {CPU, GPU}

Input: Number of Cores — Type: TextBox

number\_of\_cpu: 10

**}**