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The model fitting

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/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:36: RuntimeWarning: overflow encountered in power

return A\*(t\*\*gamma)

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/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:49: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

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/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:185: RuntimeWarning: overflow encountered in exp

return ((A)/(np.exp(np.exp(-alpha\*(t-tau)))-C))

Fitting is done!

Warning: Ignoring XDG\_SESSION\_TYPE=wayland on Gnome. Use QT\_QPA\_PLATFORM=wayland to run on Wayland anyway.

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The transformation scales increasing the age from 80 years to 160 years

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The PLM: epsilon\_PLM = 0.693147180560

The IM-III myeloma: epsilon\_IM\_III\_myeloma = 0.000295108043

The IM-III colon: epsilon\_IM\_III\_colon = 0.004408777024

The IM-III CML: epsilon\_IM\_III\_CML = 0.091144048365

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The symmetry based framework for model selection

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The scales for the framework are the following:

PLM All datasets: epsilon\_scale = 3.465735902800

IM-III myeloma: epsilon\_scale = 0.001475540214

IM-III colon: epsilon\_scale = 0.022043885118

IM-III CML: epsilon\_scale = 0.455720241824

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return A\*(t\*\*gamma)

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/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/fit\_to\_data.py:36: RuntimeWarning: overflow encountered in multiply

return A\*(t\*\*gamma)

/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:116: RuntimeWarning: invalid value encountered in log

t\_hat = np.log(np.log(np.exp(np.exp(-alpha\*(t-tau))) - (alpha\*np.exp(alpha\*tau)\*epsilon) ))

/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:116: RuntimeWarning: invalid value encountered in log

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/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:116: RuntimeWarning: invalid value encountered in log

t\_hat = np.log(np.log(np.exp(np.exp(-alpha\*(t-tau))) - (alpha\*np.exp(alpha\*tau)\*epsilon) ))

The output:

Myeloma:

PLM, number of transformation parameters: 2820

IM-III, number of transformation parameters: 368

Colon cancer:

PLM, number of transformation parameters: 2688

IM-III, number of transformation parameters: 424

CML:

PLM, number of transformation parameters: 2740

IM\_III, number of transformation parameters: 497

Symmetry framework is done!

Illustrate framework!

PLM

PLM epsilon scale: 0.693

IM-III

IM-III epsilon scale: 0.003

/home/johannes/Dropbox/Work/Projects/symmetry\_based\_model\_selsection\_carcinogenesis/Code/symmetry\_toolbox.py:116: RuntimeWarning: invalid value encountered in log

t\_hat = np.log(np.log(np.exp(np.exp(-alpha\*(t-tau))) - (alpha\*np.exp(alpha\*tau)\*epsilon) ))

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Action of symmetries!

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Epsilon scales for illustrations (i.e. the value that the transformations are pushed with twice)

PLM, 0.3465736

IM-III, 0.0001033

libGL error: MESA-LOADER: failed to open iris: /usr/lib/dri/iris\_dri.so: cannot open shared object file: No such file or directory (search paths /usr/lib/x86\_64-linux-gnu/dri:\$${ORIGIN}/dri:/usr/lib/dri, suffix \_dri)

libGL error: failed to load driver: iris

libGL error: MESA-LOADER: failed to open swrast: /usr/lib/dri/swrast\_dri.so: cannot open shared object file: No such file or directory (search paths /usr/lib/x86\_64-linux-gnu/dri:\$${ORIGIN}/dri:/usr/lib/dri, suffix \_dri)

libGL error: failed to load driver: swrast

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Calculations are done!

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