

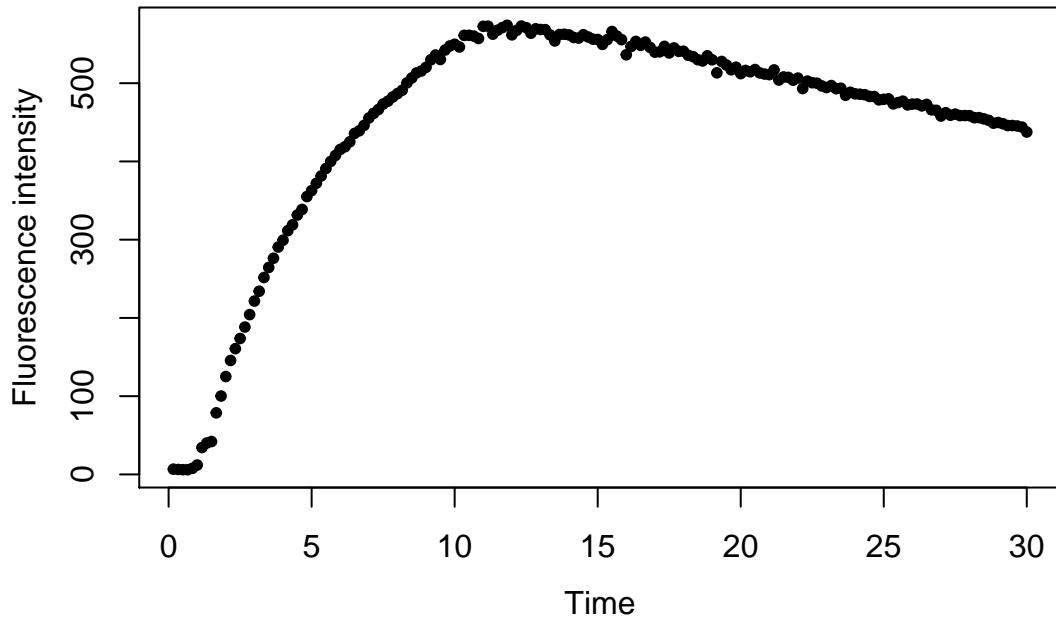
Analysis of individual stanfit objects

November 3, 2020

```
Rscript -vanilla -e 'pars <- commandArgs(trailingOnly=TRUE); rmarkdown::render(input = "R_markdown/Analysis_of_individual_stanfit_objects.Rmd", output_format = "pdf_document", knit_root_dir = getwd(), output_file = paste0("pdf_files/Analysis_of_individual_stanfit_objects", pars[1], " ", pars[2], "", pars[3], ".pdf"), params = list(dataset = pars[1], model_type = pars[2], index_trajectory = as.numeric(pars[3])))' experimental_data_d2eGFP ODE 12
```

Dataset: experimental_data_eGFP, model type: SDE

Trajectory 27



	mean	se_mean	sd	5%	50%	95%	n_eff
theta[1]	0.194	0.001	0.025	0.153	0.195	0.236	2166
theta[2]	0.547	0.041	0.629	0.102	0.326	1.729	231
theta[3]	0.020	0.000	0.003	0.015	0.019	0.026	1138
m0	281.227	12.335	196.925	48.930	238.413	662.926	255
sigma	0.020	0.000	0.001	0.018	0.020	0.022	15325
scale	1.830	0.020	0.479	1.168	1.776	2.664	592
offset	6.524	0.000	0.058	6.430	6.524	6.618	18959
prod_theta2_m0	79.871	0.877	21.742	49.380	77.240	119.151	615
prod_theta2_scale	0.903	0.065	0.966	0.209	0.577	2.677	218
prod_m0_scale	531.761	25.382	431.505	76.738	420.814	1358.557	289
prod_theta2_m0_scale	136.912	0.165	12.510	117.113	136.448	158.344	5719
x[180,1]	1.010	0.065	1.155	0.044	0.633	3.314	318
x[180,2]	253.506	2.794	65.436	163.491	244.663	371.931	548
			Rhat				
theta[1]	1.003						
theta[2]	1.036						

```
theta[3]           1.008
m0                1.031
sigma              1.000
scale              1.013
offset              1.000
prod_theta2_m0     1.012
prod_theta2_scale   1.040
prod_m0_scale      1.029
prod_theta2_m0_scale 1.001
x[180,1]           1.025
x[180,2]           1.014
```

Divergences:

0 of 20000 iterations ended with a divergence.

Tree depth:

0 of 20000 iterations saturated the maximum tree depth of 15.

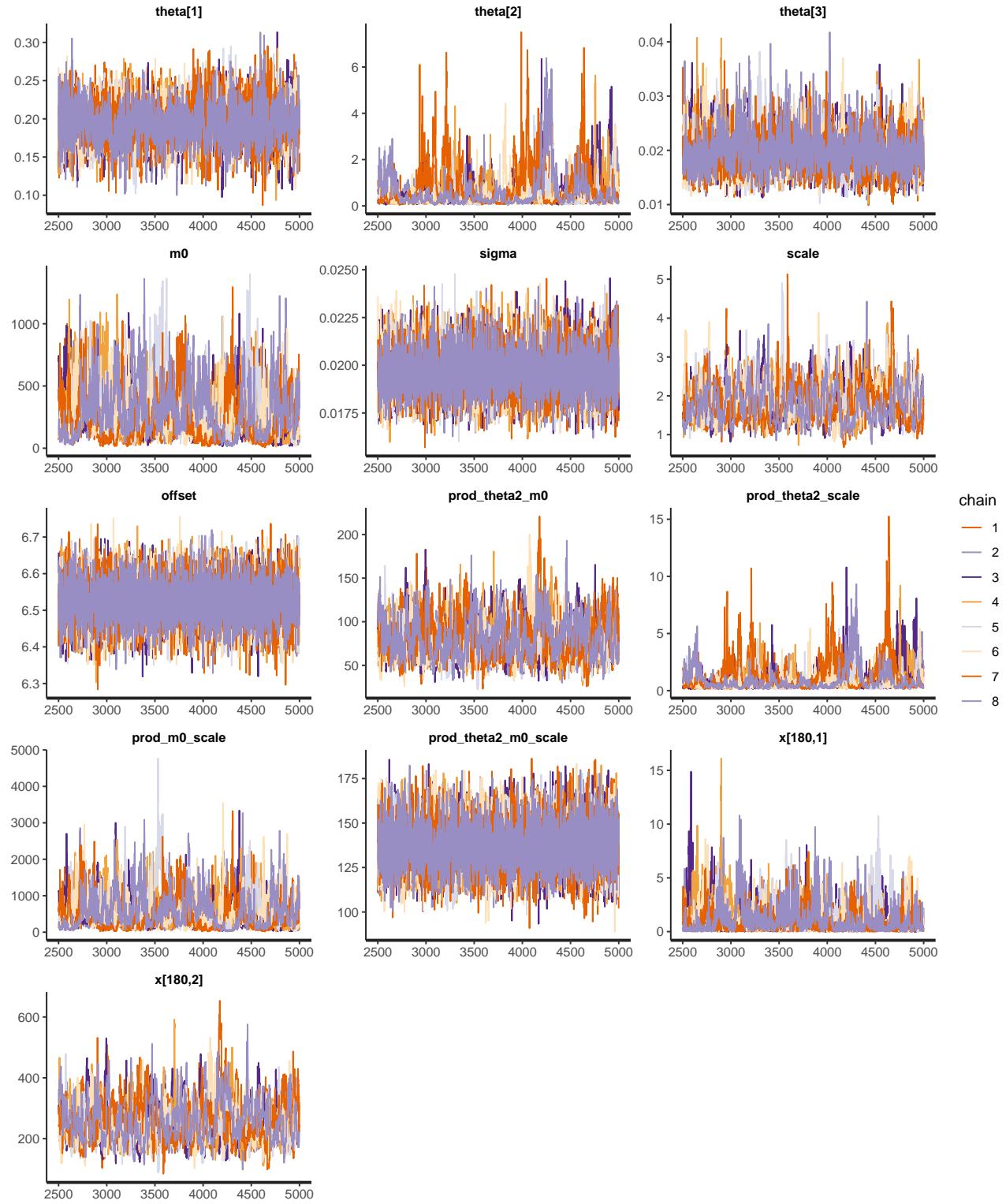
Energy:

E-BFMI indicated possible pathological behavior:

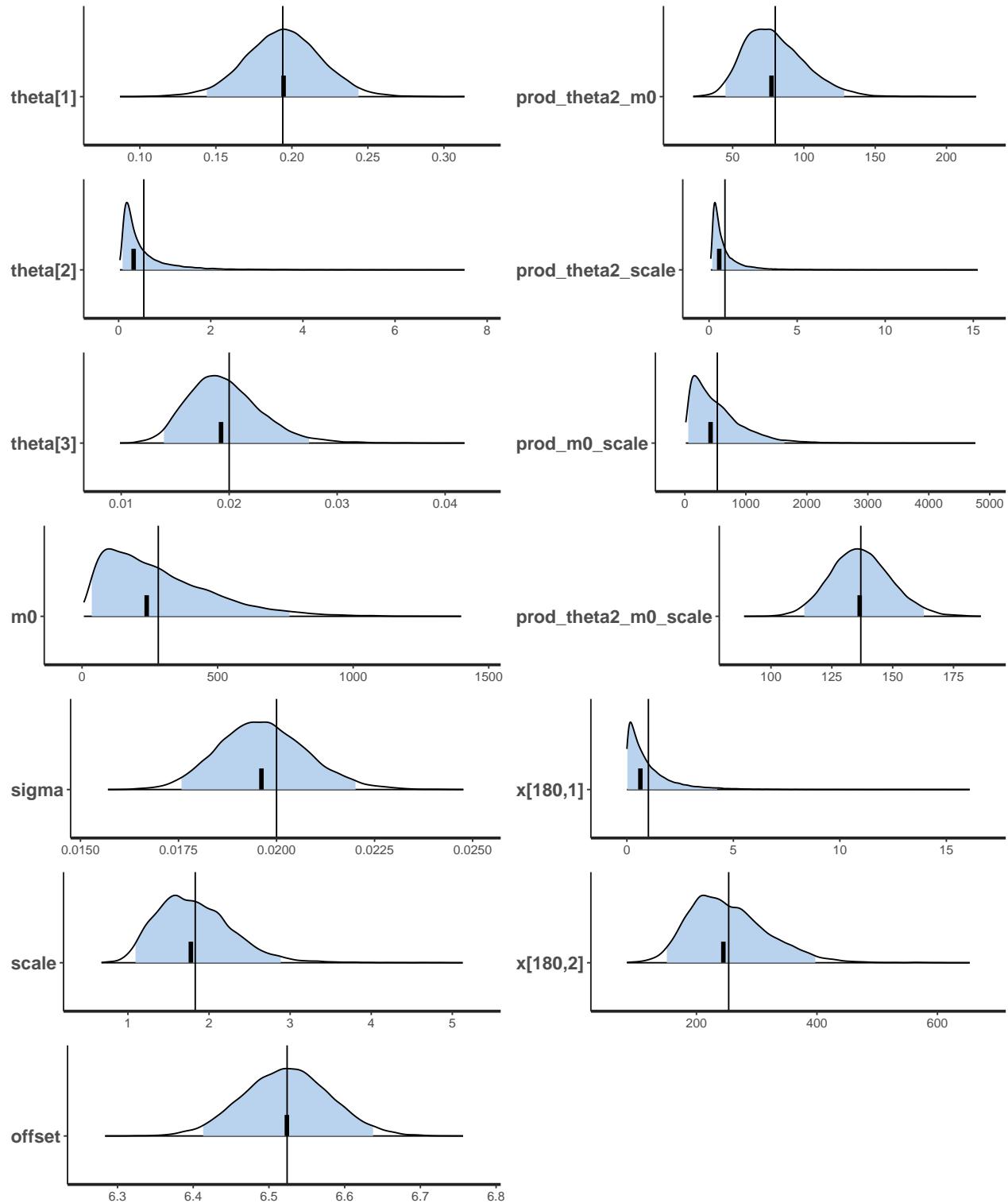
```
Chain 1: E-BFMI = 0.093
Chain 2: E-BFMI = 0.111
Chain 3: E-BFMI = 0.060
Chain 4: E-BFMI = 0.070
Chain 5: E-BFMI = 0.080
Chain 6: E-BFMI = 0.113
Chain 7: E-BFMI = 0.058
Chain 8: E-BFMI = 0.075
```

E-BFMI below 0.2 indicates you may need to reparameterize your model.

Traceplots



Density plots with 95% CI and median



Pair plots

