

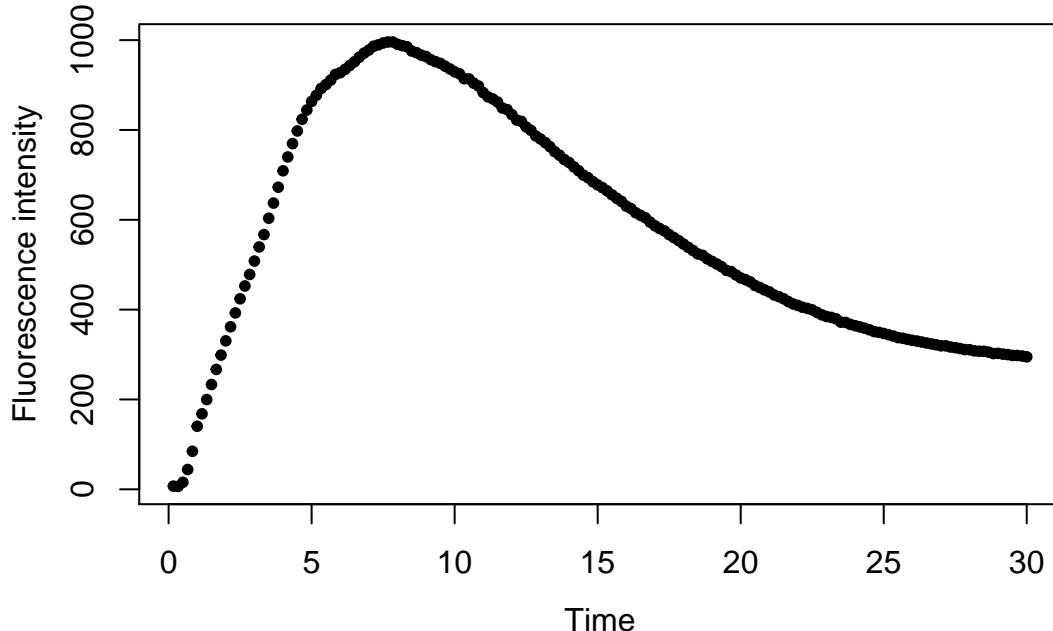
# Analysis of individual stanfit objects

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[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\_d2eGFP, model type: SDE**

**Trajectory 9**



	mean	se_mean	sd	5%	50%	95%	n_eff
theta[1]	0.164	0.002	0.041	0.099	0.162	0.234	344
theta[2]	6.494	0.123	3.142	1.907	6.216	12.143	650
theta[3]	0.096	0.002	0.021	0.073	0.091	0.138	186
m0	38.338	2.398	39.772	15.290	30.968	72.499	275
sigma	0.056	0.000	0.003	0.051	0.055	0.061	14829
scale	1.766	0.044	0.789	0.854	1.615	3.273	323
offset	8.999	0.002	0.293	8.524	8.994	9.483	21002
prod_theta2_m0	193.880	4.467	78.940	88.898	179.426	342.747	312
prod_theta2_scale	10.032	0.231	4.458	4.140	9.354	18.274	373
prod_m0_scale	76.651	10.116	178.965	23.302	46.331	158.980	313
prod_theta2_m0_scale	291.042	0.342	24.567	252.920	290.008	332.544	5156
x[180,1]	1.452	0.086	1.238	0.173	1.167	3.685	205
x[180,2]	187.942	4.353	76.246	85.884	174.032	329.680	307
			Rhat				
theta[1]	1.021						
theta[2]	1.009						

```
theta[3]           1.037
m0                1.023
sigma              1.000
scale              1.041
offset              1.000
prod_theta2_m0     1.030
prod_theta2_scale   1.016
prod_m0_scale      1.024
prod_theta2_m0_scale 1.002
x[180,1]            1.033
x[180,2]            1.031
```

Divergences:

0 of 20000 iterations ended with a divergence.

Tree depth:

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

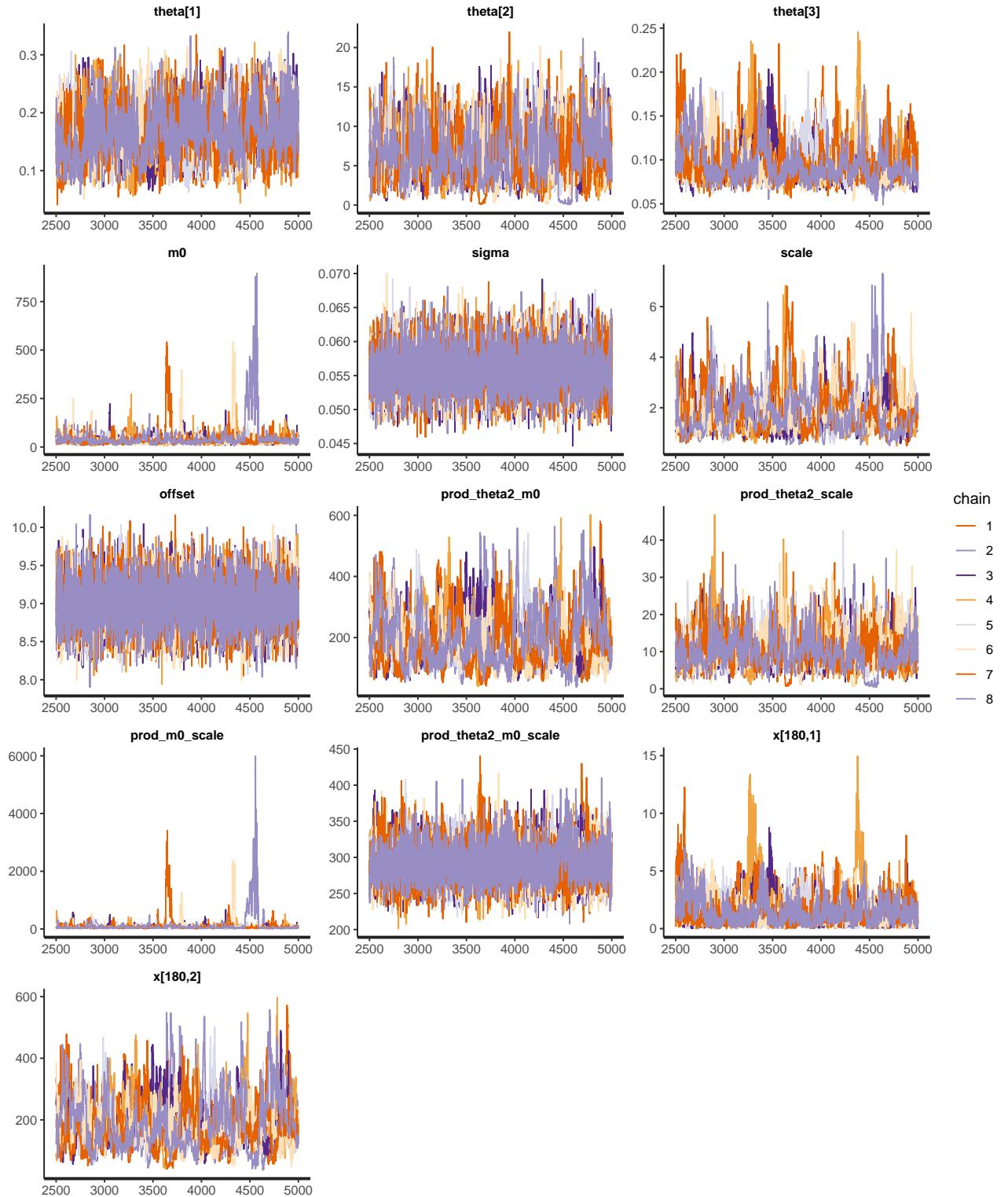
Energy:

E-BFMI indicated possible pathological behavior:

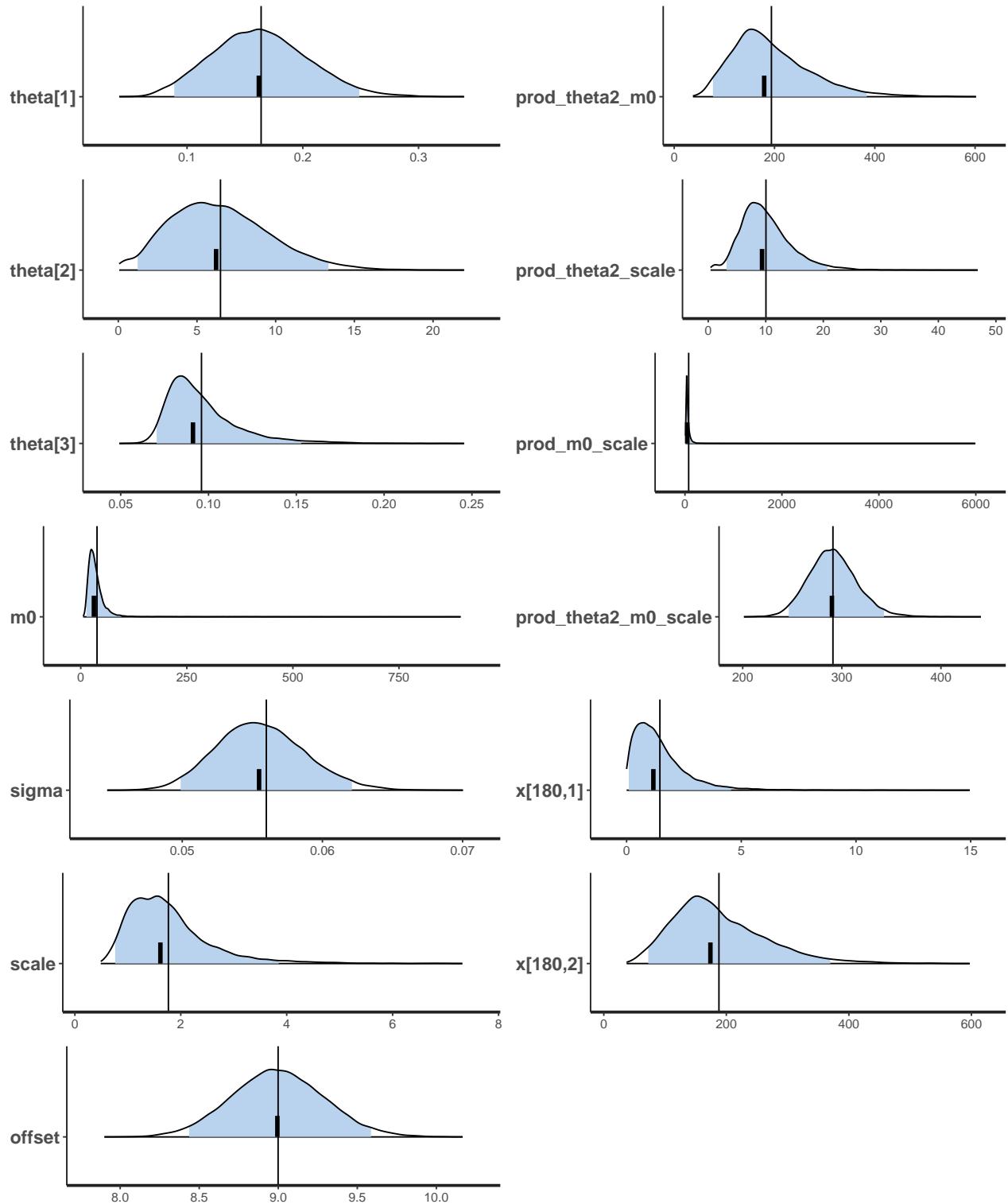
```
Chain 1: E-BFMI = 0.076
Chain 2: E-BFMI = 0.069
Chain 3: E-BFMI = 0.080
Chain 4: E-BFMI = 0.047
Chain 5: E-BFMI = 0.084
Chain 6: E-BFMI = 0.073
Chain 7: E-BFMI = 0.087
Chain 8: E-BFMI = 0.074
```

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

## Traceplots



### Density plots with 95% CI and median



## Pair plots

