

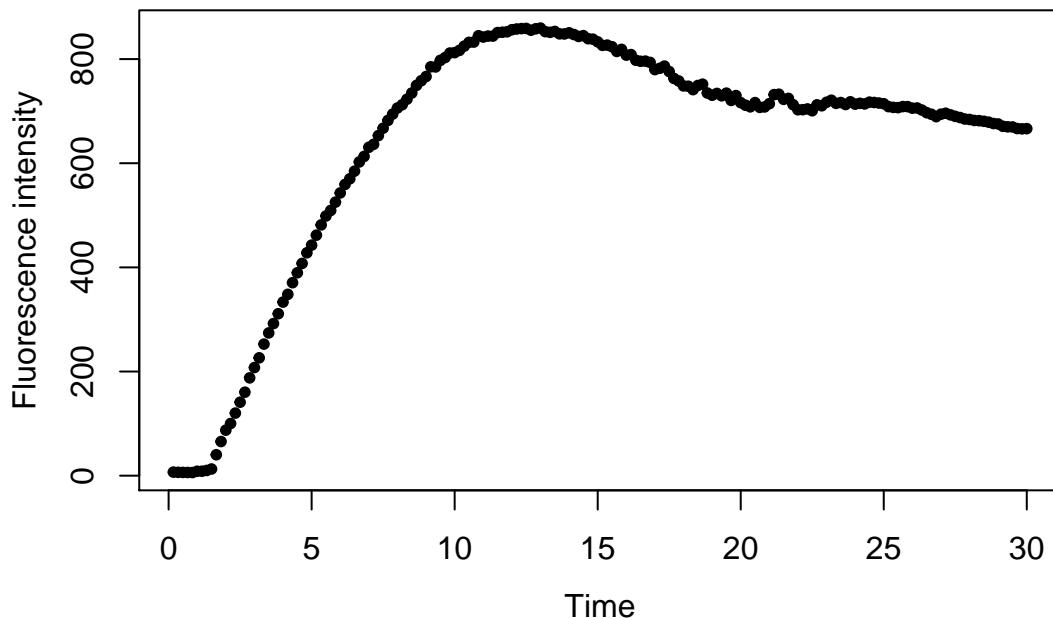
Analysis of individual stanfit objects

November 3, 2020

Dataset: experimental_data_eGFP, model type: SDE

Trajectory 33: no pathologies

Trajectory 33



	mean	se_mean	sd	5%	50%	95%	n_eff
theta[1]	0.093	0.003	0.040	0.038	0.088	0.165	130
theta[2]	7.568	0.130	3.215	2.746	7.298	13.302	614
theta[3]	0.062	0.002	0.026	0.029	0.057	0.113	111
m0	22.569	0.900	13.411	9.500	19.806	43.268	222
sigma	0.042	0.000	0.002	0.038	0.042	0.046	13000
scale	1.212	0.031	0.504	0.592	1.106	2.177	257
offset	7.240	0.001	0.109	7.064	7.239	7.420	13699
prod_theta2_m0	147.487	3.896	58.919	68.949	138.714	259.622	229
prod_theta2_scale	8.401	0.258	3.747	3.643	7.736	15.448	210
prod_m0_scale	26.437	0.925	22.814	11.164	20.960	57.410	608
prod_theta2_m0_scale	153.400	0.155	13.081	132.738	153.102	175.337	7134
x[180,1]	4.113	0.412	4.266	0.358	2.865	12.164	107
x[180,2]	628.423	16.543	246.370	300.208	590.885	1104.751	222
	Rhat						
theta[1]	1.047						
theta[2]	1.010						
theta[3]	1.063						
m0	1.034						
sigma	1.000						
scale	1.022						

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offset           1.001
prod_theta2_m0   1.027
prod_theta2_scale 1.033
prod_m0_scale    1.010
prod_theta2_m0_scale 1.001
x[180,1]         1.071
x[180,2]         1.027
```

Divergences:

0 of 20000 iterations ended with a divergence.

Tree depth:

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

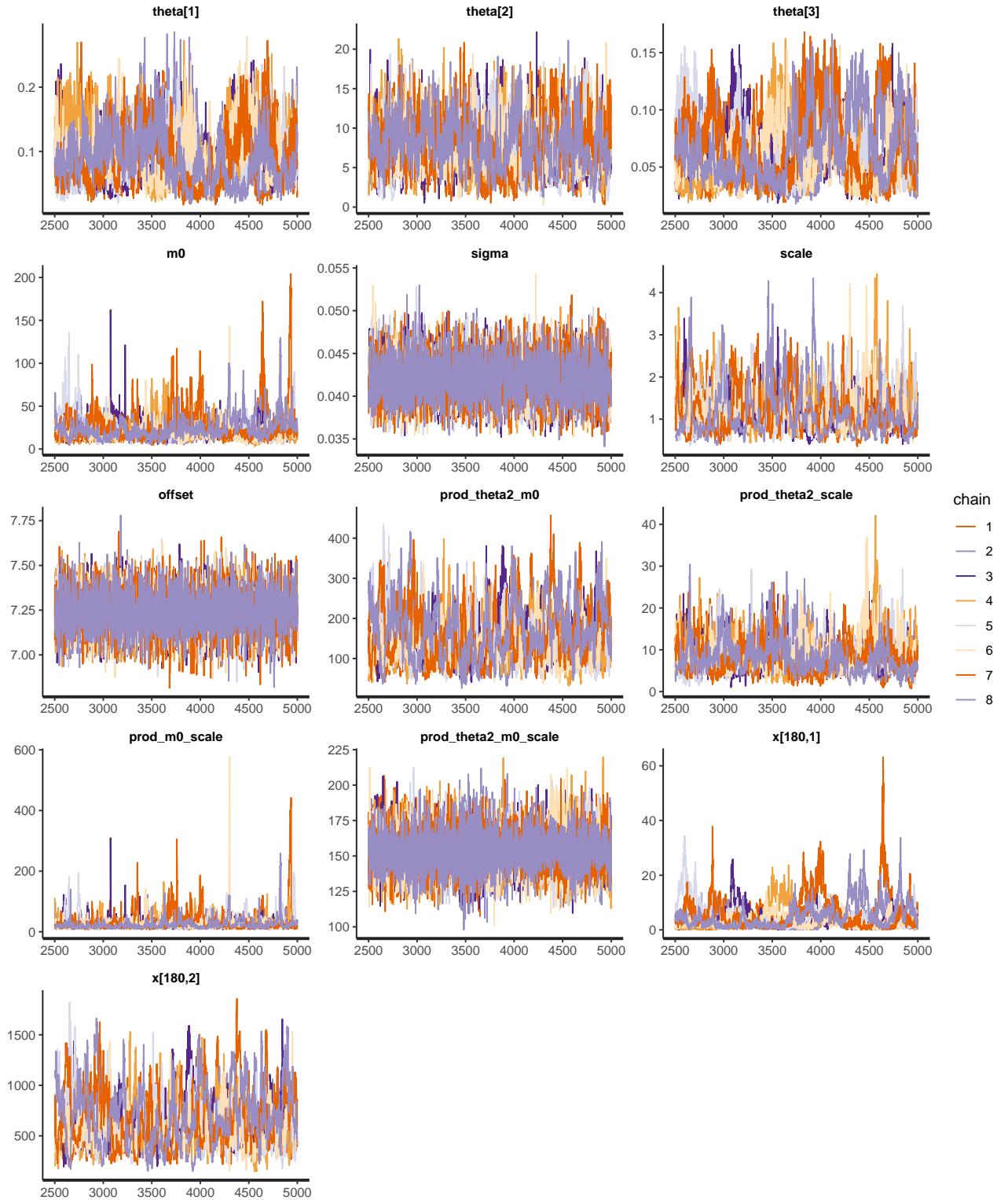
Energy:

E-BFMI indicated possible pathological behavior:

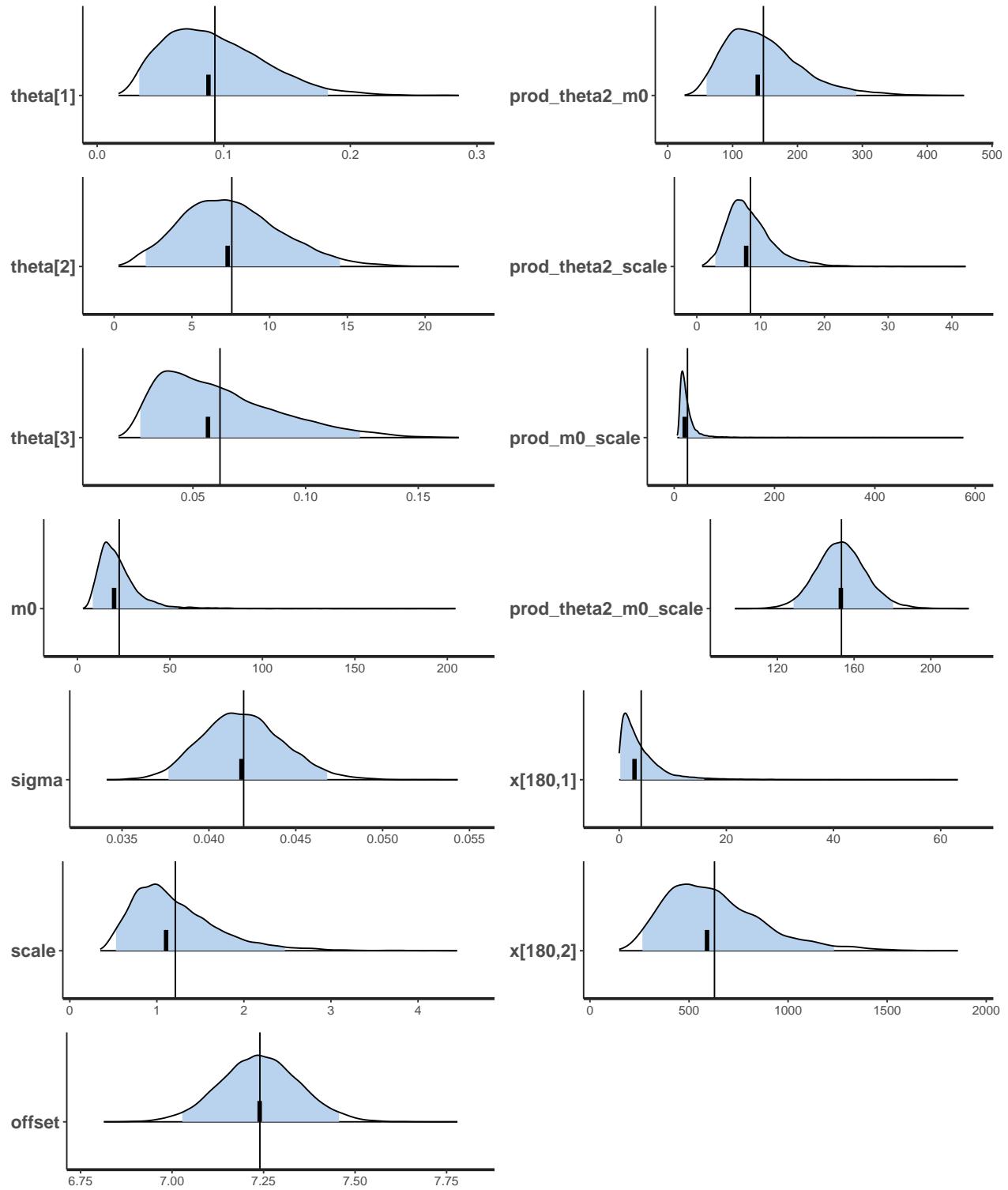
```
Chain 1: E-BFMI = 0.050
Chain 2: E-BFMI = 0.050
Chain 3: E-BFMI = 0.072
Chain 4: E-BFMI = 0.050
Chain 5: E-BFMI = 0.047
Chain 6: E-BFMI = 0.071
Chain 7: E-BFMI = 0.050
Chain 8: E-BFMI = 0.050
```

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

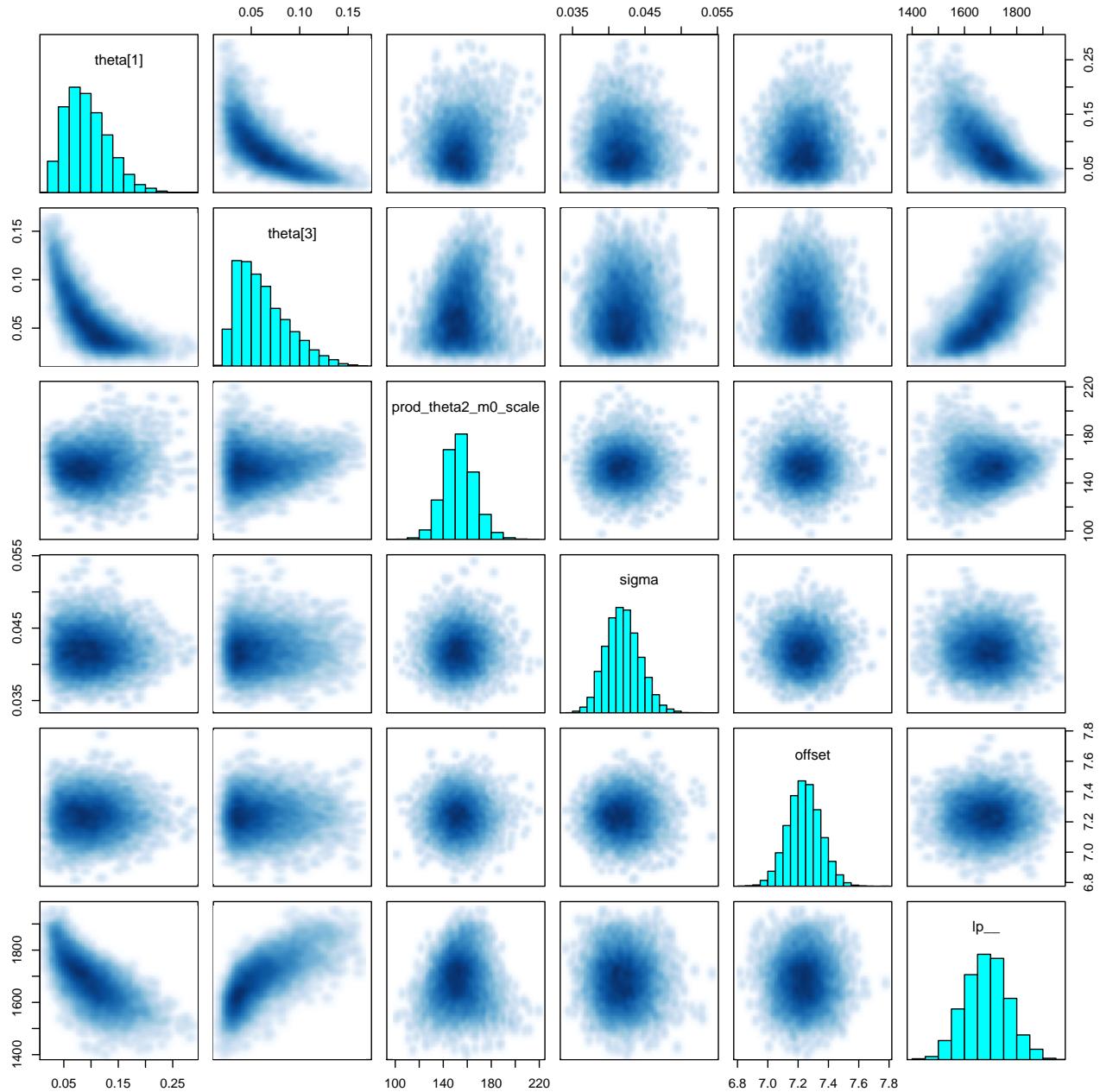
Traceplots

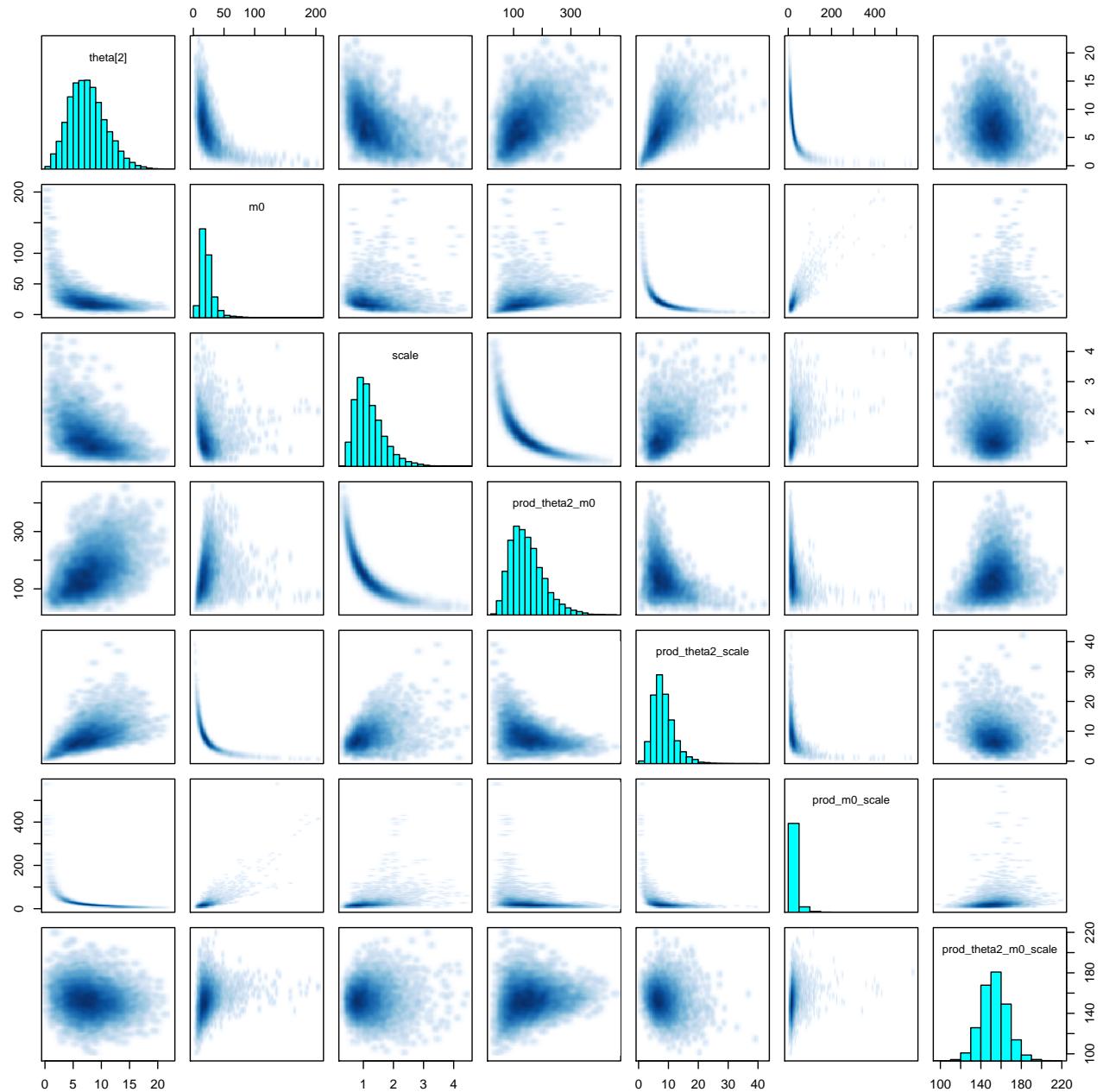


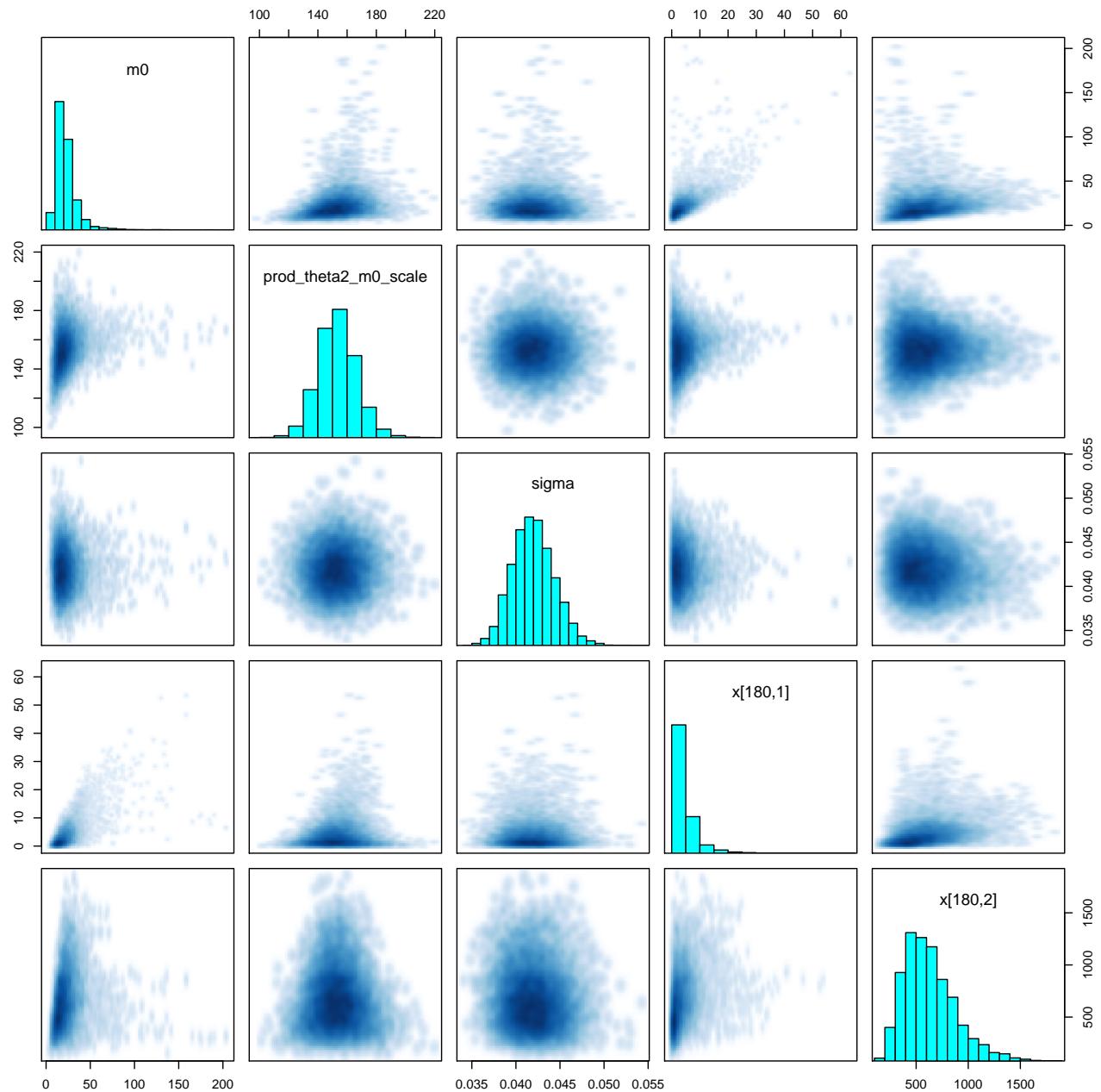
Density plots with 95% CI and median



Pair plots

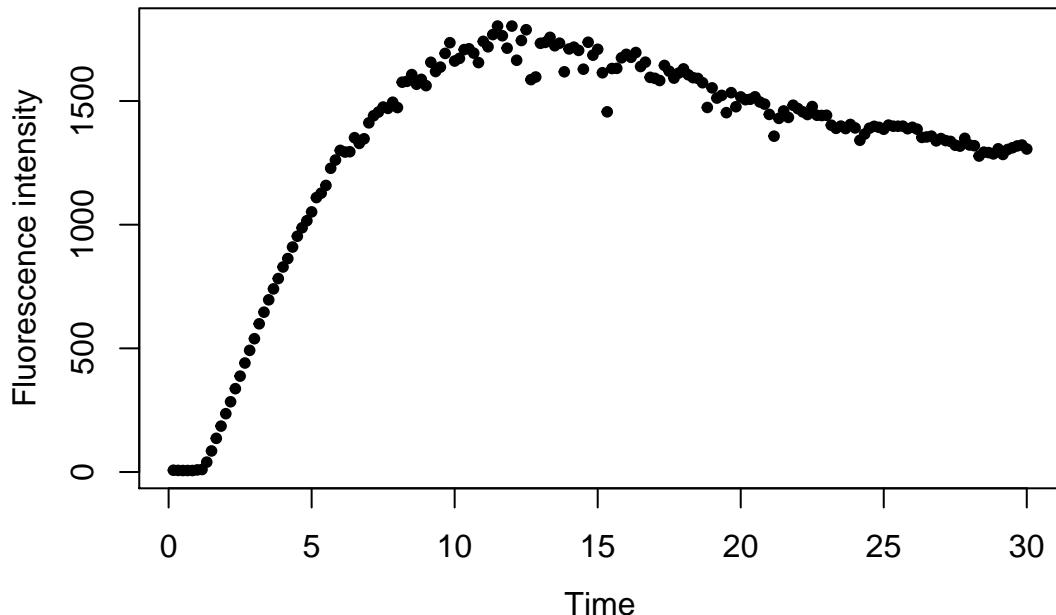






Trajectory 12: very high Rhat for theta[1] theta[3] x[180,1]

Trajectory 12



	mean	se_mean	sd	5%	50%	95%	n_eff
theta[1]	0.127	0.005	0.049	0.041	0.133	0.200	88
theta[2]	4.720	0.171	3.109	0.432	4.302	10.392	329
theta[3]	0.048	0.004	0.032	0.022	0.035	0.122	58
m0	80.003	9.170	105.746	19.059	46.740	293.108	133
sigma	0.046	0.000	0.003	0.042	0.046	0.050	11033
scale	2.282	0.087	1.296	0.903	1.921	4.842	221
offset	7.050	0.001	0.122	6.849	7.050	7.254	12105
prod_theta2_m0	206.021	7.674	106.009	76.356	188.503	397.991	191
prod_theta2_scale	8.545	0.365	5.357	1.362	7.748	18.139	215
prod_m0_scale	223.681	28.661	474.858	33.628	83.651	919.691	275
prod_theta2_m0_scale	364.741	0.818	29.861	319.961	362.705	416.457	1333
x[180,1]	7.651	3.523	27.478	0.155	1.992	20.685	61
x[180,2]	721.163	27.069	375.583	262.367	659.672	1399.841	193
	Rhat						
theta[1]	1.125						
theta[2]	1.025						
theta[3]	1.188						
m0	1.055						
sigma	1.000						
scale	1.027						
offset	1.000						
prod_theta2_m0	1.033						
prod_theta2_scale	1.029						
prod_m0_scale	1.029						
prod_theta2_m0_scale	1.005						
x[180,1]	1.167						
x[180,2]	1.032						

Divergences:

0 of 20000 iterations ended with a divergence.

Tree depth:

18 of 20000 iterations saturated the maximum tree depth of 15 (0.09%).
Try increasing 'max_treedepth' to avoid saturation.

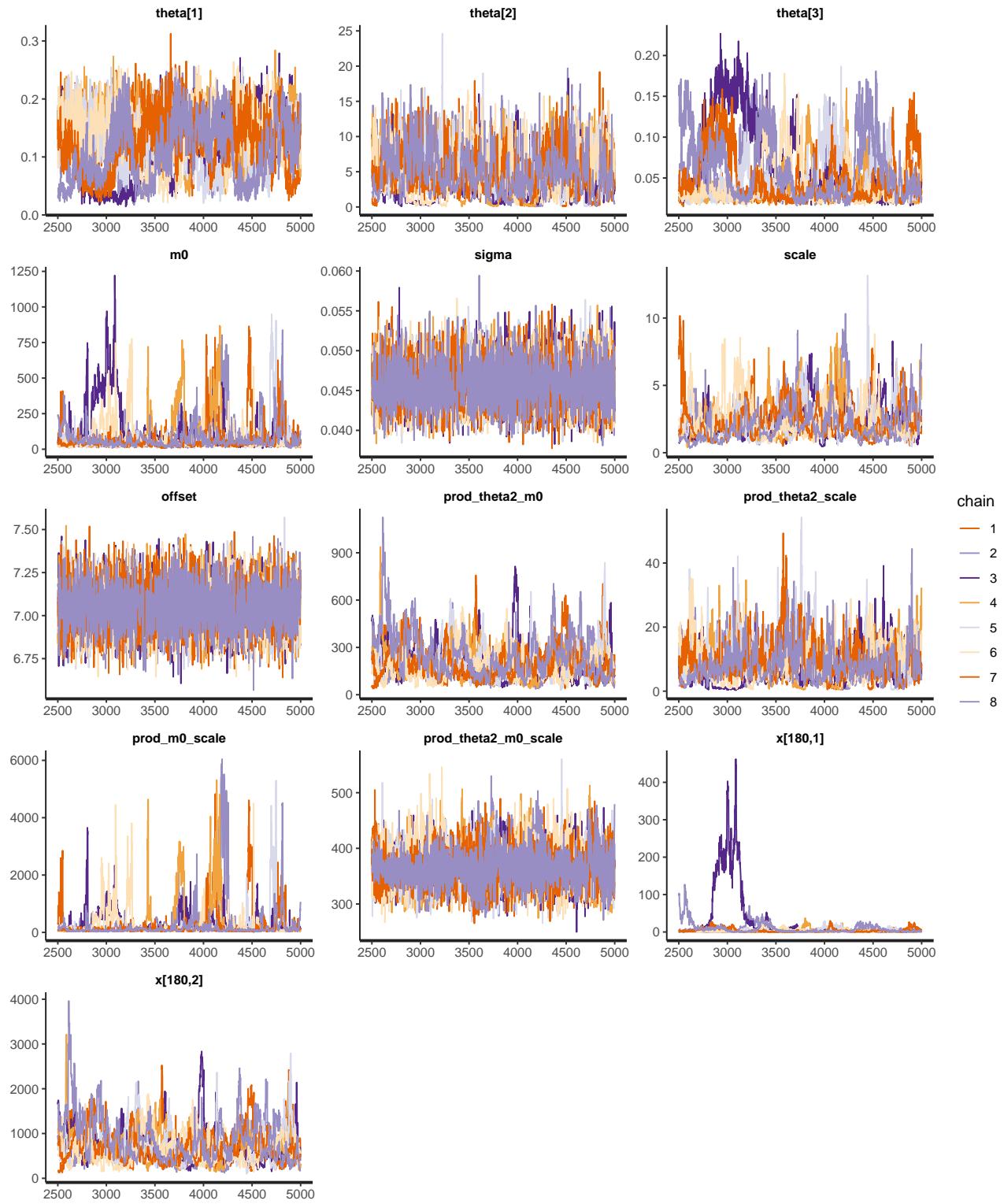
Energy:

E-BFMI indicated possible pathological behavior:

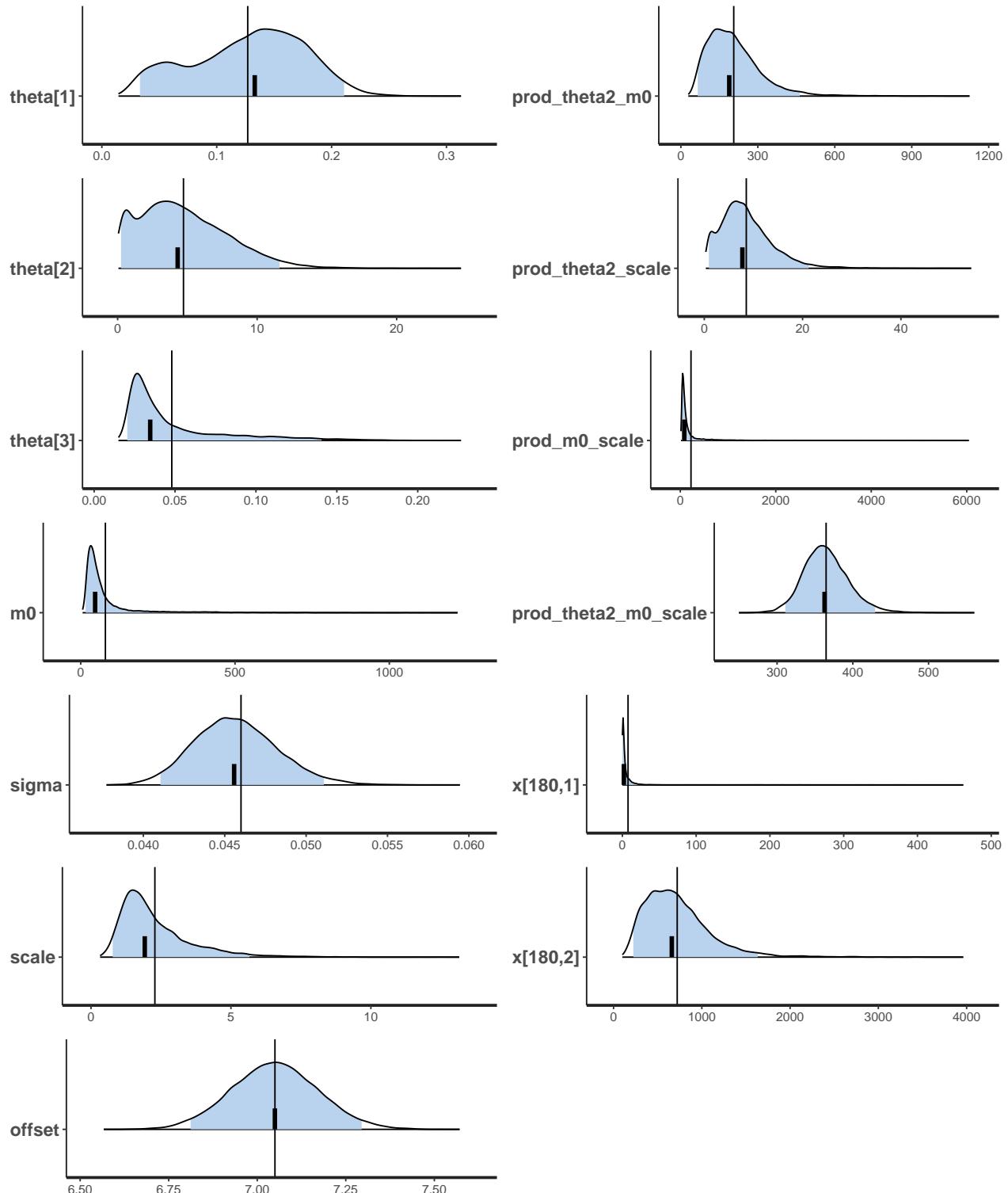
Chain 1: E-BFMI = 0.069
Chain 2: E-BFMI = 0.041
Chain 3: E-BFMI = 0.017
Chain 4: E-BFMI = 0.065
Chain 5: E-BFMI = 0.051
Chain 6: E-BFMI = 0.047
Chain 7: E-BFMI = 0.046
Chain 8: E-BFMI = 0.029

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

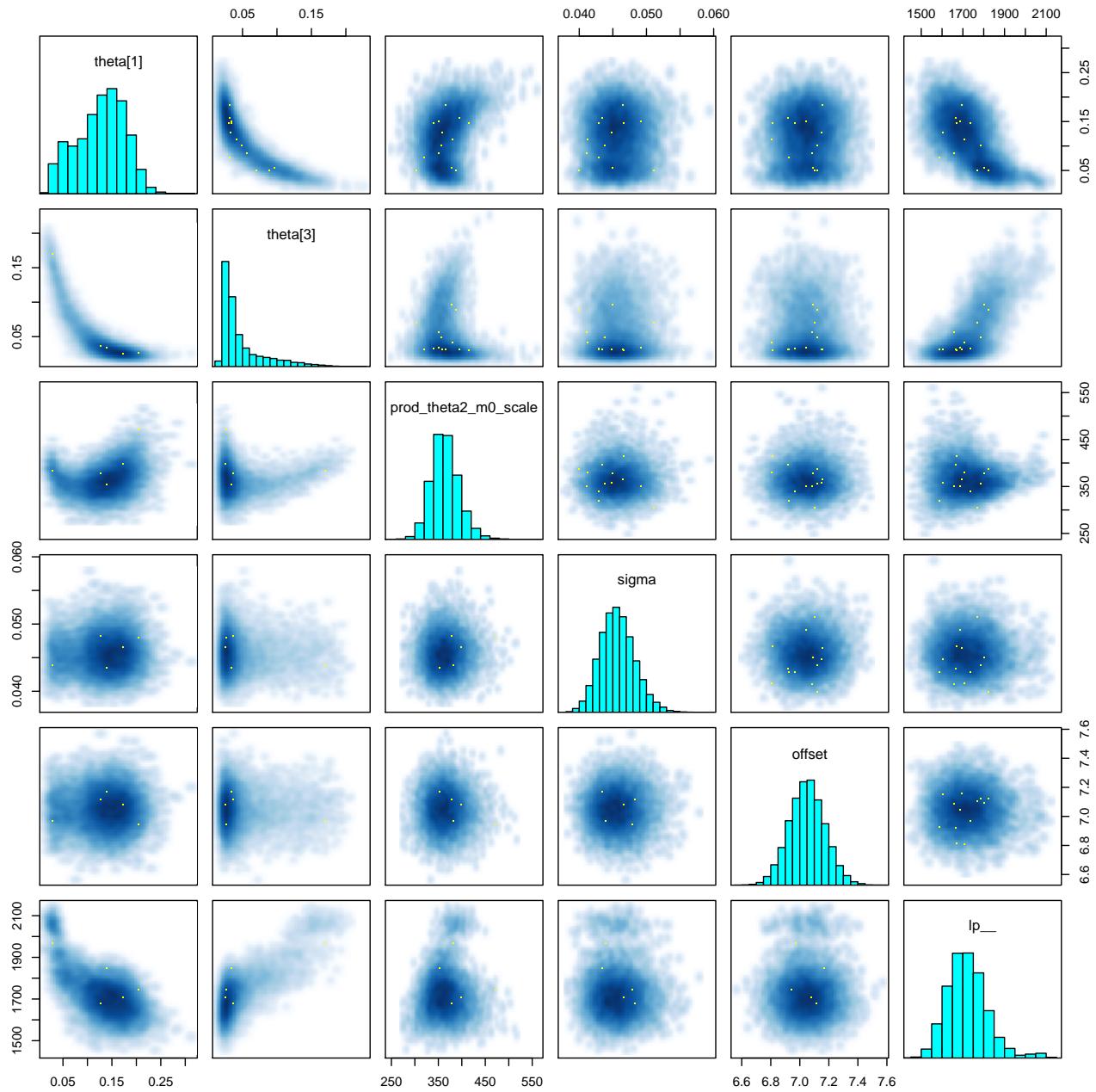
Traceplots

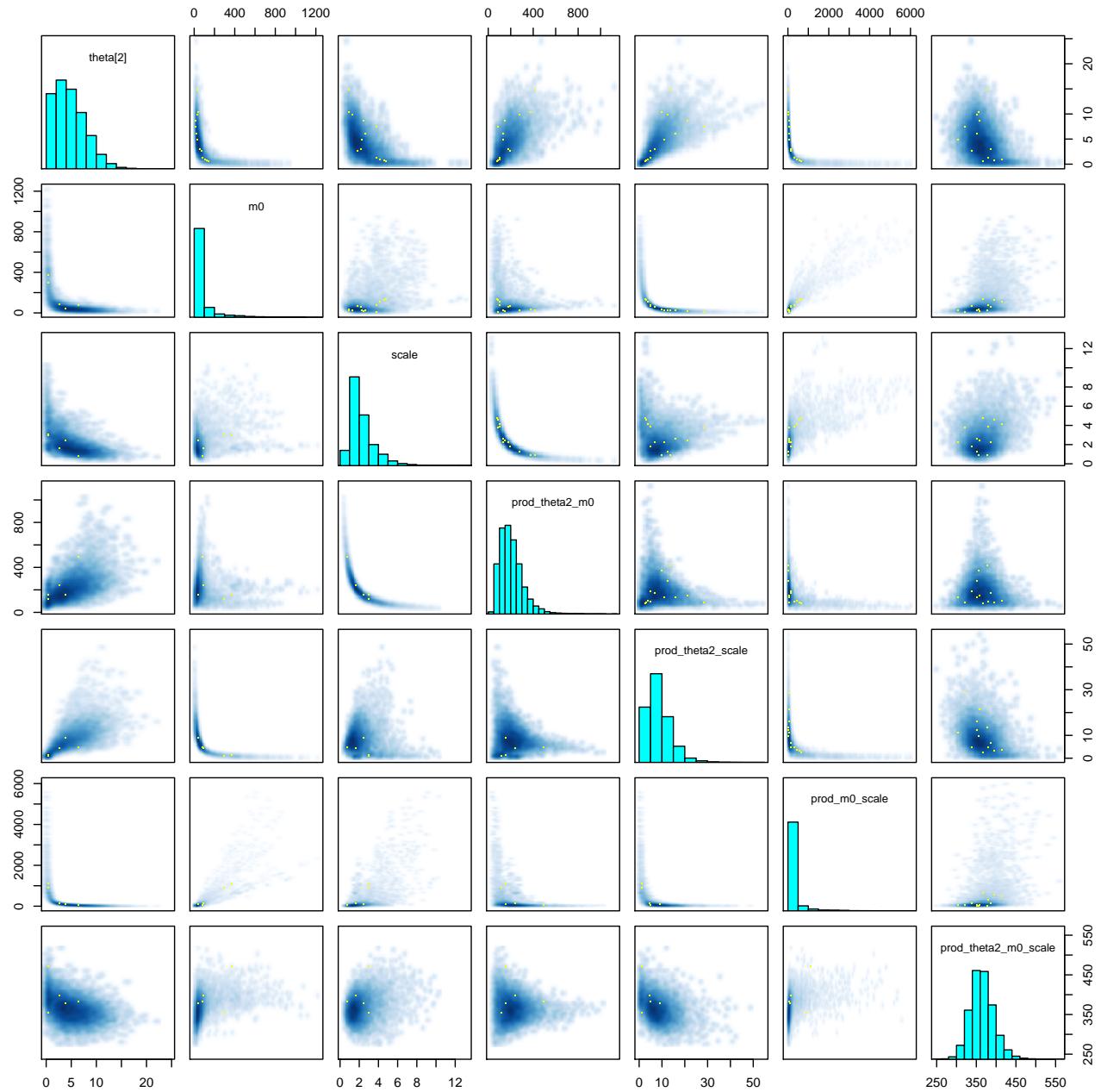


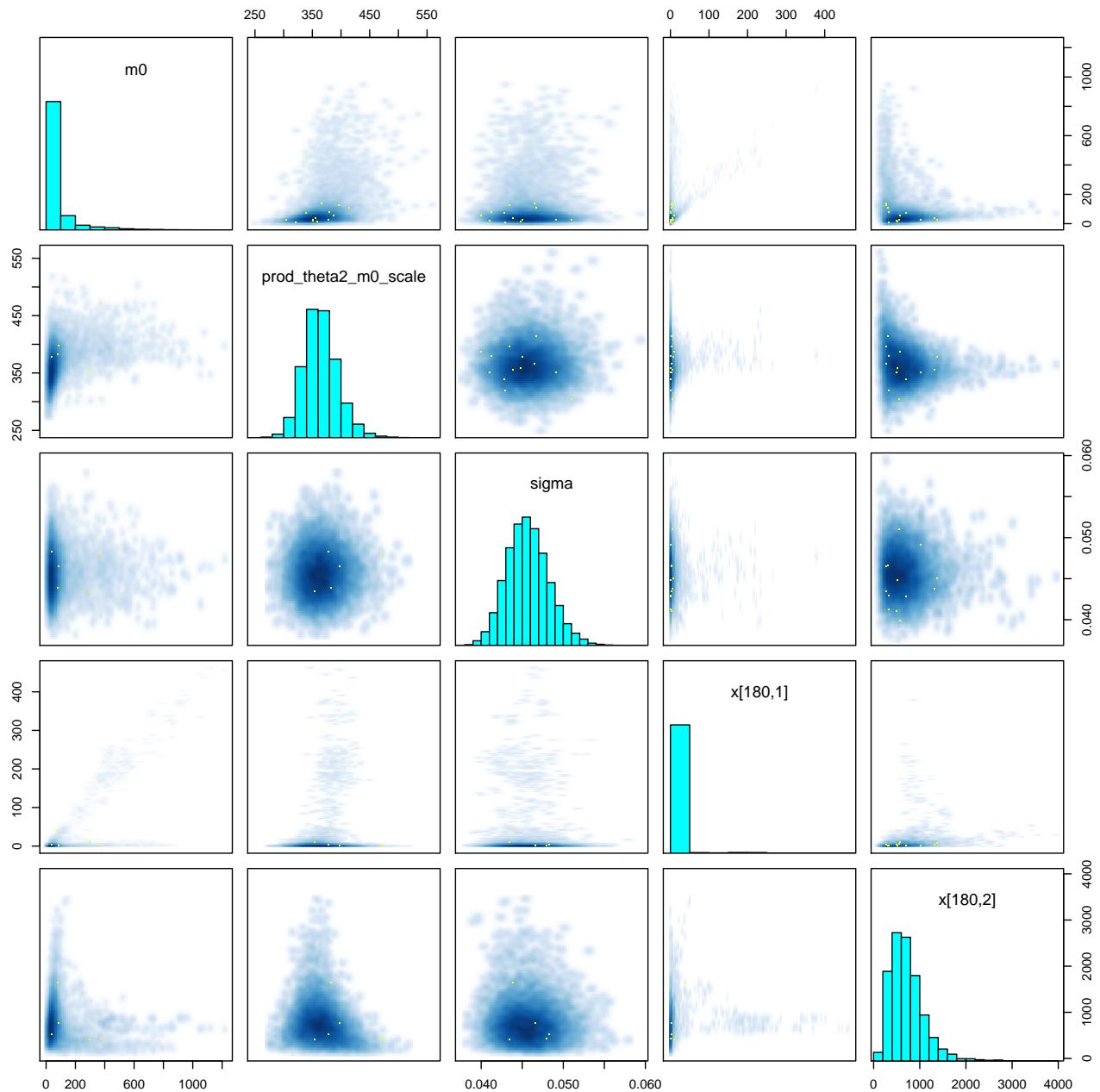
Density plots with 95% CI and median



Pair plots

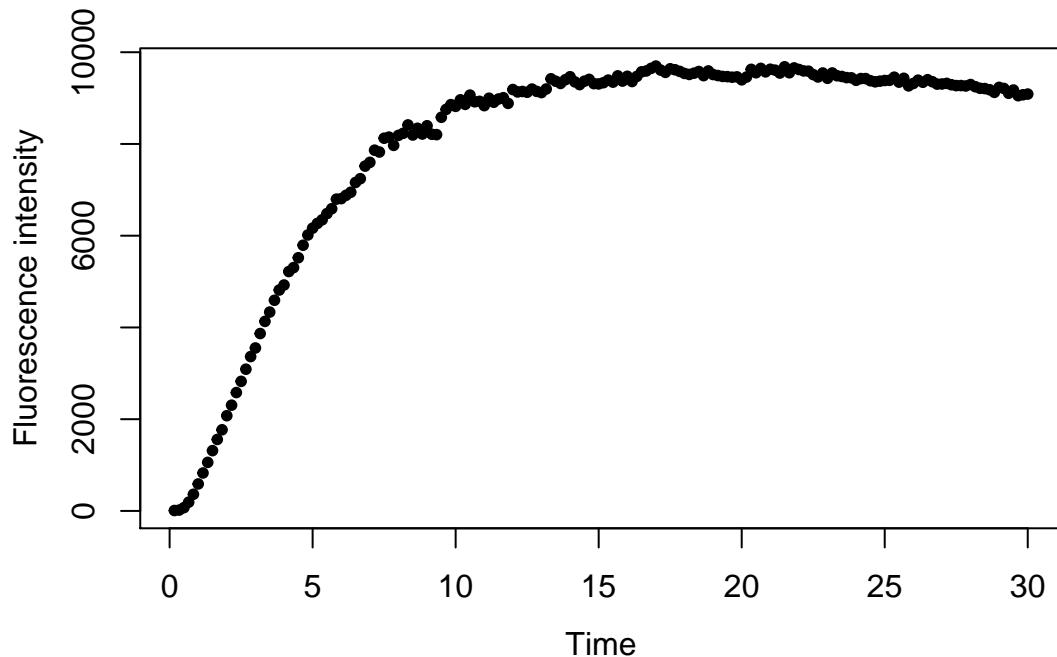






Trajectory 42: some divergent transitions

Trajectory 42



	mean	se_mean	sd	5%	50%	95%
theta[1]	0.114	0.010	0.053	0.017	0.128	0.186
theta[2]	1.624	0.117	1.929	0.152	0.847	5.796
theta[3]	0.035	0.009	0.040	0.005	0.016	0.127
m0	184.901	13.154	182.425	19.310	119.041	566.818
sigma	0.115	0.000	0.006	0.105	0.114	0.126
scale	18.247	0.319	5.958	8.731	18.039	28.258
offset	23.304	0.018	1.541	20.870	23.243	25.896
prod_theta2_m0	106.305	2.188	42.707	59.761	95.631	192.063
prod_theta2_scale	25.353	2.000	28.465	3.104	14.491	82.095
prod_m0_scale	3548.830	267.398	4016.709	273.644	2041.264	11816.385
prod_theta2_m0_scale	1715.211	5.466	164.217	1460.647	1704.788	2001.830
x[180,1]	18.084	9.685	42.913	0.147	3.216	107.203
x[180,2]	559.815	11.941	231.199	318.342	497.475	1021.359
	n_eff	Rhat				
theta[1]	31	1.206				
theta[2]	272	1.026				
theta[3]	22	1.266				
m0	192	1.036				
sigma	10214	1.001				
scale	349	1.035				
offset	7680	1.001				
prod_theta2_m0	381	1.028				
prod_theta2_scale	203	1.029				
prod_m0_scale	226	1.034				
prod_theta2_m0_scale	903	1.010				
x[180,1]	20	1.298				
x[180,2]	375	1.031				

Divergences:

15 of 20000 iterations ended with a divergence (0.075%).
Try increasing 'adapt_delta' to remove the divergences.

Tree depth:

22 of 20000 iterations saturated the maximum tree depth of 15 (0.11%).
Try increasing 'max_treedepth' to avoid saturation.

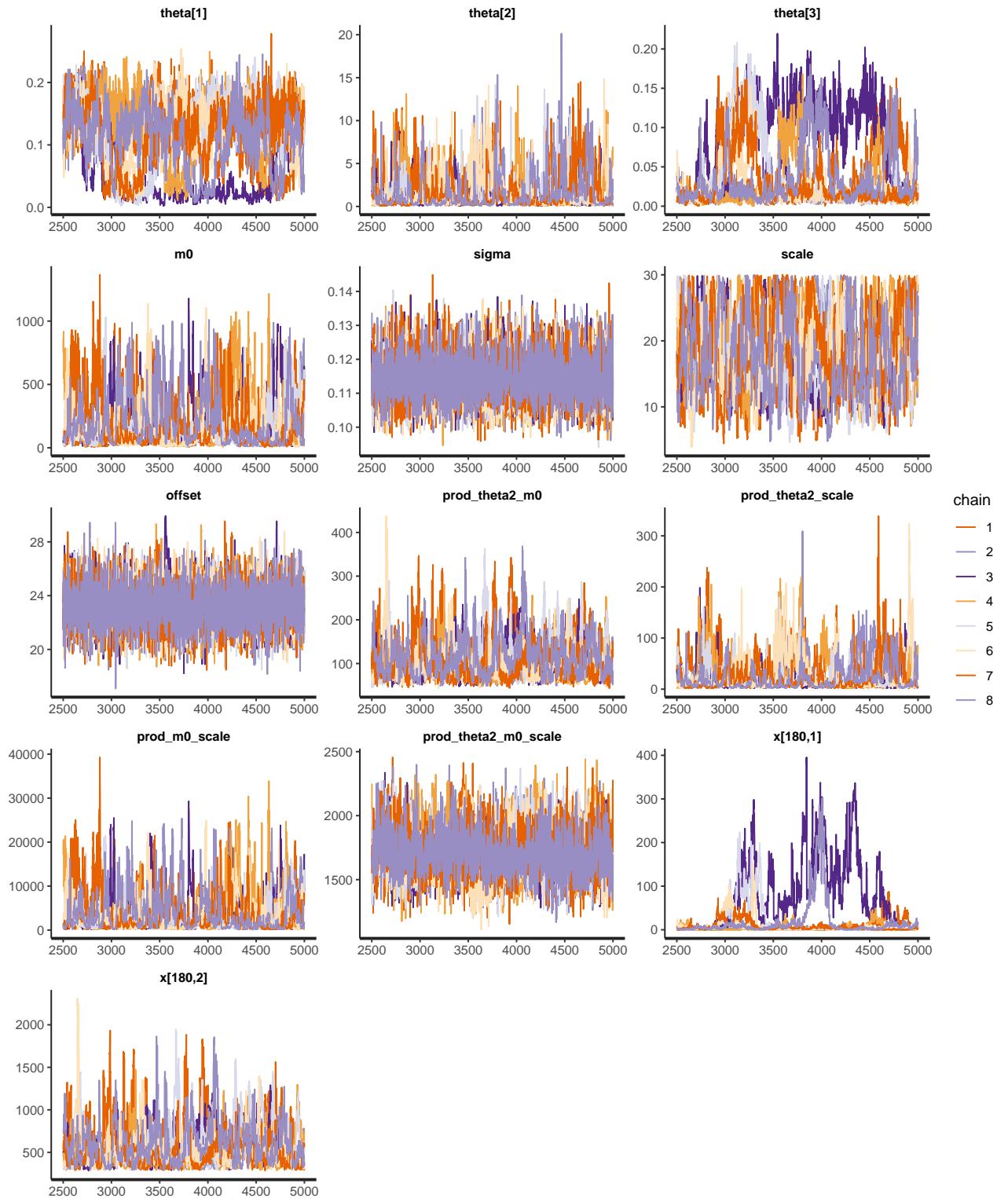
Energy:

E-BFMI indicated possible pathological behavior:

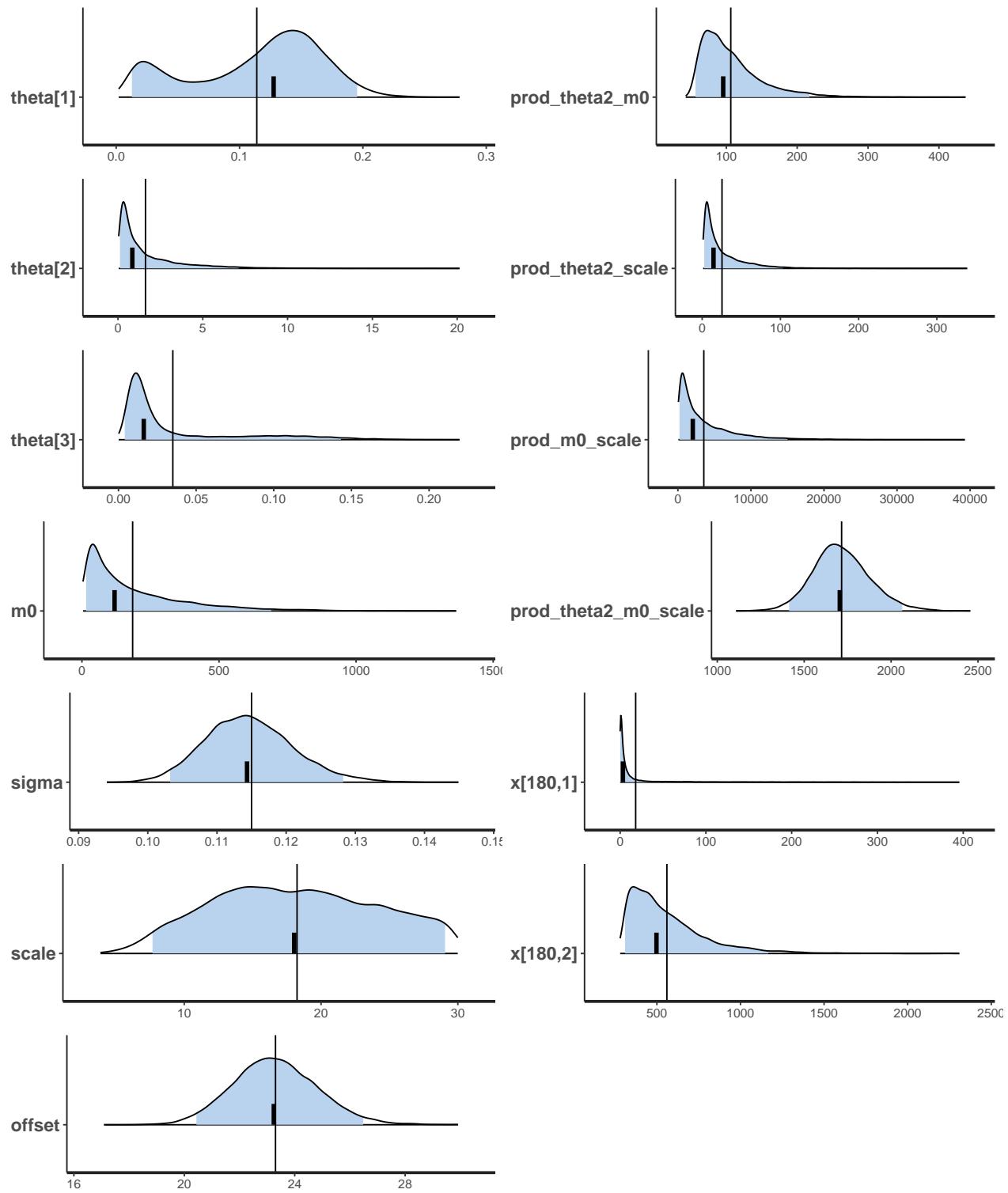
Chain 1: E-BFMI = 0.037
Chain 2: E-BFMI = 0.066
Chain 3: E-BFMI = 0.022
Chain 4: E-BFMI = 0.041
Chain 5: E-BFMI = 0.034
Chain 6: E-BFMI = 0.037
Chain 7: E-BFMI = 0.044
Chain 8: E-BFMI = 0.039

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

Traceplots



Density plots with 95% CI and median



Pair plots

