S2 File. Individual and group parameter estimates, and statistical and graphical convergence tests from the Hierarchical Bayesian Drift Diffusion Model (HDDM) output of analysis of the anti-saccade data, using the Python HDDM package. For further details, see (1) manuscript text; (2) Wiecki, Sofer & Frank (2013). Frontiers in Neuroinformatics, 7, 1-10: doi: 10.3389/fninf.2013.00014; and (3) http://ski.clps.brown.edu/hddm_docs/.

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In [9]: model1.print_stats()

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DIC: 17317.836397
deviance: 17060.069395
pD: 257.767002


In [10]: model1.plot_posteriors(['a', 'a_var'])
    ...: model1.plot_posteriors(['v', 'v_var'])
Plotting a(0)
Plotting a(1)
Plotting v(coke)
Plotting v(neutral)
Plotting v(shape)
/home/sdl/anaconda2/lib/python2.7/site-packages/matplotlib/figure.py:1999:
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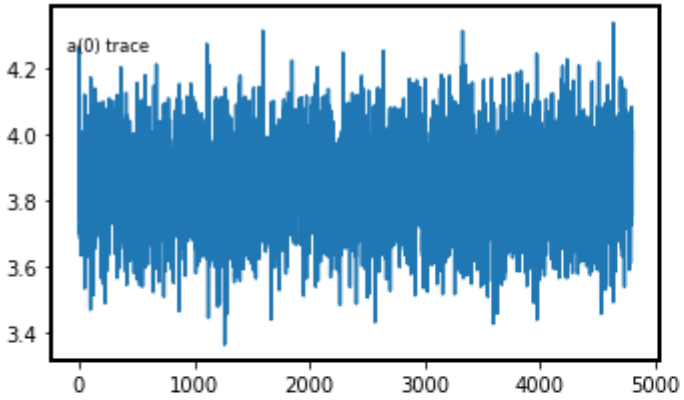
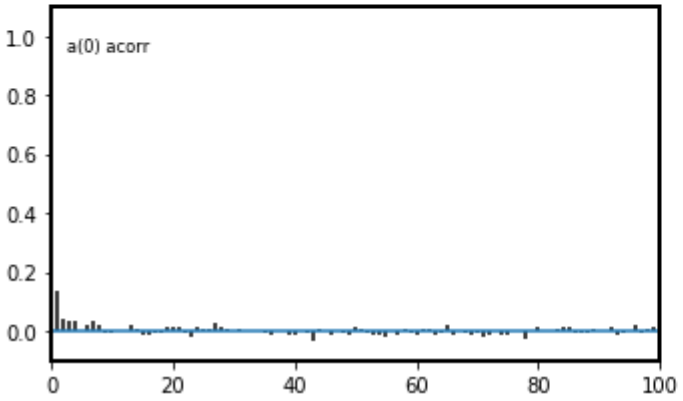

a(0) trace
4.2
4.0
3.8
3.6
3.4
0
1000
2000
3000
4000
5000


a(0) acorr
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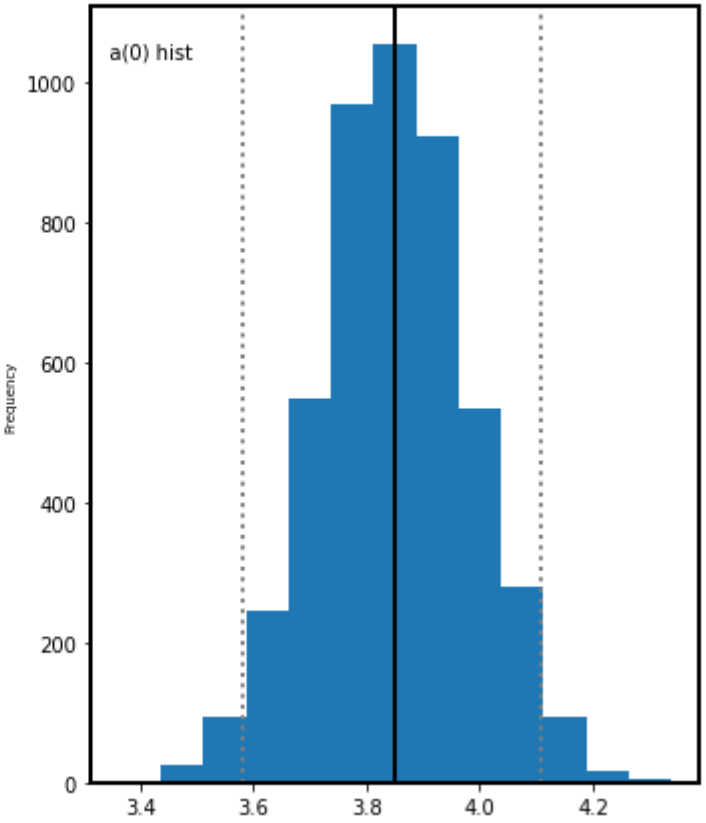
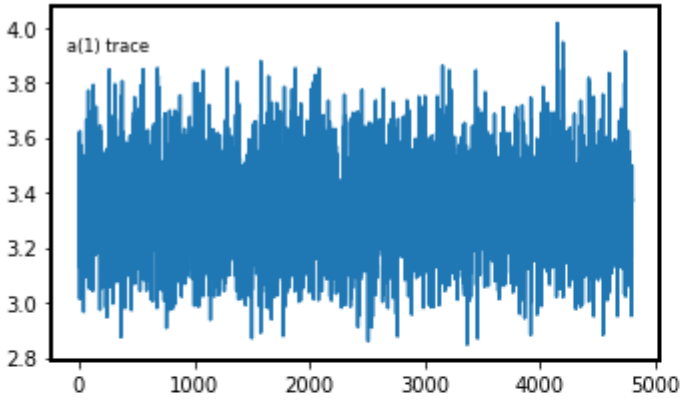
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100


a(0) hist
Frequency
1000
800
600
400
200
0
3.4
3.6
3.8
4.0
4.2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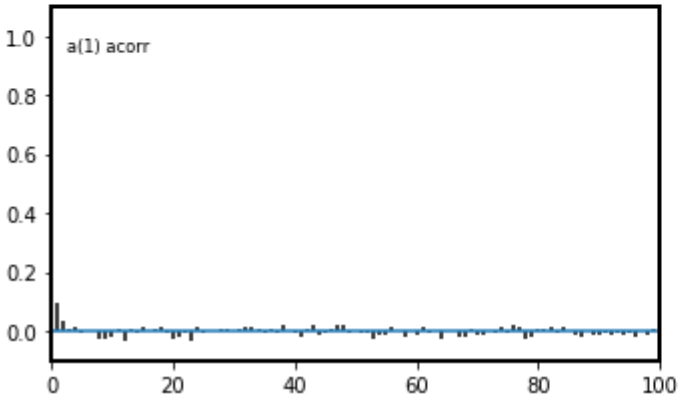
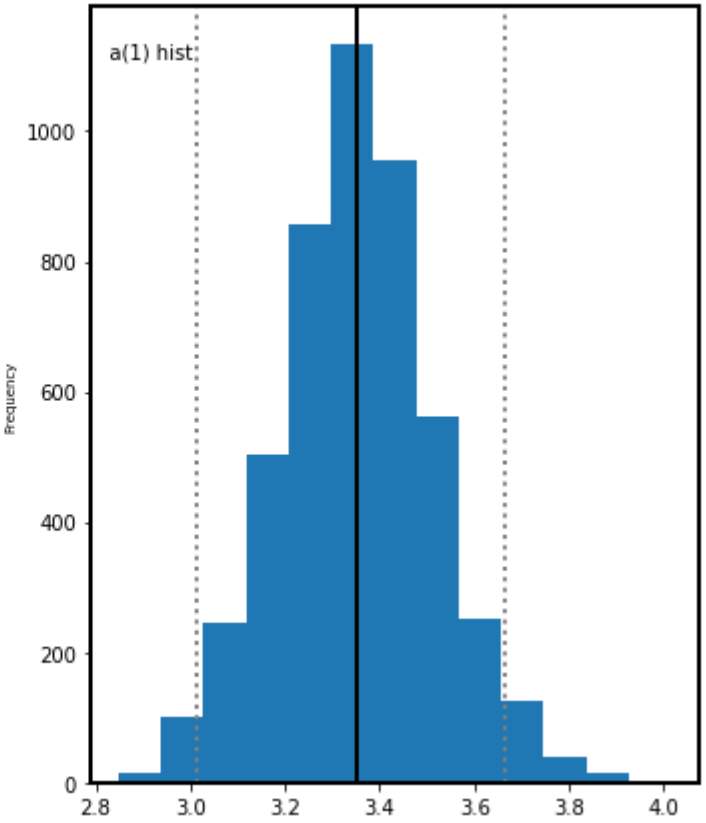
3.8
3.6
3.4
3.2
3.0
2.8
0
1000
2000
3000
4000
5000


a(1) acorr
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100


a(1) hist
Frequency
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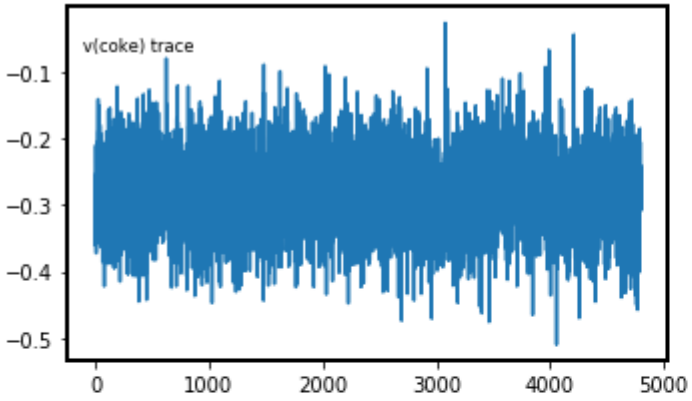
800
600
400
200
0
2.8
3.0
3.2
3.4
3.6
3.8
4.0


v(coke) trace
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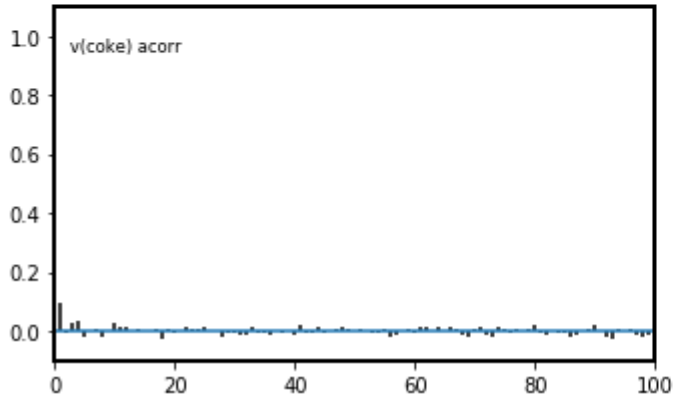
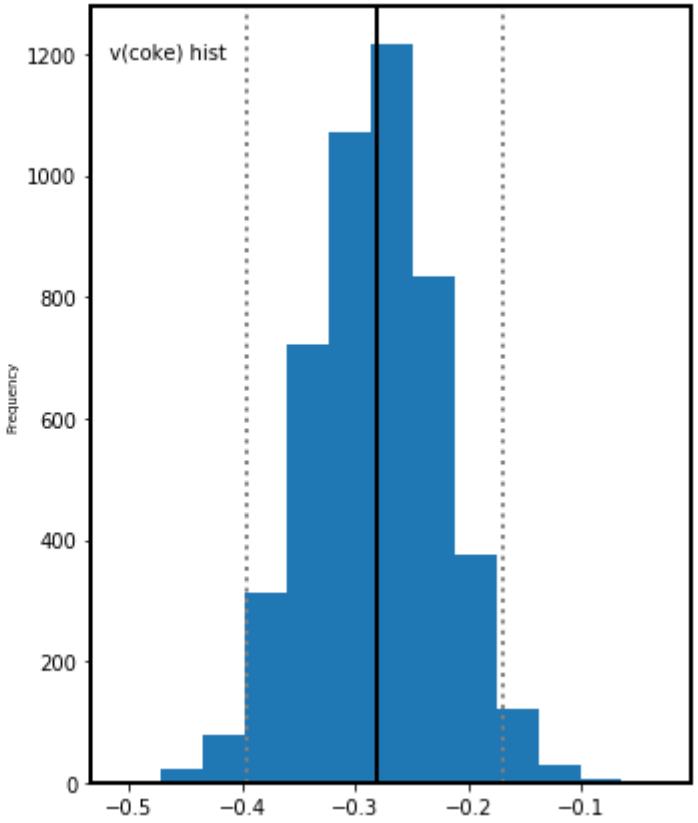
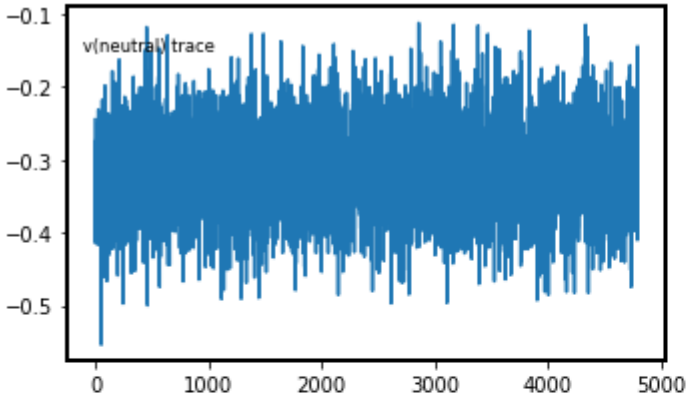
−0.2
−0.3
−0.4
−0.5
0
1000
2000
3000
4000
5000


v(coke) acorr
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100


v(coke) hist
Frequency
1200
1000
800
600
400
200
0
−0.5
−0.4
−0.3
−0.2
−0.1


v(neutral) trace
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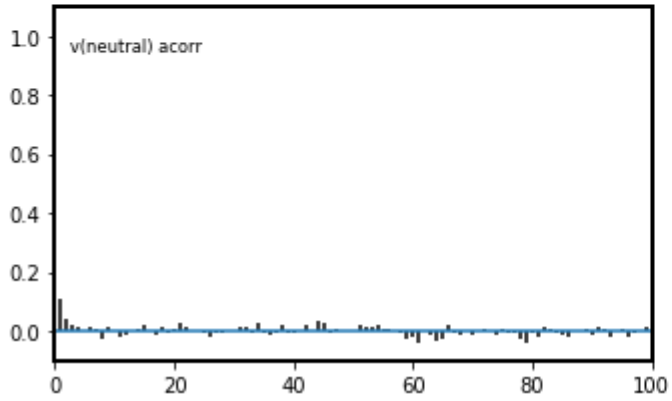
−0.2
−0.3
−0.4
−0.5
0
1000
2000
3000
4000
5000


v(neutral) acorr
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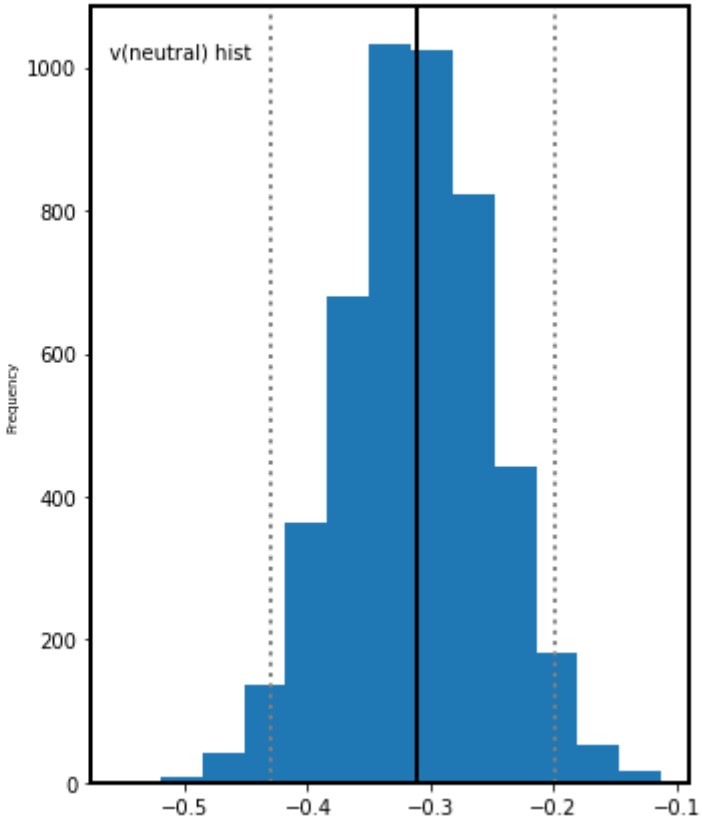
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100


v(neutral) hist
Frequency
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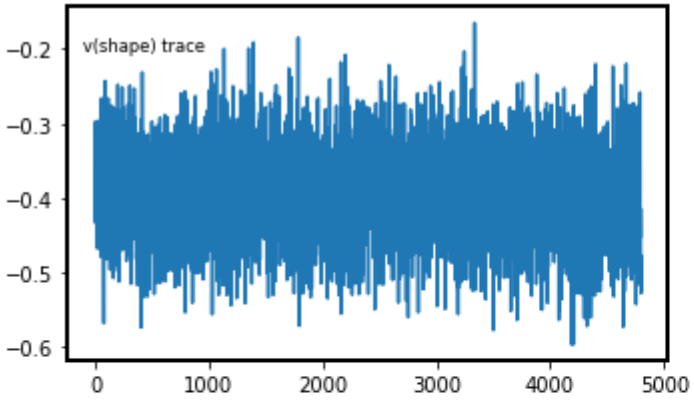
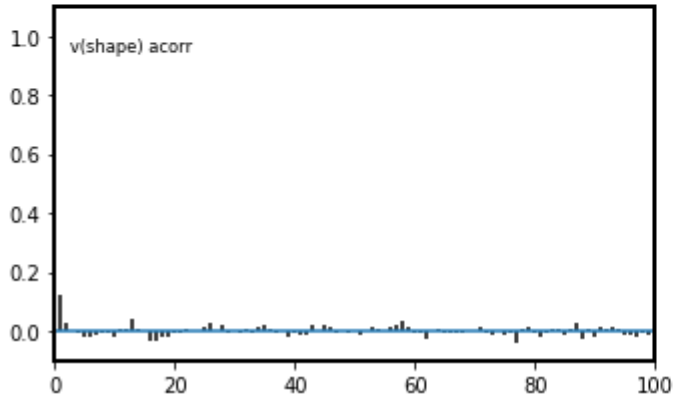
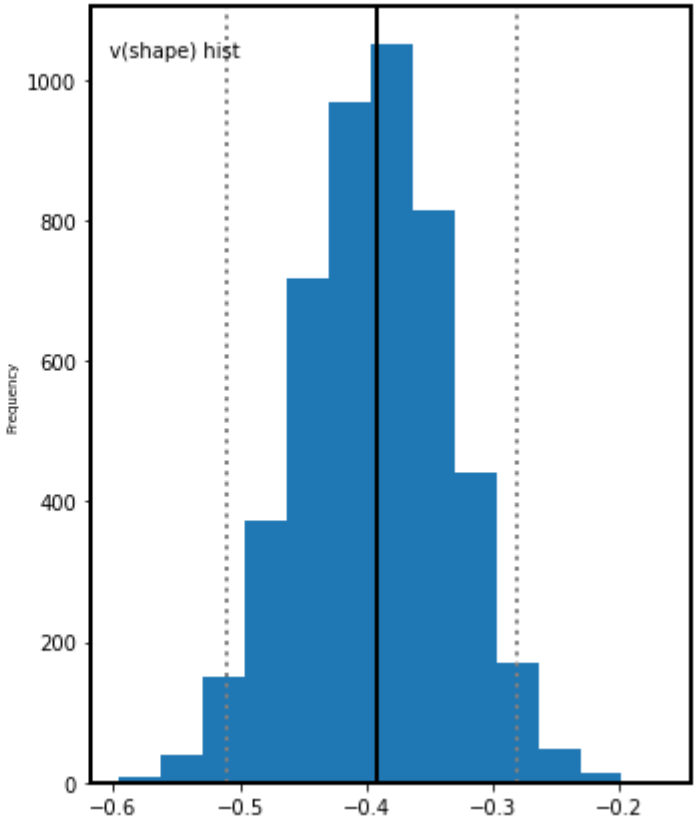
800
600
400
200
0
−0.5
−0.4
−0.3
−0.2
−0.1


v(shape) trace
−0.2
−0.3
−0.4
−0.5
−0.6
0
1000
2000
3000
4000
5000


v(shape) acorr
1.0
0.8
0.6
0.4
0.2
0.0
0
20
40
60
80
100


v(shape) hist
Frequency
1000
800
600
400
200
0
−0.6
−0.5
−0.4
−0.3
−0.2