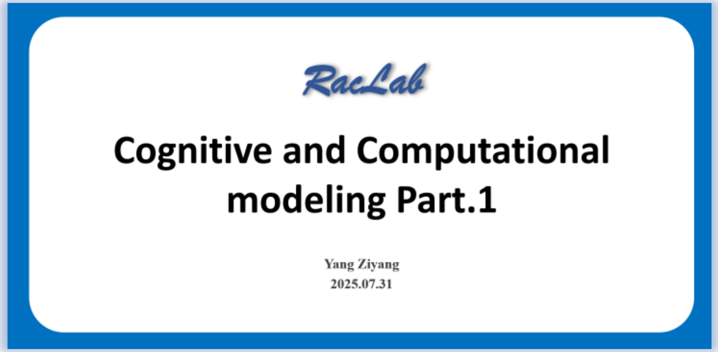
RacLab

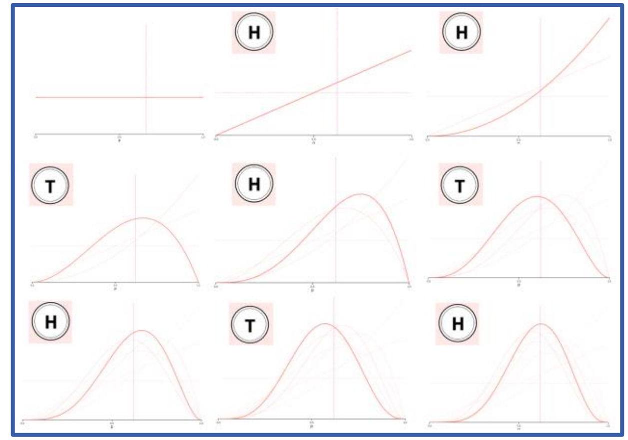
Introduction to Drift Diffusion Model pt.2

Yang Ziyang

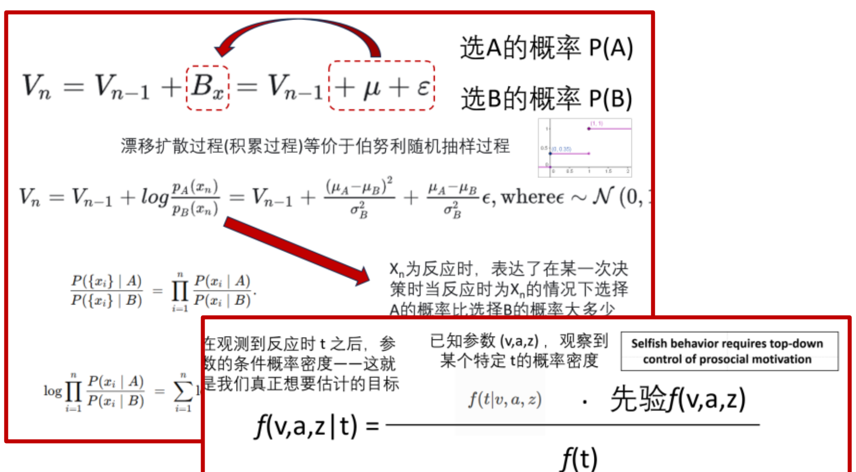
2025.09.22

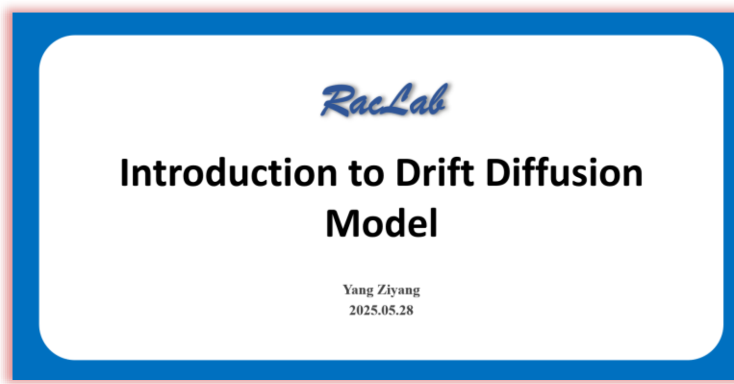
Introduction





Hierarchical Bayesian parameter estimation of the Drift Diffusion Model





Environment

How to install HDDM (suitable for docker and linux)

https://huchuanpeng.com/post/hddm_installation_tutorial/

dockerHDDM:
从安装到入土

https://www.bilibili.com/video/BV17T421Y7MX/?spm_id_from=333.337.search-card.all.click&vd_source=30501c1c4b33ad073b7b7c3b06ab8a93

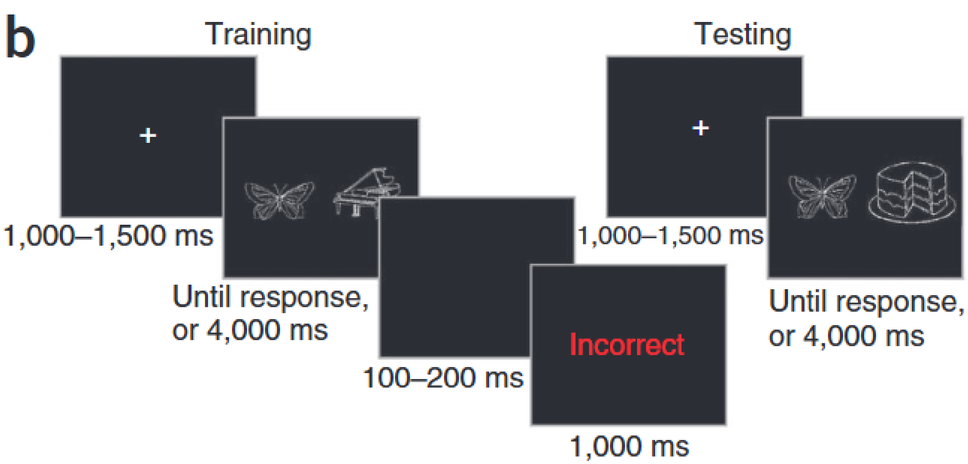
Introduction

Dataset

Article | Published: 25 September 2011

Subthalamic nucleus stimulation reverses mediofrontal influence over decision threshold

James F Cavanagh, Thomas V Wiecki, Michael X Cohen, Christina M Figueroa, Johan Samanta, Scott J Sherman & Michael J Frank



subject	stim	rt	choice	conf
0	LL	1210	1	HC
0	WL	1630	1	LC
0	WW	1030	1	HC
0	WL	2770	1	LC
0	WW	1140	0	HC
0	WL	1150	1	LC

		Stim		
Conflict	High	WW		LL
	Low		WL	

Dataset

subject	stim	rt	choice	conf
0	LL	1210	1	HC
0	WL	1630	1	LC
0	WW	1030	1	HC
0	WL	2770	1	LC
0	WW	1140	0	HC
0	WL	1150	1	LC

→

	subj_idx	stim	rt	response	conf
0	0	LL	1.210	1	HC
1	0	WL	1.630	1	LC
2	0	WW	1.030	1	HC
3	0	WL	2.770	1	LC
4	0	WW	1.140	0	HC

HDDM requires the inclusion of three columns of variables

"subj_idx" *"rt"* *"response"*

- ✓ *"rt" must be seconds*
- ✓ *NaN values are not available.*

- ✓ *accuracy-coding*
  correct (1) and error (0)
- ✓ *stimulus-coding*
  upper (1) and lower (0)

Modelset

 # Model 0: base model: full model

mm0 = hddm.HDDM(df, include=['a', 'v', 't', 'z'])

 # Model 1: treat within-subj as between-subj: full model

mm1 = hddm.HDDM(df, include=['a', 'v', 't','z'],

depends_on={'v': 'conf'})

```
# Model 2: regression model (varying intercept and slope)
mm2 = hddm.HDDMRegressor(
  df, "v ~ 1 + C(conf, Treatment('LC'))",
  include=['a', 'v', 't', 'z'],
  group_only_regressors=False,
  keep_regressor_trace=True)
```

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```
# Model 1: treat within-subj as between-subj: full model
mm1 = hddm.HDDM(df, include=['a', 'v', 't','z'],
depends_on={'v': 'conf'})
```

- **漂移率**依赖于一个**分类变量(HC/LC)**
- **漂移率的均值(Mean)和变异性(Std)**是基于群体水平共享的

⬇

漂移率是通过先验(统一的群体先验)来建模的

Hyper-parameter
(Group distribution)

⬇

群体先验：
高冲突慢(v_HC 低)，低冲突快(v_LC 高)

?

所有被试的两个参数都强制受到群体先验的影响

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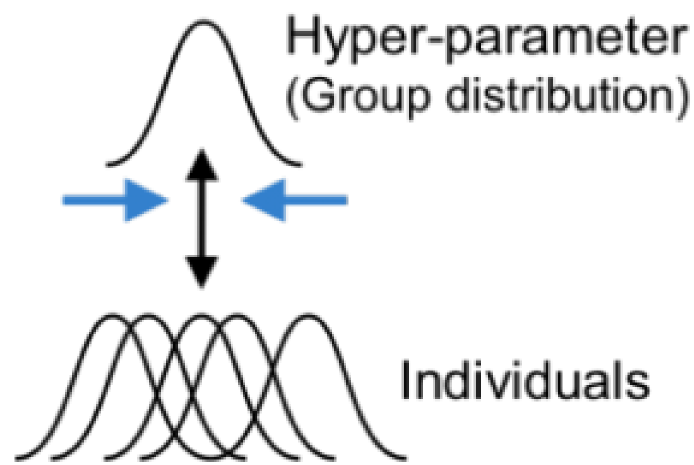
```
# Model 2: regression model (varying intercept and slope)
mm2 = hddm.HDDMRegressor(
  df, "v ~ 1 + C(conf, Treatment('LC'))",
  include=['a', 'v', 't', 'z'],
  group_only_regressors=False,
  keep_regressor_trace=True)
```

允许为每个个体的参数设置独立的先验

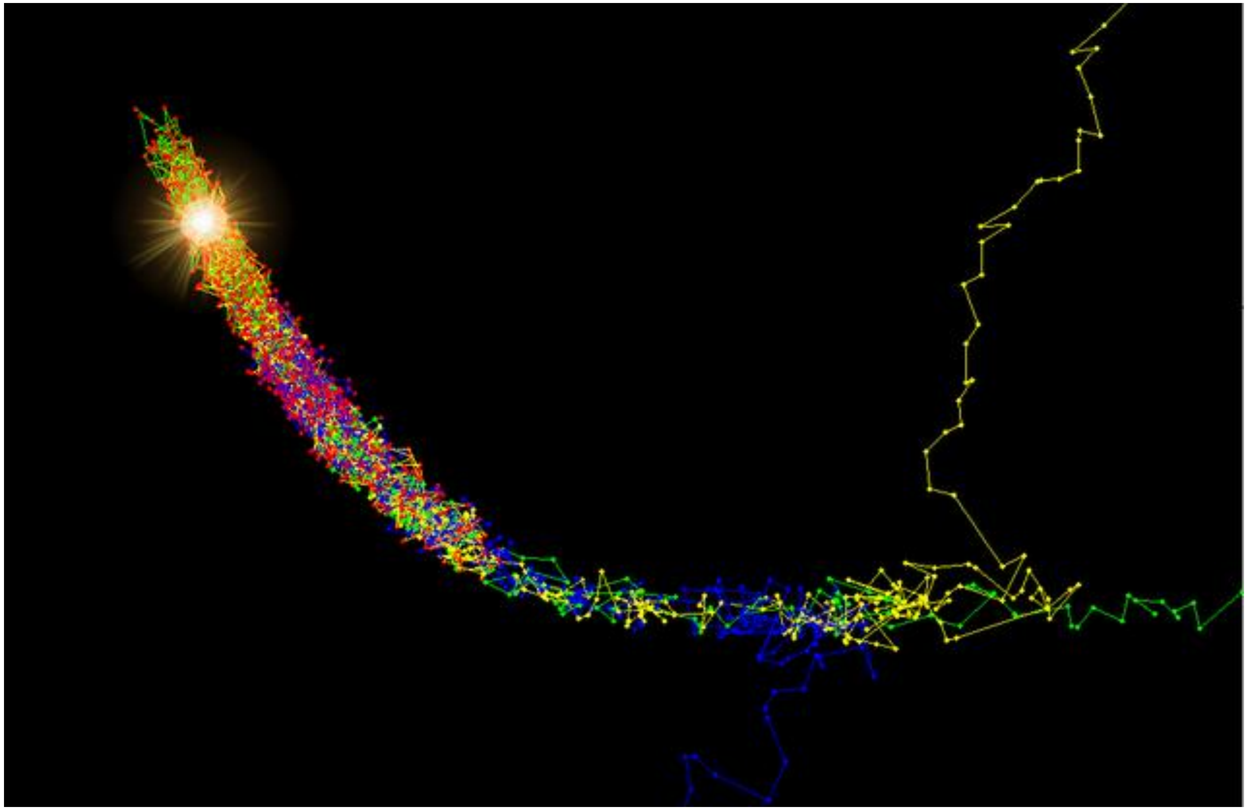


个体的参数会收缩到群体的先验上
但个体之间的差异会被保留下来

即同时考虑的群体差异和个体差异

Introduction

Markov chain Monte Carlo



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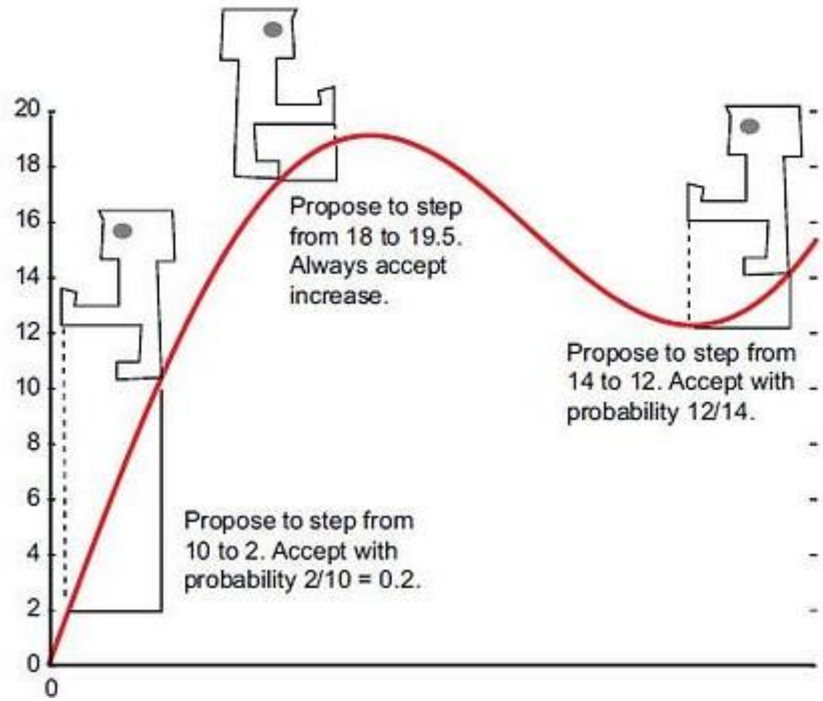
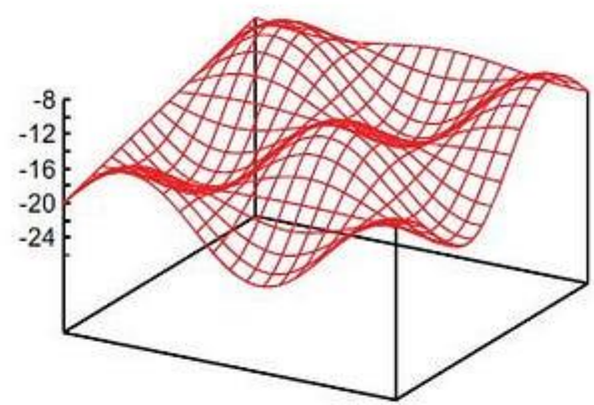
The MCMC sampler's objective is to generate more samples from high target distribution regions and fewer from low target distribution regions.





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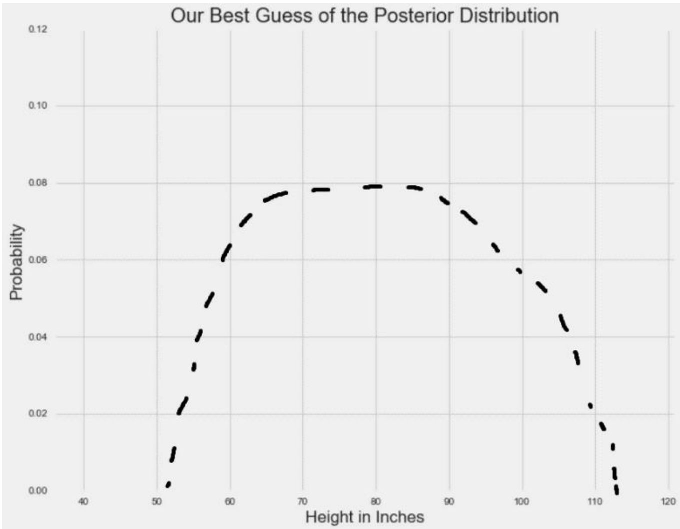
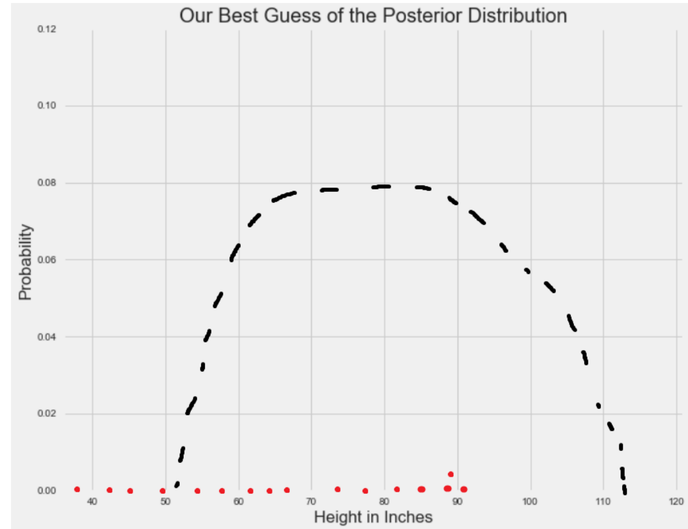
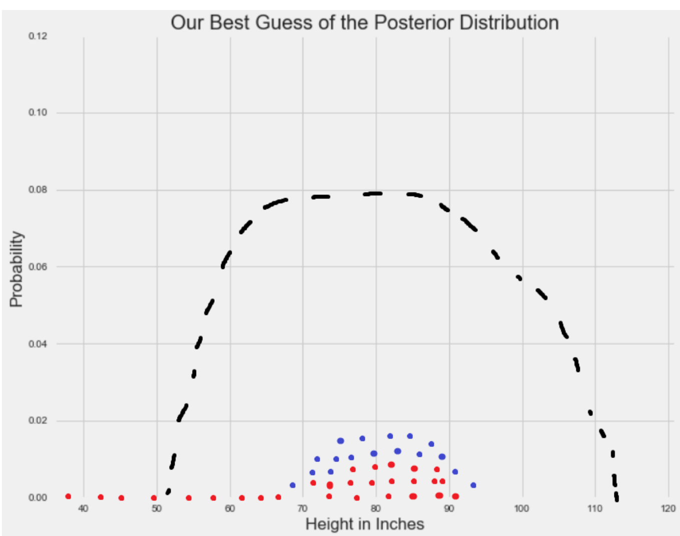
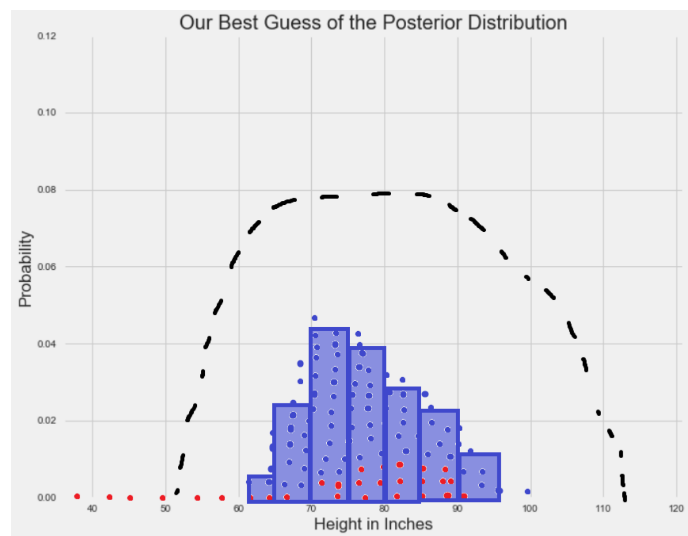
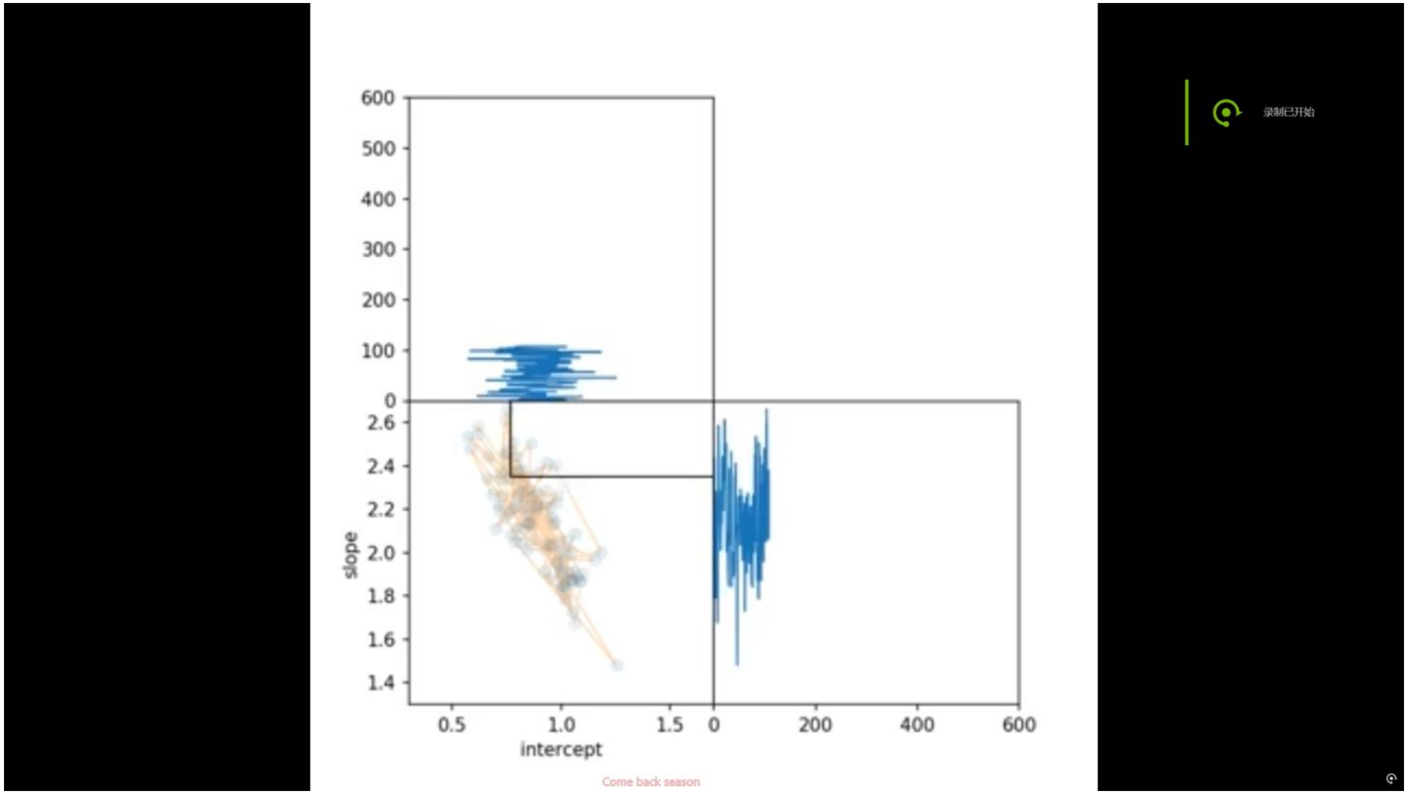








Introduction



MCMC chains are ***valid and reliable*** when they fluctuate around a value and different chains are ***indistinguishable*** from each other, a scenario often referred to as a "***caterpillar***" shape.

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