

Module 4: Coping with Multiple Predictors

Multidimensional Kernel Methods

STAT/BIOSTAT 527, University of Washington

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Kernel Density Estimation

- Kernel methods are often used for density estimation (actually, classical origin)

- Assume random sample $x_1, \dots, x_n \stackrel{\text{iid}}{\sim} P$

- Choice #1: empirical estimate? $\hat{p} = \frac{1}{n} \sum \delta_{x_i}$ 

- Choice #2: as before, maybe we should use an estimator


$$\hat{p}(x_0) = \frac{\#x_i \in \text{Nbhd}(x_0)}{n \lambda}$$

width of nbhd

- Choice #3: again, consider kernel weightings instead

$$\hat{p}(x_0) = \frac{1}{n\lambda} \sum K_\lambda(x_0, x_i)$$

Parzen est.

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Kernel Density Estimation

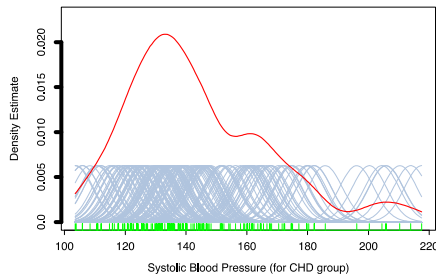
- Popular choice = Gaussian kernel → **Gaussian KDE**

$$\hat{p} = \frac{1}{n} \sum_{i=1}^n \phi_{\lambda}(x - x_i)$$

ϕ_{λ}

$$= (\hat{p} * \phi_{\lambda})(x)$$

↑ empirical dist.



From Hastie, Tibshirani, Friedman book

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Multivariate KDE

- In 1d
$$\hat{p}(x_0) = \frac{1}{n\lambda} \sum_{i=1}^n K_{\lambda}(x_0, x_i)$$

- In $\mathbb{R}^d$, assuming a product kernel,

$$\hat{p}(x_0) = \frac{1}{n\lambda_1 \cdots \lambda_d} \sum_{i=1}^n \left\{ \prod_{j=1}^d K_{\lambda_j}(x_{0j}, x_{ij}) \right\}$$

- Typical choice = Gaussian RBF

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Multivariate KDE

$$\hat{p}(x_0) = \frac{1}{n\lambda_1 \cdots \lambda_d} \sum_{i=1}^n \left\{ \prod_{j=1}^d K_{\lambda_j}(x_{0j}, x_{ij}) \right\}$$

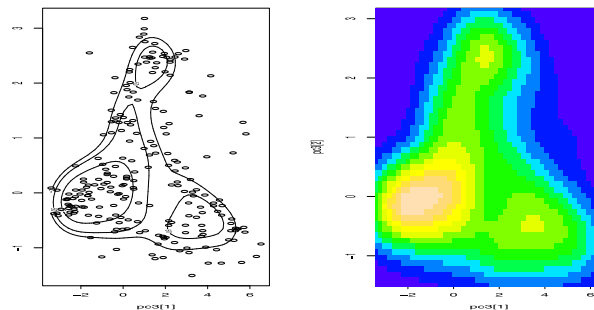
- Risk grows as $O(n^{-4/(4+d)})$
- Example: To ensure relative MSE < 0.1 at 0 when the density is a multivariate norm and optimal bandwidth is chosen
- Always report confidence bands, which get wide with d

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Multivariate KDE Example

- Data on 6 characteristics of aircraft (Bowman and Azzalini 1998)
- Examine first 2 principle components of the data
- Perform KDE with independent kernels

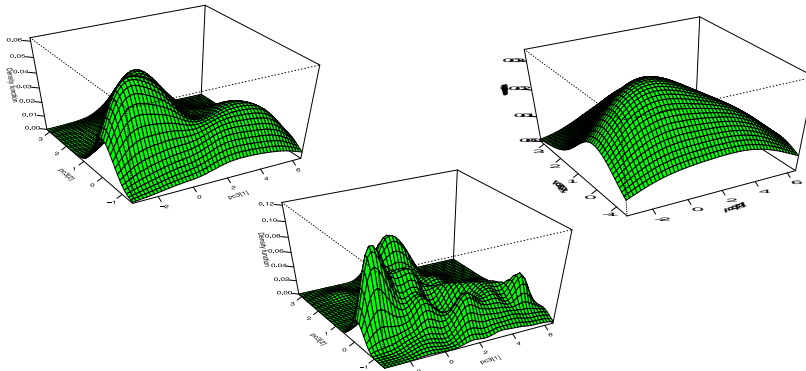


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Multivariate KDE Example

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- Examine first 2 principle components of the data
- Perform KDE with independent kernels



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Module 4: Coping with Multiple Predictors

Regression Trees

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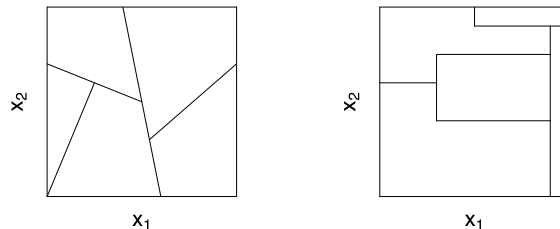
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Regression Trees Overview

- An alternative adaptive regression technique
 - Conceptually simple
 - Powerful
- Partition the covariate space into regions and then fit a simple model in each (e.g., constant)
- How to partition?

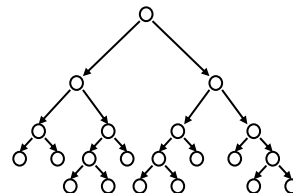
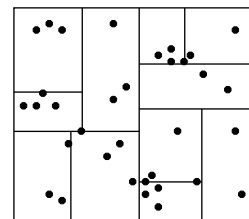


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Recursive Binary Partitions

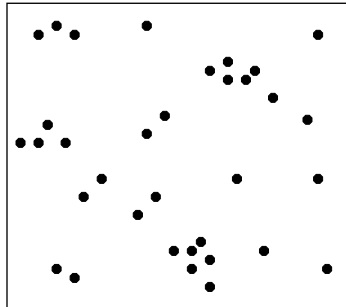
- To simplify the process and interpretability, consider **recursive binary partitions**
- Described via a rooted tree
 - Every node of the tree corresponds to split decision
 - Leaves contain a subset of the data that satisfy the conditions



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Recursive Binary Partitions



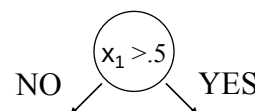
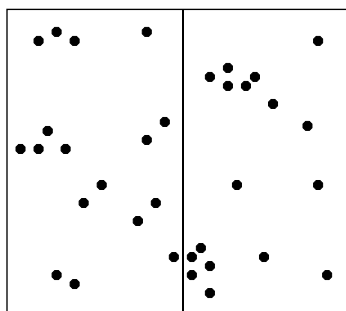
Pt	x_1	x_2
1	0.00	0.00
2	1.00	4.31
3	0.13	2.85
...	...	...

- Start with a list of d -dimensional points.

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Recursive Binary Partitions



Pt	x_1	x_2
1	0.00	0.00
3	0.13	2.85
...	...	...

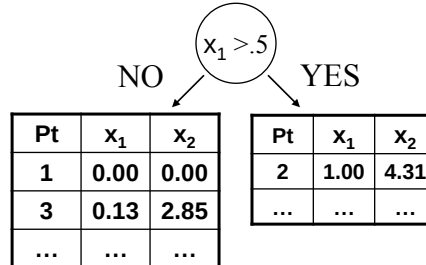
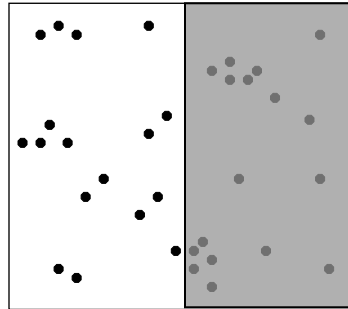
Pt	x_1	x_2
2	1.00	4.31
...	...	...

- Split the points into 2 groups by:
 - Choosing dimension d_j and value t_j (methods to be discussed...)
 - Separating the points into $x_{id_j} > t_j$ and $x_{id_j} \leq t_j$.

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Recursive Binary Partitions

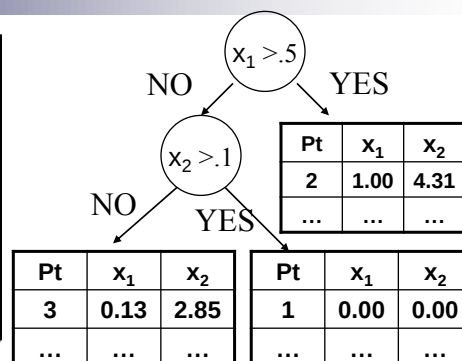
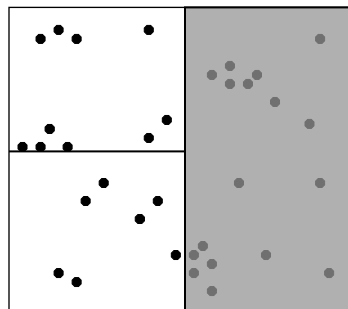


- Consider each group separately and possibly split again (along same/different dimension).
 - Stopping criterion to be discussed...

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Recursive Binary Partitions

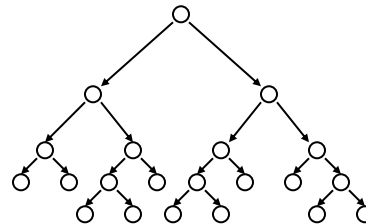
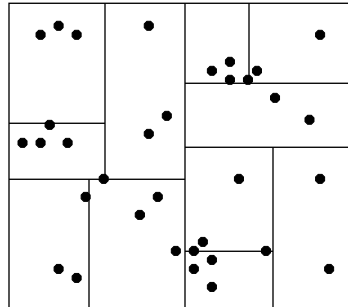


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Recursive Binary Partitions

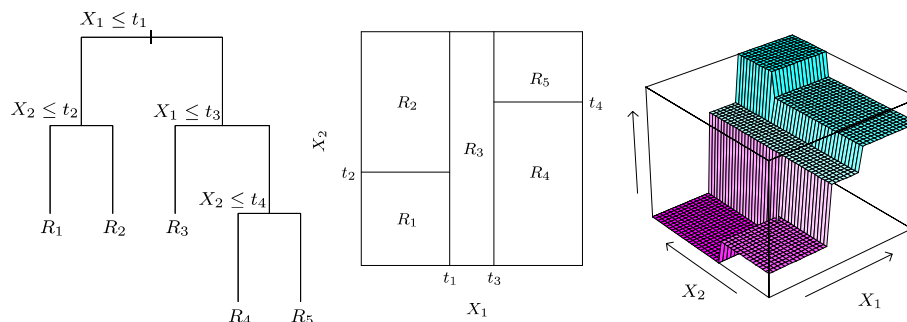


- Continue splitting points in each set
□ creates a binary tree structure
- Each leaf node contains a list of points

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Resulting Model



- Model the response as constant within each region

$$f(x) = \sum_{m=1}^M \beta_m I(x \in R_m)$$

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Basis Expansion Interpretation

- Equivalent to a basis expansion

$$f(x) = \sum_{m=1}^M \beta_m h_m(x)$$

- In this example:

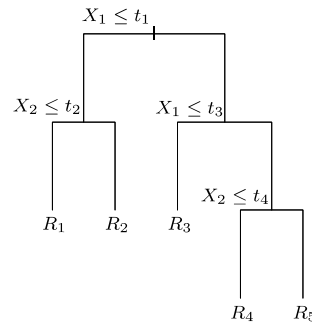
$$h_1(x_1, x_2) = I(x_1 \leq t_1)I(x_2 \leq t_2)$$

$$h_2(x_1, x_2) = I(x_1 \leq t_1)I(x_2 > t_2)$$

$$h_3(x_1, x_2) = I(x_1 > t_1)I(x_1 \leq t_3)$$

$$h_4(x_1, x_2) = I(x_1 > t_1)I(x_1 > t_3)I(x_2 \leq t_4)$$

$$h_5(x_1, x_2) = I(x_1 > t_1)I(x_1 > t_3)I(x_2 > t_4)$$



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Questions on Building the Tree

- Which variable should we split on?
- What threshold value should we consider?
- When should we stop the process?

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Building the Tree

$$f(x) = \sum_{m=1}^M \beta_m I(x \in R_m)$$

- Assume the partition $(R_1, \dots, R_M)$ is given
- If criterion is to minimize RSS, then

$$\hat{\beta}_m =$$

- How do we find the partition $(R_1, \dots, R_M)$?
 - Finding the optimal tree that minimizes RSS is generally computationally infeasible
 - Consider a greedy algorithm instead

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Choosing a Split Decision

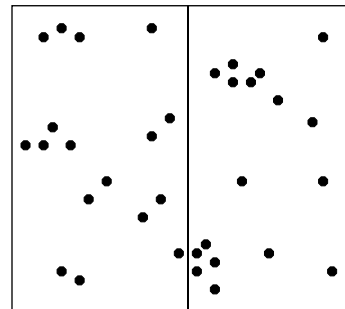
- Starting with all of the data, consider splitting on variable j at point s

- Define

$$R_1(j, s) = \{x \mid x_j \leq s\}$$

$$R_2(j, s) = \{x \mid x_j > s\}$$

- Our objective is



- For any (j, s) , the inner minimization is solved by

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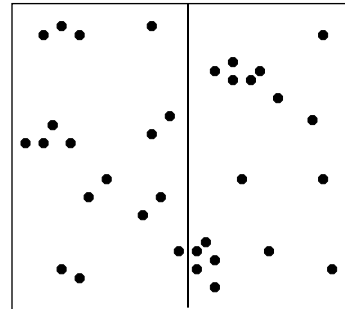
Choosing a Split Decision

$$\min_{j,s} \left[\sum_{x_i \in R_1(j,s)} (y_i - \hat{\beta}_1)^2 + \sum_{x_i \in R_2(j,s)} (y_i - \hat{\beta}_2)^2 \right]$$

$$\hat{\beta}_1 = \text{avg}(y_i \mid x_i \in R_1(j,s))$$

$$\hat{\beta}_2 = \text{avg}(y_i \mid x_i \in R_2(j,s))$$

- For each splitting variable j , finding the optimal s can be done efficiently
 - Why?



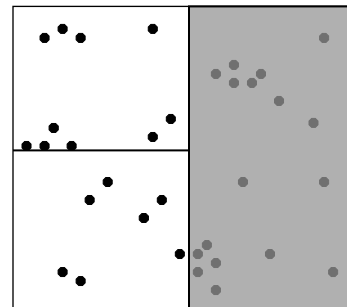
- Max of $d(n-1)$ partitions to consider
- So, determining (j,s) is feasible

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Choosing a Split Decision

- Conditioning on the best split just found, we recurse on each of the two regions
- Repeat on all resulting regions
- When do we stop recursing?



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How Large of a Tree?

- Large tree, like partitioning until each node has one observation
→
- Small tree →
- Tree size is a tuning parameter that governs model complexity
 - Optimal tree size should be chosen adaptively from the data
- Stopping criterion
 - Stop when decrease in RSS due to a split falls below some threshold
 - Stop when a minimum node size (e.g., 5) is reached. Go back and prune.

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Cost-Complexity Pruning

- Searching over all subtrees and selecting using AIC or CV is not possible since there is an exponentially large set of subtrees
→
- Define a subtree $T \subset T_0$ to be any tree obtained by pruning T_0

and $|T| =$

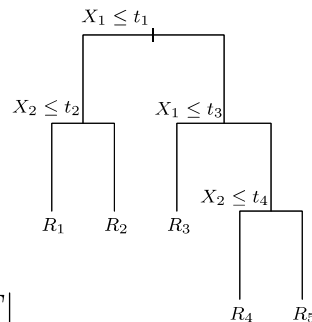
$n_m =$

$\hat{\beta}_m =$

$Q_m(T) =$

- We examine a complexity criterion

$$C_\lambda(T) = \sum_{m=1}^{|T|} n_m Q_m(T) + \lambda |T|$$



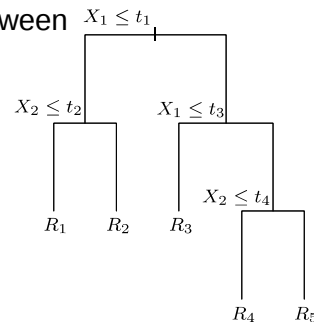
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Cost-Complexity Pruning

$$C_\lambda(T) = \sum_{m=1}^{|T|} n_m Q_m(T) + \lambda |T|$$

- For a given λ , want to find $T_\lambda \subset T_0$ to minimize $C_\lambda(T)$
- Tuning parameter λ governs tradeoff between tree size and goodness of fit to the data
 - Large $\lambda \rightarrow$
 - $\lambda = 0 \rightarrow$
- For each λ , can show that there is a unique smallest subtree T_λ



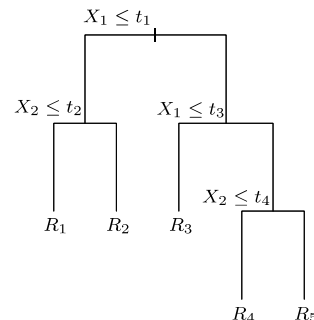
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Cost-Complexity Pruning

$$C_\lambda(T) = \sum_{m=1}^{|T|} n_m Q_m(T) + \lambda |T|$$

- Can find using *weakest link pruning*
 - Successively collapse the internal node that produces smallest increase in RSS
 - Continue until at single-node (root) tree
 - Produces a finite sequence of subtrees, which must contain T_λ
 - See Breiman et al. (1984) or Ripley (1996)
- Choose λ via 5- or 10-fold CV
- Final tree:



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Comments on Regression Trees

- Partition is not specified apriori, so regression trees provide a *locally adaptive* technique
- Effectively performs variable selection by discovering the relevant interaction terms
 - Implicit in the process
- In the construction, we are assuming that
 - Error terms are uncorrelated
 - Constant variance

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Example: Prostate Cancer

- Fit binary regression tree to log PSA with splits based on eight covariates
- Grow tree with condition of at least 3 observation per leaf
- Results in a tree with 27 splits
- Run weakest-link pruning for each candidate λ , with λ chosen according to CV

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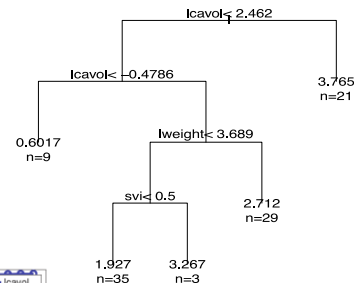
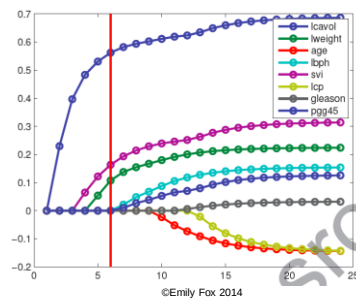
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Example: Prostate Cancer

■ Compare results to LASSO

- $lcavol$ most “important”
- Then $lweight$ and svi

$$\begin{aligned}
 h_1(x) &= I(lcavol < -0.4786) \\
 h_2(x) &= I(lcavol < -0.4786) \quad I(lweight < 3.689) \quad I(svi < 0.5) \\
 h_3(x) &= I(lcavol < -0.4786) \quad I(lweight < 3.689) \quad I(svi > 0.5) \\
 h_4(x) &= I(lcavol < -0.4786) \quad I(lweight = 3.689) \\
 h_5(x) &= I(lcavol = 2.462).
 \end{aligned}$$



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Issues

■ Unordered categorical predictors

- With unordered categorical predictors with q possible values, there are $2^{q-1}-1$ possible choices of partition points to consider for each variable
- Prohibitive for large q
- Can deal with this for binary y ...will come back to this in “classification”

■ Missing predictor values...how to cope?

- Can discard
- Can fill in, e.g., with mean of other variables
- With trees, there are better approaches
 - Categorical predictors: make new category “missing”
 - Split on observed data. For every split, create an ordered list of “surrogate” splits (predictor/value) that create similar divides of the data. When examining observation with a missing predictor, when splitting on that dimension, use top-most surrogate that is available instead

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Issues

■ Binary splits

- Could split into more regions at every node
- However, this more rapidly fragments the data leaving insufficient data and subsequent levels
- Multiway splits can be achieved via a sequence of binary splits, so binary splits are generally preferred

■ Instability

- Can exhibit high variance
- Small changes in the data → big changes in the tree
- Errors in the top split propagates all the way down
- **Bagging** averages many trees to reduce variance

■ Inference

- Hard...need to account for stepwise search algorithm

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Issues

■ Lack of smoothness

- Fits piecewise constant models...unlikely to believe this structure
- **MARS** address this issue (can view as modification to CART)

■ Difficulty in capturing additive structure

- Imagine true structure is

$$y = \beta_1 I(x_1 < t_1) + \beta_2 I(x_2 < t_2) + \epsilon$$

- No encouragement to find this structure

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What you need to know

- Regression trees provide an adaptive regression method
- Fit constants (or simple models) to each region of a partition
- Relies on estimating a binary tree partition
 - Sequence of decisions of variables to split on and where
 - Grown in a greedy, forward-wise manner
 - Pruned subsequently
- Implicitly performs variable selection
- MARS is a modification to CART allowing linear fits

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Readings

- Wakefield – 12.7
- Hastie, Tibshirani, Friedman – 9.2.1-9.2.2, 9.2.4, 9.4
- Wasserman – 5.12

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