Institut für Informatik, Universität Zürich

MSc Project Report

Implementing Learned Indexes on 1 and 2 Dimensional Data

Neeraj Kumar, Nivedita Nivedita, Xiaozhe Yao

Matrikelnummer: 19-759-570

Email: xiaozhe.yao@uzh.ch

April 28, 2021

supervised by
Prof. Dr. Michael H. Böhlen and
Mr. Qing Chen

University of Zurich[UZH]

Department of Informatics

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Databases use indexes to find records efficiently. Among these indexes, B-tree and KD-tree are the two indexes used for 1-dimensional and 2-dimensional data. In this project, we first implement these two indexes from scratch and then we implemented the learned indexes, including a fully connected neural network and a recursive model for 1-dimensional data [KBC+18] and the LISA model for 2-dimensional data [LLZ+20]. Afterwards, we conduct several experiments to evaluate the performance of learned indexes. In addition to the implementation and evaluation, we then theoretically analyse some properties that the learned indexes hold. Beyond that, we also explore and discuss the properties that the learned indexes should hold.

As an extension to the existing learned indexes, we explore the possibilities of using convolution operation and convolutional neural network as learned indexes.

Contents

1. Introduction

Over the years, indexes have been widely used in databases to improve the speed of data retrieval. In the past decades, the database indexes generally fall into the hand-engineered data structures, such as B-Tree, KD-Tree, etc. These indexes have played a crucial role in databases and have been used widely in modern data management systems (DBMS) such as PostgreSQL. Despite their huge success, a shortcoming of these data structures is the lack of consideration of how the database records distributed. We use an example to demonstrate how distributions can affect the efficiency of database indexes.

Example 1.1 For example, if the dataset contains integers from 1 to 1 million, then the keys can be used directly as offsets. With the keys used as offsets, the value with a given key can be retrieved in $\mathcal{O}(1)$ time complexity while B-Tree requires $\mathcal{O}(\log n)$ time complexity for the same query. From the perspective of space complexity, we do not need any extra overhead by using the key as an offset directly, while the B-Tree needs extra $\mathcal{O}(n)$ space complexity to save the tree.

From the above example, we found that there are two promising advantages of leveraging the distribution of the data:

1. It may be faster when performing queries, especially when the number of entries in the database are rather huge.

2. It may take less memory space, as we only need to save the model with constant size.

Nowadays, to learn the distribution and apply it to database indexes, researchers proposed learned indexes [KBC+18], where machine learning techniques are applied to automatically learn the distribution of the database entries and build the data-driven indexes. In this project, we implemented hand-engineered indexes and the learned index. After that, we explore the possibilities of using complex convolutional neural networks as database indexes. This report is organised into the following chapters:

1. **Introduction**. In this chapter, we illustrate the organisation of this report. Besides, we go through the modern computer systems and introduce the general information about database indexes.

2. **Implementation**. In this chapter, we thoroughly describe the implementation of one and two dimensional indexes, including B-Tree, baseline learned index, recursive model, KD-Tree and LISA.

3. **Evaluation**. In this chapter, we perform evaluation among the indexes we implemented with different evaluation dataset.

4. **Insights and Findings**. We demonstrate our findings during the implementation in this chapter. Besides, we also discuss the advantages and disadvantages of different indexes.

5. **Convolution and CNN for Learned Indexes**. In this chapter we explore the possibilities of using convolution operation and convolutional neural network to build learned indexes.

6. **Conclusions**.

1.1. Notations

In this report, we will use the following notations:

Sets and Spaces	
$\mathbb{R}$	The set of real numbers
$\mathbb{R}^d$	The set of d dimensional real space
Random Variables	
$\boldsymbol{X}$	A vector or matrix
x	A single value in $\mathbf{X}$
(x, y)	A tuple contains two values
Hyper-Parameters	
N	A pre-set hyper parameter
Functions	
$\mathcal{LR}$	Linear Regression Function
$\mathcal{P}$	Polynomial Function
$\mathcal{M}$	Mapping Function
$\mathcal{O}$	Big-O notation for complexity
$\mathcal{SP}$	Shard Prediction Function
$\mathcal{Q}$	Range Query
$\mathcal{K}$	KNN Query

1.2. Terminologies

In the following chapters, we will use the following terminologies

Index model is a function that maps the index of a row of data into the location (e.g. page index) of the data. For example, in one-dimensional case, the index models include B-Tree, Linear Regression models, etc.

Key is a special attribute in the database that could identify a record. In our work, the key could be a scalar in one-dimensional case, or a (x, y) pair in two-dimensional case.

Order of a tree is the maximum number of children that a node can have.
Internal node is any node of a tree that has child nodes and is not a root node.
Leaf node is any node that does not have child nodes.
Level of a node is defined as the number of edges between this node and the root node.

1.3. Assumptions

Formally, we define the index of each record as x and the corresponding location as y and we represent the whole data as (X, Y) pairs with the total number of pairs defined as N. We could then normalise the Y into $\tilde{Y} \in [0, 1]$ so that the $\tilde{y}$ represents the portion of the y among the whole Y. With these definitions, we can then define a function $F : X \to \tilde{Y}$ that maps the index into the portion of the y. We have $y = F(x) * N$. As the output of this function can be considered as the probability of $X \leq x$, we can regard this function $F(x)$ as the cumulative distribution function (CDF) of X, i.e. $F(x) = \mathbb{P}(X \leq x)$. Now that N is determined by the length of data records, we only need to learn such CDF and we called the learned CDF function as **learned index model**.

Example 1.2 From the perspective of the distribution of data records, our previous example can be rephrased as following. Our data records are (X, Y) pairs with a linear relation, i.e. $y = x, \forall y \in Y$. We are looking for a function F such that $y = x = F(x) * N$, and hence we end up with $F(x) = \frac{1}{N} * x$. If we use this linear function $F(x)$ as the index model, then we could locate the data within $\mathcal{O}(1)$ time complexity and we only need to store the total number of records as the only parameter. Compared with B-Tree and other indexes, the advantages are enormous.

In order to ensure the learned index model to be the desired CDF, we need to make the following assumptions:

1. All data records are stored statically in database, hence we do not take insertion and deletion into consideration. If there is some insertion or deletion, then the total size of the data records, N, will be different. Therefore, if insertion or deletion are involved, we cannot calculate the position as we show above.

2. All data records are sorted according to theirs keys $\boldsymbol{X}$. Only when the data records are sorted according to the keys, we can regard the index model as CDF, i.e. $F(x) = \mathbb{P}(X \leq x)$.

3. For simplicity, we assume that our data records are stored in a continuous memory space. In other words, the indices of pages in this project is continuous integers and all the data records are loaded into memory.

2. Implementation

Summary In this chapter, we first describe how we implement the B-Tree, Baseline model and recursive model for one-dimensional data. After that, we illustrate the implementation of LISA and LISA Baseline, which are two index models for two-dimensional data. At the end, we describe how we use these indexes to perform point query, range query and KNN query.

2.1. One Dimensional Data

2.1.1. B-Tree

B-tree and its variants have been widely used as indexes in databases. B-trees can be considered as a generalisation of binary search tree: In binary search tree, there is only one key and two children at most in the internal node. B-tree extends the nodes such that each node can contain several keys and children. The keys in a node serve as dividing points and separate the range of keys. With this structure, we make a multi-way decision based on comparisons with the keys stored at the node x.

In this section, we introduce the construction process of B-trees and then analyse its properties.

Attributes and Properties

Each node `x` in a B-tree has the following attributes:

- `x.n`: the number of keys currently stored in the node x.
- `x.keys`: the stored keys of this node.
- `x.leaf`: a bool value that determines if current node is a leaf node.
- `x.children`: a list of its children. If `x` is a leaf node who has no children at all, then the list will be empty. We assume the children are `x.`c_1`,` $\cdots$ `,x.`$c_{x.n+1}$, i.e. there will be `x.n` $+ 1$ children at most.

With these attributes, a B-tree has the following properties:

- The number of children of a node is always 1 bigger than the number of keys in a node.

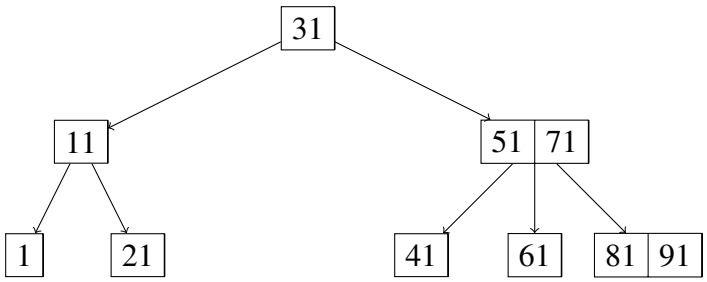


Figure 2.1.: An example of B-tree with the degree $t = 2$.

- Nodes in this tree have lower and upper bounds on the number of keys they can contain. These two bounds can be expressed in terms of a fixed integer t, which we call the **degree** of this tree.
  1. Each node, other than the root node, must contain at least $t - 1$ keys. The root of the tree must have at least one key if the tree is not empty.
  2. Each node can contain at most $2t - 1$ keys. A node is called **full** if it contains exactly $2t - 1$ keys.
- Inside each node, the keys are sorted in the non-decreasing order, so that we have $\texttt{x.keys}_1 \leq \texttt{x.keys}_2 \leq \cdots \leq \texttt{x.keys}_{\texttt{x.n}}$.
- The keys $\texttt{x.key}_i$ separate the ranges of keys stored in each subtree: if k_i is any key stored in the subtree with a root $\texttt{x.c}_i$, then we have $k_1 \leq \texttt{x.keys}_1 \leq k_2 \leq \texttt{x.keys}_2 \leq \cdots \leq \texttt{x.keys}_n \leq k_{\texttt{x.n}+1}$.

In Fig. 2.1, we demonstrate an example B-tree whose degree is 2. In the following section, we will illustrate how to construct and insert keys into a B-tree.

Insertion in a B-tree

With a B-tree, we cannot simply create a new leaf node and insert the new key as we do with binary search tree, as the resulting tree will fail to be a valid B-tree. Instead, we need to insert the new key into an existing leaf node. If the node is not full, we can safely insert the new key. Otherwise, we will need to split the node around the median of its keys into two new nodes and promote the median key into its parent. In this process, we need to split the parent if its parent is also full.

In our implementation of insertion, we travel down the tree and search for the position where the key should be inserted and we split each full node along the way. By doing so, whenever we want to split a full node, we are assured that its parent is not full. The overall algorithm is shown in Algo. 1, which contains methods `splitChild` and `InsertNonFull`

as described in Algo. 2 and Algo. 3 respectively.

Algorithm 1: B-tree Insertion

input: T: The tree with the root T.root; k: The key to be inserted
Result: T: The tree with the inserted key k

```
1  r=T.root
2  if T.n==2t-1 then
3  |  s = NewNode()
4  |  T.root = s
5  |  s.leaf = False
6  |  s.n = 0
7  |  s.c_1 = r
8  |  SplitChild(s, 1)
9  |  InsertNonFull(s, k)
10 else
11 |  InsertNonFull(r, k)
```

In the Algo. 1, we first check if the root node r is full. If it is full, then the root splits and a new node s becomes the root. Then we insert the key k into the tree rooted at the non-full root node, i.e. s or r.

In the Algo. 2, the node y originally has $2t$ children (i.e. $2t-1$ keys) and is full. We take the following steps to split it:

1. We first (from Line 1 to Line 11) create a new node z and give it the largest $t-1$ keys and the corresponding t children of y.
2. Then we adjust the count of keys for y on Line 12: after the split, y will have $t-1$ keys.
3. After that, from Line 13 to Line 21, we insert z as a child of x, move the median key from y up to x, and adjust the key count in x.

Algorithm 2: Split a Child Node in B-Tree

input: x: The node whose children are being split; i: The index of x's child who is full originally

Result: x: The parent node whose children are not full

```
1  z = NewNode()
2  y = x.c_i
3  z.leaf = y.leaf
4  z.n = t-1
5  for j ← 1 to t − 1 do
6  |  z.keys_j = y.keys_{j+t}
7  end
8  if not y.leaf then
9  |  for j ← 1to t do
10 |  |  z.c_j = y.c_{j+t}
11 |  end
12 y.n = t-1
13 for j ← x.n to i + 1 do
14 |  x.c_{j+1} = x.c_j
15 end
16 x.c_{i+1} = z
17 for j ← x.n to i do
18 |  x.keys_{j+1}=x.keys_j
19 end
20 x.key_i = y.key_t
21 x.n = x.n+1
```

The Algo. 3 works as follows:

1. From Line 3 to Line 6, We first check if x is a leaf. If it is a leaf, then we insert the key k into x.

2. If x is not a leaf, then we must insert k into the appropriate leaf node in the subtree rooted at internal node x. From Line 8 to Line 11, we traverse the subtree rooted at x and determine the child of x to which the recursion descends. Then we check on Line 12 if the child where the recursion descends is a full node.

3. If the child is a full node, we then split the child on Line 13 into two non-full children. We then determine from Line 14 to Line 15 which of the two children is the appropriate node to insert.

4. At the last, on Line 16 we look into the ith children of x and recursively insert the key k into it.

Algorithm 3: Insert into a Non-Full Node in B-Tree

input: x: The node to be inserted; k: The key to be inserted
Result: x: The node with the inserted key k

```
i=x.n
if x.leaf then
    while i ≥ 1 and k < x.keys_i do
        x.key_{i+1}=k
        x.n = x.n+1
    end
else
    while i ≥ 1 and k < x.keys_i do
        i=i-1
    end
    i=i+1
    if x.c_i.n==2t-1 then
        SplitChild(x,i)
        if k>x.key_i then
            i=i+1
    InsertNonFull(x.c_i, k)
```

2.1.2. Baseline Learned Index

Overview

The B-Tree can be regarded as a function $\mathcal{F}$ that maps the key x into its corresponding page index y. It is known to us that the pages are allocated in a way that the every S entries are allocated in a page where S is a pre-defined parameter. For example, if we set S to be 10 items per page, then the first page will contain the first 10 keys and their corresponding values. Similarly, the second 10 keys and their corresponding values will be allocated to the second page.

If we know the CDF of X as $F(X \leq x)$ and the total number of entries N, then the position of x can be estimated as $p = F(x) * N$ and the page index where it should be allocated to is given by

$$y = \lfloor \frac{p}{S} \rfloor = \lfloor \frac{F(x) * N}{S} \rfloor$$

Example 2.1 For example, if the keys are uniformly distributed from 0 to 1000, i.e. the CDF of X is defined as $F(X \leq x) = \frac{x}{1000}$ and we set $S = 10, N = 1001$. Then for any key x, we immediately know it will be allocated into $y = \lfloor \frac{1000}{10} * \frac{x}{1000} \rfloor = \lfloor \frac{x}{10} \rfloor$. Assume that we have a key 698, then we can calculate $y = \lfloor \frac{698}{10} \rfloor = 69$. By doing so, the page index is calculated in constant time and space.

In this example, we see that the distribution of X is essential and our goal of learned

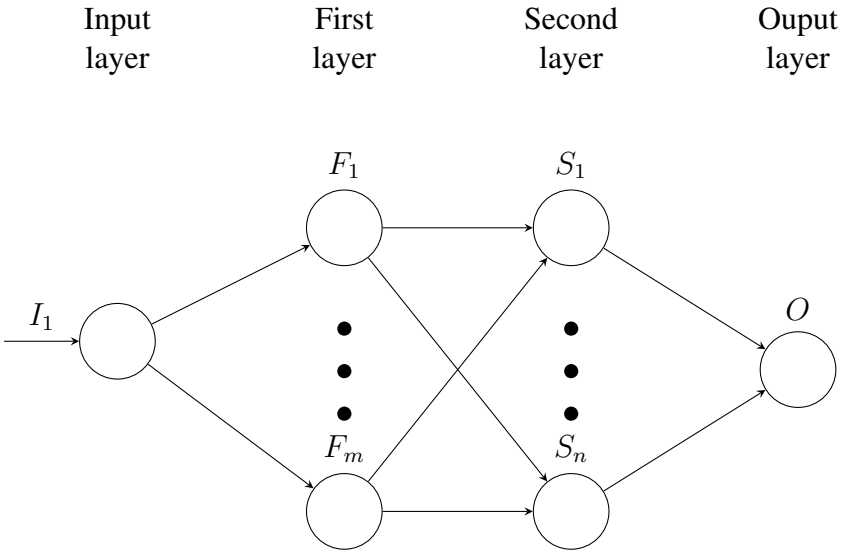


Figure 2.2.: The architecture of the fully connected neural network used as baseline learned index. In this neural network, we use only 2 fully connected layers. The input of this neural network is only one neuron such that it represents the given query key. The output of this neural network is limited to 1 neuron such that it represents the predicted proportional position of the key-value pair.

index in one-dimensional data is to learn such distribution. To do so, we apply two different techniques as the baseline, the polynomial regression and fully connected neural network.

To train such a learned index, we first manually generate the X with respect to a certain distribution. We then save the generated X into a dense array with the length N. Then we use the proportional index, i.e. the index of each x divided by N as the expected output y.

Fully Connected Neural Network

After generating the training dataset X and its corresponding Y, we build a fully connected neural network as the baseline learned index. The architecture of the fully connected neural network is illustrated in Figure 2.2.

We apply the Rectified Linear Unit (ReLU) activation function at the end of F_i and S_i. Formally, assume the output of F_i is $\boldsymbol{a}$, then we define the output of $\textit{ReLU}(F_i)$ as $y = \max(\boldsymbol{a}, 0)$ where max returns the larger value between each entry of $\boldsymbol{a}$ and 0. Then we train this fully connected neural network with standard stochastic gradient descent (SGD), and we set the learning rate to be $\alpha = 0.001$. We use the mean square error (MSE) $\ell = \frac{1}{n}\sum(y - \hat{y})^2$ as the loss function.

Formally, we can induce the output of this fully connected neural network as following:

1. In the input layer, we have the input as a scalar value x.

2. The first fully connected layer has m nodes, and the output is defined as $\boldsymbol{y_1} = \boldsymbol{w_1}x + \boldsymbol{b_1}$ where $\boldsymbol{w_1}$ and $\boldsymbol{b_1}$ is a $m \times 1$ matrix. Hence, the output of the first fully connected layer is a $m \times 1$ matrix. Then we apply the ReLU activation function to $\boldsymbol{y_1}$ and we get $\boldsymbol{z_1} = \max(\boldsymbol{y_1}, 0)$.

3. The second fully connected layer has n nodes, and the output is defined as $\boldsymbol{y_2} = \boldsymbol{w_2}\boldsymbol{z_1} + \boldsymbol{b_2}$. Similarly, after the ReLU operation, we get $\boldsymbol{z_2} = \max(\boldsymbol{y_2}, 0)$.

4. For the output layer, in order to get a scalar as output, we apply a n node fully connected layer here. The final output is defined as $\hat{y} = \boldsymbol{w_3}\boldsymbol{z_2} + \boldsymbol{b_3}$ where $\boldsymbol{w_3}$ is a $1 \times n$ matrix.

In summary, the output of the fully connected neural network can be calculated as

$$\hat{y} = \boldsymbol{w_3}\max(\boldsymbol{w_2}\max(\boldsymbol{w_1}x + \boldsymbol{b_1}, 0) + \boldsymbol{b_2}, 0) + \boldsymbol{b_3} \tag{2.1}$$

In the above fully connected neural network, there are 6 parameters to optimise: $\boldsymbol{w_1}, \boldsymbol{w_2}, \boldsymbol{w_3}$ and $\boldsymbol{b_1}, \boldsymbol{b_2}, \boldsymbol{b_3}$ and we apply the gradient descent and back propagation to optimise them. Formally, the steps are illustrated below:

1. **Initialisation**. For $\boldsymbol{w_i}$ and $\boldsymbol{b_i}$ of the shape $m \times n$, we randomly initialise the values of each entry using a uniform distribution $U(-\frac{1}{\sqrt{n}}, \frac{1}{\sqrt{n}})$.

2. **Forward Pass**. With the initialised $\boldsymbol{w_i}$ and $\boldsymbol{b_i}$, we calculate the output as formulated be the equation 2.1. We then calculate the error as $\ell = \frac{1}{n}\sum(y - \hat{y})^2$.

3. **Backward Pass**. After getting the error, we start from the last layer to perform the backward propagation operation. Formally, we do the following operations:
   a) We first calculate the partial derivatives: $\frac{\partial \ell}{\partial \boldsymbol{w_3}} = \boldsymbol{z_2}^T$, $\frac{\partial \ell}{\partial \boldsymbol{b_3}} = 1$ and $\nabla_3 = \frac{\partial \ell}{\partial \boldsymbol{z_2}} = \boldsymbol{w_3}^T$. Then we can update $\boldsymbol{w_3}$ and $\boldsymbol{b_3}$ as $\boldsymbol{w_3}^{\text{new}} = \boldsymbol{w_3} - \alpha * \frac{\partial \ell}{\partial \boldsymbol{w_3}}$ and $\boldsymbol{b_3}^{\text{new}} = \boldsymbol{b_3} - \alpha * \frac{\partial \ell}{\partial \boldsymbol{b_3}}$.
   b) Then we pass the ∇_3 to previous layer, and calculate the partial derivatives as $\frac{\partial \ell}{\partial \boldsymbol{w_2}} = \boldsymbol{z_2}^T\nabla_3$, $\frac{\partial \ell}{\partial \boldsymbol{b_2}} = \nabla_3$ and $\nabla_2 = \frac{\partial \ell}{\partial \boldsymbol{z_1}} = \nabla_3\boldsymbol{w_2}^T$. Then we update $\boldsymbol{w_2}$ and $\boldsymbol{b_2}$.
   c) After that, we pass the ∇_2 to the first layer, and calculate the partial derivatives as $\frac{\partial \ell}{\partial \boldsymbol{w_1}} = x^T\nabla_2$, $\frac{\partial \ell}{\partial \boldsymbol{b_1}} = \nabla_2$. Then we update $\boldsymbol{w_1}$ and $\boldsymbol{b_1}$.

4. **Loop between 2 and 3**. We perform the forward pass and the backward several times until the loss is acceptable or a maximum number of loops reached.

We will discuss more findings and insights about the baseline model in the *Chapter 4*.

2.1.3. Recursive Model Index

In our baseline models, it is not very difficult to reduce the mean square error from millions to thousands. However, it is much harder to reduce it from thousands to tens. This is the so called last-mile problem.

In order to solve this problem, recursive model index was proposed [KBC+18]. The idea is to split the whole set of data into smaller pieces and assign each piece an index model. By doing so, each model is only responsible for a small range of keys. Ideally, in each smaller range, the keys are distributed in a way that is easier to be learned by our index models, such as polynomial model, fully connected model or even traditional B-Tree model.

As shown in Fig. 2.3. A recursive model can be regarded as a tree structure, which contains a root model that receives the full dataset for training. Then the root model will split the dataset into several parts. Each sub-model will then receive one part of the full dataset. Then we train the sub-models one by one with the partial training dataset.

Example 2.2 For example, in the Fig. 2.3, the full dataset will be split into three parts and each sub-model receives one part. To train this recursive model, we first train the root model with the whole dataset. Then the root model will split the dataset into 3 parts according to the predicted value of each data point in the dataset. Then each sub-model will receive one part and we train the sub-model accordingly.

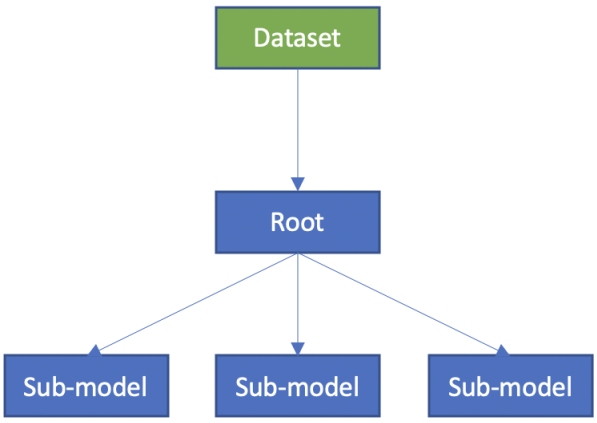


Figure 2.3.: An example recursive model index with one root model and three leaf model.

Properties

Similar to a tree, we define the following terms in a recursive model:

1. **Node Model**. Every node is responsible for making decisions with given input data. In one dimensional case, it can be regarded as a function $f : \mathbb{R} \to \mathbb{R}, x \to y$ where x is the input index and y is the corresponding page block. In principle, each node can be implemented as any machine learning model, from linear regression to neural network, or a traditional tree-based model, such as B-Tree.

2. **Internal Node Model**. Internal nodes are all nodes except for leaf nodes and the root node. Every internal node receives a certain part of training data from the full dataset, and train a model on it.

In the following sections, we will use the notations defined below:

1. $N_M^{(i)}$ is the number of models in the ith stage.

Training

In order to construct a recursive model, we need to have several parameters listed below:

1. The training dataset, notated as (X, Y) with entries notated as (x, y).
2. The number of stages, notated as N_S. It is an integer variable.
3. The number of models at each stage, notated as N_M. It is a list of integer variable. $N_M^{(i+1)}$ represents the number of models in the ith stage.

The training process of recursive model is an up-bottom process. There will be only one root model that receives the whole training data. After the root model is trained, we iterate over all the training data and predict the page by the root model. After the iteration, we get a new set of pairs (X, Y_0). Then we map $\forall y_0 \in Y_0$ into the selected model id in next stage by

next $= y_0 * N_M^{(i+1)}/$max(Y).

Algorithm 4: Training of Recursive Model Index

```
input: N_S: A scalar representing the number of stages;
       N_M: An array representing the number of models at
  each stage;
       x; y
trainset=[[(x,y)]]
stage← 0
while stage <N_S do
    while model <N_M[stage] do
        model.train(trainset[stage][model])
        models[stage].append(model)
    end
    if stage<N_S-1 then
        for i ← 0 to len(x) do
            next_model = 0
            for j ← 0 to stage-1 do
                output = models[stage][next_model]
                next_model = output * N_M[stage+1]/max_y
            end
            model = models[next_model]
            output = model.predict(x[i])
            next = output * N_M[stage+1]/max_y
            trainset[stage+1][next].add((x[i],y[i]))
        end
    stage=stage+1
end
```

Polynomial Internal Models

In the recursive model index, we use internal models to learn the CDF of a part of the full training data. In order to learn the CDF, we need to know or assume the distribution of a specific part of the data. In this report, we support the following distributions.

Linear Regression	$wx + b$
Quadratic Regression	$ax^2 + bx + c$
B-Tree	N/A
Fully Connected Neural Network	N/A

Here we describe how we fit a polynomial model.
The polynomial regression model with degree m can be formalised as

$$\hat{y}_i = \beta_0 + \beta_1 x_i + \beta_2 x_i^2 + \cdots + \beta_m x_i^m$$

and it can be expressed in a matrix form as below

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_1 & x_1^2 & \cdots & x_1^m \\ 1 & x_2 & x_2^2 & \cdots & x_2^m \\ \vdots & & & & \\ 1 & x_n & x_n^2 & \cdots & x_n^m \end{bmatrix} \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_m \end{bmatrix}$$

which can be written as $Y = \boldsymbol{X}\boldsymbol{\beta}$.

Proof 2.1 Our goal is to find β such that the sum of squared error, i.e.

$$\mathrm{S}(\boldsymbol{\beta}) = \sum_{i=1}^{n} (\hat{y} - y)^2$$

is minimal. This optimisation problem can be resolved by ordinary least square estimation as shown below.

First we have the error as

$$\begin{aligned} \mathrm{S}(\boldsymbol{\beta}) = ||\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta}|| &= (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta})^T (\boldsymbol{y} - \boldsymbol{X}\boldsymbol{\beta}) \\ &= \boldsymbol{y}^T\boldsymbol{y} - \boldsymbol{\beta}^T\boldsymbol{X}^T\boldsymbol{y} - \boldsymbol{y}^T\boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\beta}^T\boldsymbol{X}^T\boldsymbol{X}\boldsymbol{\beta} \end{aligned} \tag{2.2}$$

Here we know that $(\boldsymbol{\beta}^T\boldsymbol{X}^T\boldsymbol{y})^T = \boldsymbol{y}^T\boldsymbol{X}\boldsymbol{\beta}$ is a 1×1 matrix, i.e. a scalar. Hence it is equal to its own transpose. As a result we could simplify the error as

$$\mathrm{S}(\boldsymbol{\beta}) = \boldsymbol{y}^T\boldsymbol{y} - 2\boldsymbol{\beta}^T\boldsymbol{X}^T\boldsymbol{y} + \boldsymbol{\beta}^T\boldsymbol{X}^T\boldsymbol{X}\boldsymbol{\beta} \tag{2.3}$$

In order to find the minimum of $S(\boldsymbol{\beta})$, we differentiate it with respect to $\boldsymbol{\beta}$ as

$$\nabla_{\boldsymbol{\beta}} S = -2\boldsymbol{X}^T\boldsymbol{y} + 2(\boldsymbol{X}^T\boldsymbol{X})\boldsymbol{\beta} \tag{2.4}$$

By let it to be zero, we end up with

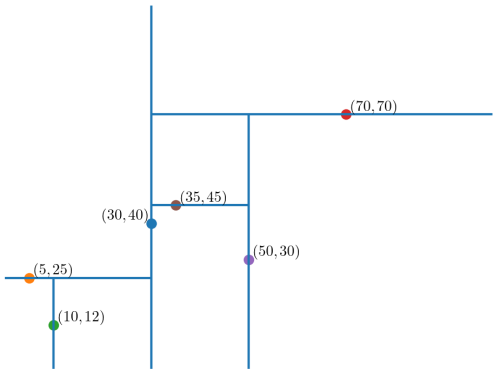
$$\begin{aligned} &-\boldsymbol{X}^T\boldsymbol{y} + (\boldsymbol{X}^T\boldsymbol{X})\boldsymbol{\beta} = 0 \\ &\implies \boldsymbol{\beta} = (\boldsymbol{X}^T\boldsymbol{X})^{-1}\boldsymbol{X}^T\boldsymbol{y} \end{aligned} \tag{2.5}$$

■

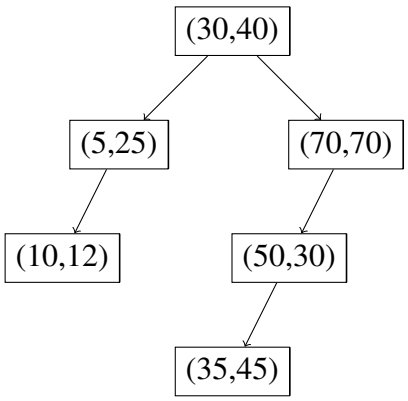
2.2. Two Dimensional Data

2.2.1. KD-Tree

KD-tree is a space partitioning structure that can be used to organise data points in k dimensional space. In this project, we limit the dimension k to be 2. We implement the KD-tree as a binary tree in which every node is a 2-dimensional point. Every non-leaf node is representing a splitting line that divides the space into two parts. Then every points to the left (or down) of this line are represented by the left subtree and points to the right (or up) of this line are represented by the right subtree. In Fig. 2.4 we illustrate an example of KD-tree.



(a) The 2D space and the partition of KD-tree



(b) The tree structure of the KD-tree

Figure 2.4.: An example of KD-Tree

Insertion of KD-tree

Similar to a binary search tree, we need to traverse the tree when we need to insert a point to the KD-tree. The only difference is that we need to switch the axes when inserting into a KD-tree. For example, since the dimension is 2 in our case, we compare the x-coordinate at the root level. Then in the root's direct children, we compare the y-coordinate at that level. Formally, the insertion algorithm is expressed as in Algo. 5.

Algorithm 5: KD-tree Insertion

input: `t`: The node to be inserted; `k`: The key to be inserted; `cd`: Current dimension
Result: `t`: The node with the inserted key `k`

```
1 DIM=2;
2 if t==NULL then
3 |  t = NewNode(k)
4 else if x[cd]<t.data[cd] then
5 |  t.left=insert(x, t.left, (cd+1) % DIM )
6 else
7 |  t.right=insert(x, t.right, (cd+1)% DIM)
8 return N
```

To insert a key `k` into the KD-tree with `T` as its node, we only need to apply this function with the root node as `insert(T, k, 0)`.

In the Algo. 5, the insertion of a key is performed in the following steps:

1. On Line 1, we specify the dimension to be 2.
2. Then we first check if the node is `NULL`. If it is `NULL`, which means we should have a new leaf node, then we create a new node and give it our key.

3. Otherwise, from Line 4 to 7, we check the data at current dimension. If it is smaller than the data in the node `t` at current dimension, then we should insert into the left subtree. Otherwise, we should insert into the right subtree.

4. When we moves down to the left or right subtree, we switch the current dimension by calculating `(cd+1)% DIM`.

Example 2.3 In Fig. 2.4, we present an example of KD-tree. In this example, we will illustrate how it is constructed. Assume our data points is

$$[(30, 40), (5, 25), (10, 12), (70, 70), (50, 30), (35, 45)]$$

The construction of the KD-tree follows the steps below:

1. We start with $(30, 40)$ by creating a new node and give it the data point, which results in the root node in the figure.

2. After that we insert $(5, 25)$, since `x[0]<t.data[0]`, we insert this node as the left subtree to the root.

3. Then we insert $(10, 12)$. First we compare the x-coordinate at the root level. As $10 < 30$, we go to the left subtree. Then we compare at the root's children level and compare the y-coordinate. As $12 < 25$, we go to the left subtree and create a new node there.

4. Similarly, we insert other keys one-by-one.

2.2.2. LISA: Learned Index for Spatial Data

Spatial data and query processing have become ubiquitous due to proliferation of location-based services such as digital mapping, location-based social networking, and geo-targeted advertising. Motivated by the performance benefits of learned indices for one-dimensional data, this section explores the application of learned index for spatial data. The main motivation is to map spatial data into one-dimensional data through several steps and apply machine learning techniques to generate a learned index for the one-dimensional data.

Motivation

In the last section, we described a recursive model index (RMI) that consists of a number of machine learning models staged into a hierarchy to enable synthesis of specialised index structures, termed learned indexes. Provided with a search key x, RMI predicts the position of x's data with some error bound, by learning the CDF over the key search space. However, the idea of RMI is not applicable in the context of spatial data as spatial data invalidates the assumption required by RMI that the data is sorted by key and that any imprecision can

be easily corrected by a localised search. Although it is possible to learn multi-dimensional CDFs, such CDFs will result in searching local regions qualified on one dimension but not all dimensions.

For the one-dimensional data, we can learn the CDF by using a recursive model as shown in previous section. However, when the data is two-dimensional, the learned CDF (the marginal CDF) through recursive model cannot be applied directly to predict the position of the key. Formally, we could learn the marginal CDF for each dimension by using recursive model, i.e. $F(X)$ and $F(Y)$. However, to predict the position of a 2-dimensional key, we need to joint CDF $F(X, Y)$, which cannot be induced from the marginal CDFs. We show an example as below to illustrate this limitation.

Example 2.4 Assume that X and Y are distributed as shown in Fig 2.5. In this example, we have $F(x \leq A) = \frac{1}{3}$, which means that the point A should be assigned into the first third pages. With learned indexes in one-dimensional, then there comes the problem below:

1. There will be duplicate keys. In this example, if we only consider the X axis, we will get an array $[0.7, 0.7, 1.5]$ which contains duplicate keys.
2. If we remove the duplicate keys, then $F(x \leq A) = \frac{1}{2}$, which is not what we expect.
3. If we do not remove the duplicate keys, then $F(x \leq A) = F(x \leq B)$, which is still not we expect.

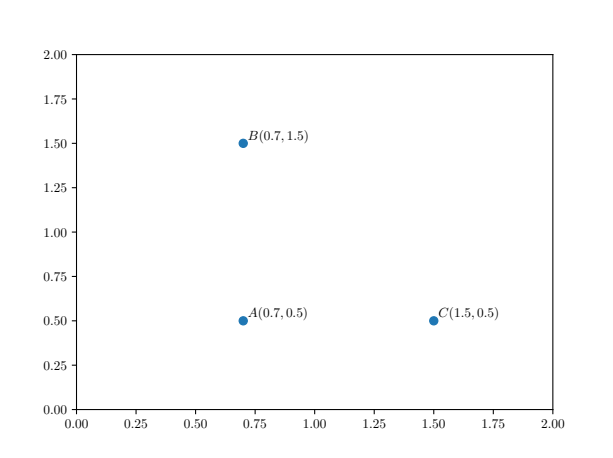


Figure 2.5.: An example demonstrating the limitations of one-dimensional learned index in two-dimensional data. In this graph we have $F(x \leq A) = \frac{1}{3}$ but with learned index in one-dimensional, we cannot learned such joint CDF.

LISA solves this problem by partitioning search space into a series of grid cells based on the data distribution and building a function map the data from $\mathbb{R}^d$ into $\mathbb{R}$, in our case, we have $d = 2$. We call this function as *Mapping Function*.

Definitions

This section presents the definition

1. **Key**. A key k is a unique identifier for a data record with $k = (x_0, x_1) \in \mathbb{R}^2$.
2. **Cell**. A grid cell is a rectangle whose lower and upper corners are points (l_0, l_1) and (u_0, u_1), i.e., cell = $(l_0, u_0) \times [l_1, u_1)$.
3. **Mapping Function**. A mapping function $\mathcal{M}$ is a function on the domain $\mathbb{R}^2$ to the non-negative range, i.e $\mathcal{M} : [0, X_0] \times [0, X_1] \to [0, +\infty)$ such that $M(x_0, x_1) \leq \mathcal{M}(y_0, y_1)$ when $x_0 \leq y_0$ and $x_1 \leq y_1$.

2.2.3. Baseline Method

We can extend the learned index method for range queries on spatial data by using a mapping function. This baseline method works as follows. We first sort all keys according to their mapped values and divide the mapped values into some cells such that each cell contains the same number of keys (except the last one). If a point (x, y)'s mapped value is larger than those of the keys stored in the first i cells, i.e. $\mathcal{M}(x, y) > \sup \bigcup_{j=0}^{i-1} M(C_j)$, we store (x, y) in the $(i + 1)$th cell.

For a range query, represented by the query rectangle $qr = [l_0, u_0) \times [l_1, u_1)$, We only need to predict the indices of (l_0, l_1) and (u_0, u_1) namely i_1 and i_2 respectively. Then we scan the keys in $i_2 - i_1 + 1$ cells, and find those keys that fall in the query rectangle qr.

Example 2.5 As shown in Fig. 2.6, the key space is divided into 3 cells using the mapping function $\mathcal{M}((x, y)) = x + y$. The query rectangle consisting of only 1 key, falls inside the second cell. During prediction, we need to find out the cell to which our query rectangle belongs (the 2^{nd} cell in our example). Once the cell is identified, we need to compare the 2 dimensional key value of the query point, against all the possible keys in that cell until a match is found. This results in 8 irrelevant points accessed for the range query that only contains one relevant key.

Training

The training dataset for the baseline model can be notated as $(\boldsymbol{X}, Y)$ with entries notated as $(\boldsymbol{x}, y)$. $\boldsymbol{X}$ represents the two dimensional key coordinates, and Y represents the corresponding data item.

In order to construct the baseline model, we need to have several parameters listed below:

1. N, which represents the number of cells into which the key's mapped value space will be divided.

As described in Algorithm 8, during training, we perform the following operations:

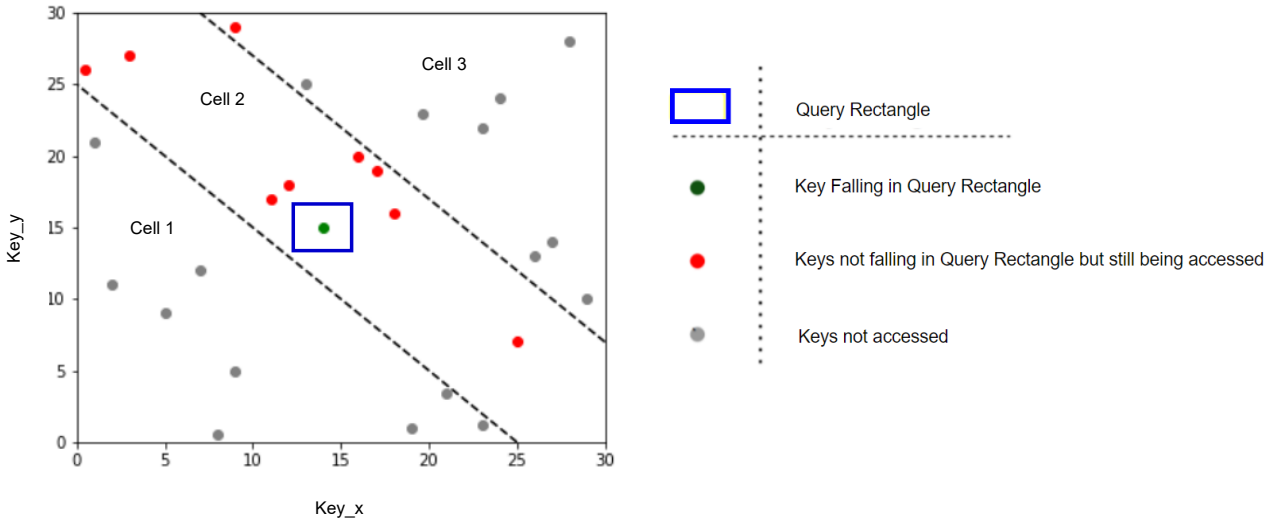


Figure 2.6.: LISA Baseline Method
a) Key space is divided into 3 cells with equal number of keys
b) To search for a query, we first need to find out the cell which contain the query point
c) Once the query point is found, we need to compare the query point 2 dimensional key value with all the keys in the cell until a match is found

1. Sort all keys according to their mapped values.
2. Divide the keys into equal sized cells
3. Store the mapped values of first and last key for each cell into an array

Algorithm 6: Training Algorithm for Lisa Baseline Method

input : N; trainset=$[(x, y); x \in \mathbb{R}^2; y \in \mathbb{R}]$
Output: $\mathcal{M}$:Mapped Function

for $i \leftarrow 0$ **to** $len(x)$ **do**
  `x[i].mapped_value = x[i][0]+x[i][1]`
end
`sortXBasedOnMappedValue()`
`Divide` x `into` N `equal size cells`
for $i \leftarrow 0$ **to** N **do**
  `denseArray[`i`].lower = first key in cell` i
  `denseArray[`i`].upper = last key in cell` i
end

For prediction, we find the cell corresponding to mapped value of the query point using binary search, scan this cell sequentially and compare the values of keys in the cell against the query point, until a match is found.

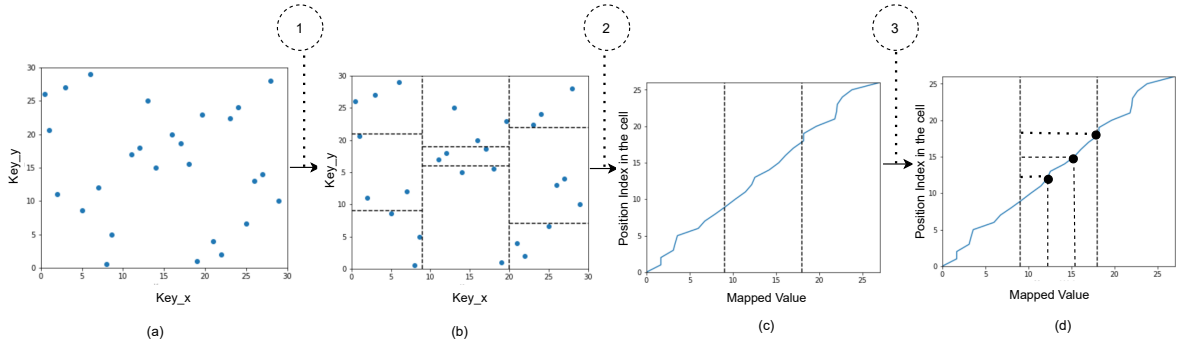


Figure 2.7.: Lisa Framework
1) Generate grid cells, and apply Lebesgue Measure to each cell to map two dimensional key value to a scalar.
2) Sort mapped values and divide them across equal length intervals termed as mapped intervals (3 in our figure)
3) For each mapped interval, divide the mapped value range in shards (3 in our figure) and learn a linear regression function to partition the keys belonging to a particular interval, into different shards

Prediction

Algorithm 7: Prediction Algorithm for Lisa Baseline Model

input: `x_test`: Key; `d`: Array with metadata for each cell

```
x_test.mapped_value = x_test[0]+x_test[1]
for i ← 0 to len(denseArray) do
    if M(x_test) ∈ [d[i].lower, d[i].upper] then
        Key is in Page i
        break
    end
end
Sequentially search for x_test in page i
```

2.2.4. Lisa Overview

Given a spatial dataset, we generate the mapping function $\mathcal{M}$ and the shard prediction function $\mathcal{SP}$. Based on them, we build our index structure, LISA, to process point, range and KNN queries. LISA consists of four parts: the representation of grid cells, the mapping function $\mathcal{M}$, the shard prediction function $\mathcal{SP}$, and the local models for all shards. As illustrated in the Fig 2.7. the procedure of building LISA is composed of four parts.

1. Grid cell partition.
2. Mapping spatial coordinates into scalars, i.e. $\mathbb{R}^d \to \mathbb{R}$.
3. Build shard prediction function $\mathcal{SP}$.

4. Build local models.

Definitions

This section presents the additional definition specific to Lisa implementation.

4. **Shard**. The shard S is the pre-image of an interval $[a, b) \subseteq [0, +1)$ under the mapping function $\mathcal{M}$, i.e., $S = M^{-1}([a.b))$.
   Given an initial data set, we divide the key space into cell grids based on the data distribution, map keys values to an one dimensional space using mapping function, followed by learning several monotonic shard prediction functions. After sorting, the one dimensional mapped value space is divided into equal-length intervals. One shard prediction function is learned for each interval, to partition the keys belonging to a particular interval, into different shards. As keys are sorted by mapped values before partitioning them into equal sized intervals, and all shards exhibit a total order with respect to their corresponding intervals in the mapped range(Shard Prediction function for each interval is monotonically increasing), following relationship holds
   $inf(M(S_i)) > sup(M(S_j))$ when $i > j$.

5. **Local Model**. Local model L_i is a model that processes operations within a shard S_i . It keeps dynamic structures such as the addresses of pages contained by S_i. Local models are not relevant to our implementation as full data-set is loaded in the main memory

2.2.5. Design and Implementation Details

Grid Cells Generation

The first task in Lisa implementation is to partition the 2 dimensional key space into a series of grid cells based on the data distribution along a sequence of axes. Then we number the cells along these axes as well. The principal idea behind this partition strategy is to divide the key space into cell boundaries and apply a mapping function to create monotonically increasing mapping values at the cell boundaries.

$M(x_i \in V) < M(x_j \in V)$ when $i < j$, where $x_i \in C_i$ and $x_j \in C_j$

i.e. mapped value of a key in cell i will always be less than mapped values of a key in cell j, if $i < j$.

Example 2.6 Consider the example shown in the figure 2.8: 27 keys are partitioned into 9 cell, resulting in 3 keys per cell. To partition the key space, we first sort the keys values according to 1^{st} dimension and divide the keys into 3 vertical columns each containing 9 keys. Then for each vertical column of 9 keys, we sort the keys again according to 2^{nd} dimension, and divide the keys in each column into 3 new cells. The number of cells N into which the keys space is divided, is a hyper-parameter and found empirically using grid search.

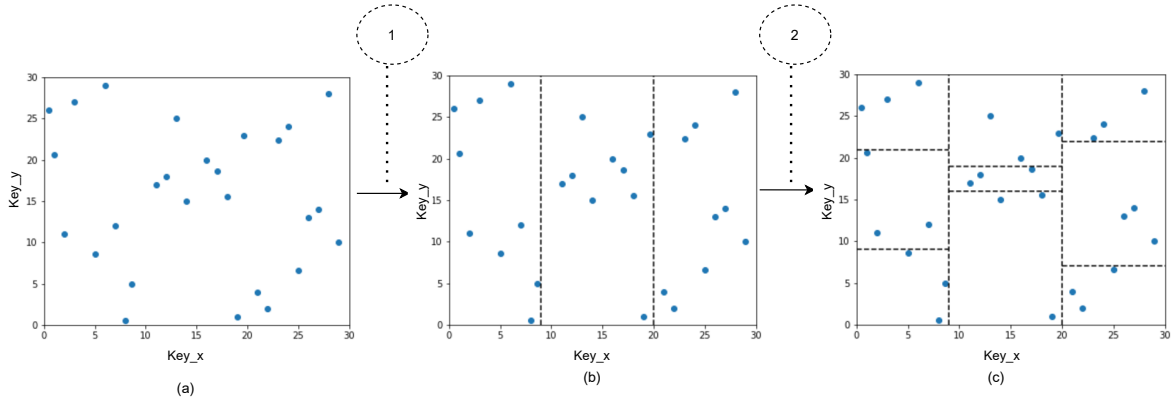


Figure 2.8.: Cell Partition Strategy:
1) : Sort Keys on 1^{st} dimension and divide into 3 vertical columns each containing 9 keys
2) : Sort each vertical column keys on 2^{nd} dimension and divide into 3 horizontal columns each containing 3 keys

We need to sort the key space along the sequence of axis before we partition the keys value along that axis to make sure that cells don't contain overlapping keys.

Algorithm 8: Grid Cell Generation Algorithm for Lisa Method

input: `N;` x`;` y

`trainset=[`$(x, y); x \in \mathbb{R}^2; y \in \mathbb{R}$`]`
$keysPerCell = len(x)/(N \times N)$
`sort`x`BasedOnDimension_0()` // Sort x based on 1^{st} dimension.
for $i \leftarrow 0$ **to** N **do**
    `Store the 1st dimensional coordinates of first and last key in cell` i
    `Sort keys in cell` i `based on 2nd dimension,x[:][1]`
end
for $i \leftarrow 0$ **to** N **do**
    for $j \leftarrow 0$ **to** N **do**
        `Store the 2nd dimensional coordinate of first and last key of cell[`i`][`j`] .`
    end
end

Mapping Function

A mapping function $\mathcal{M}$ is a function on the domain $\mathbb{R}^2$ to the non-negative range, i.e $M : [0, X_0] \times [0, X_1] \rightarrow [0, +\infty)$ such that $M(x_i \in V) < M(x_j \in V)$ if $i < j$, where $x_i \in C_i$ and $x_j \in C_j$. That means the mapped value of a key in cell i will always be less than mapped values of a key in cell j, if $i < j$.

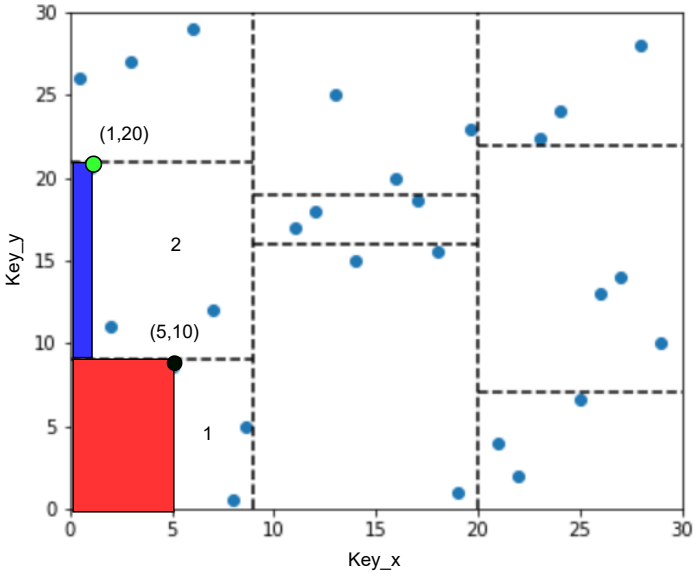


Figure 2.9.: Lebesgue Measure Representation for 2 dimensional data
1) Lebesgue Measure for the black point in first cell will be ratio of area of red rectangle divided by the total area of 1^{st} cell = $50/100 = 0.5$
1) Lebesgue Measure for the green point in second cell will be ratio of area of blue rectangle divided by the total area of 2^{nd} cell = $20/100 = 0.2$

Suppose $x = (x_0, x_1)$ and $x \in C_i = [\theta^{(0)}_{i_0}, \theta^{(0)}_{i_0+1}) \times [\theta^{(1)}_{i_1}, \theta^{(1)}_{i_1+1})$ then we define

$$M(x) = i + \frac{\mu(H_i)}{\mu(C_i)}$$

where $H_i = [\theta^{(0)}_{i_0}, x_0) \times [\theta^{(1)}_{i_1}, x_1)$ and μ is the Lebesgue measure on $\mathbb{R}^2$.

As shown in figure 2.9, in 2-dimensional case, $\frac{\mu(H_i)}{\mu(C_i)}$ represents the fraction of the area covered by the key(x_0, x_1) to the total area of the cell. Since we are adding i, the index of the cell, to this fraction, the mapped value of a key in cell i will always be less than mapped values of a key in cell j, if $i < j$. After calculating the mapped values of the data set, we sort the keys in each cell according to the mapped value. This results in the whole key space to be sorted according to the mapped value. Figure 2.10 shows the mapping of 2 dimensional key space to one dimensional CDF.

Shard Prediction Function

After the mapping function, we get a dense array of mapped values. Then we partition them evenly into U parts and let $\boldsymbol{M}_p = [m_1, \cdots, m_U]$. We train linear regression functions $\mathcal{F}_i$ on each interval and suppose $V+1$ is the number of mapped values that each $\mathcal{F}_i$ needs to process and D is the number of shards per interval. $\Psi = \lfloor \frac{V+1}{D} \rfloor$ is the number of keys falling in a shard.

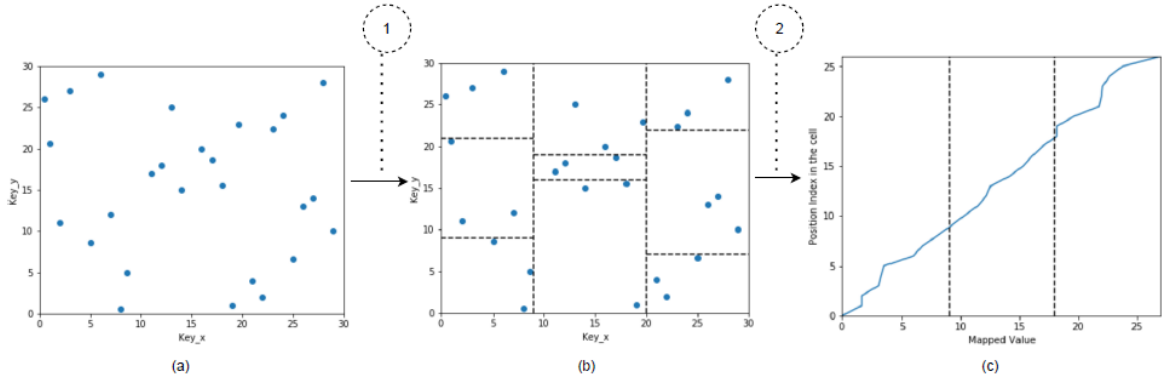


Figure 2.10.: Mapping 2 dimensional key Values to one dimensional cdf
1) Generate grid cells, and apply Lebesgue Measure to each cell.
2) Sort key in each cell according to mapped value. Mapped values in consecutive cells are already sorted by mapping function definition. Plot the cdf of mapped values.

Example 2.7 For example, assume we have a dense array of 9 mapped values as

$$[1, 1.2, 2, 2.2, 3, 3.3, 3.4, 4, 4.5]$$

and U and D are initialized as 3. So we have $\boldsymbol{M}_p = [9]$ which is divided into 3 equal intervals, $\boldsymbol{M}_p = [m_1, m_2, m_3]$, each containing 3 keys. In this case we have $V+1 = 3$ and will train 3 linear regression functions, 1 for each interval. Each $\mathcal{F}_i$ generates D shards and number of keys falling in a shard will be $\Psi = \lfloor \frac{V+1}{D} \rfloor = 1$.

Then with a given x, the predicted shard is given by $\mathcal{SP}(x) = \mathcal{F}_i(x) + i \times D$, where $i = \text{binary-search}(\boldsymbol{M}_p, x)$. More specifically, we first determine i by using binary search. The result tells which interval this x should belong to. Then we find the corresponding linear regression function $\mathcal{F}_i$ and calculate $\mathcal{F}_i(x)$, which is the predicted shard.

Example 2.8 In the above example, given a key $x = 1.2$, we first perform binary search in $\boldsymbol{M}_p$ and we found $i = 1$. Then we find the first linear regression function $\mathcal{F}_1$ and calculate $\mathcal{F}_1(x)$. Since each linear regression function will yield $D = 3$ shards, the shards that the first linear regression function generates will be from 0 to 2 and the shards that the second linear regression function generates will be from 3 to 5. Hence, the predicted shard id is given by

$$\mathcal{SP}(x) = \mathcal{F}_i(x) + i \times D$$

Then the problem left is to train the linear regression functions $\mathcal{F}_i$. Let $\boldsymbol{x} = (x_0, \cdots, x_v)$ be the keys' mapped value that fall in $[m_{i-1}, m_i)$. Suppose that $\boldsymbol{x}$ is sorted, i.e. $x_i \leq x_j, \forall 0 \leq i < j \leq v$. Let $\boldsymbol{y} = (0, \cdots, V)$. Then we build a piecewise linear regression function f_i with

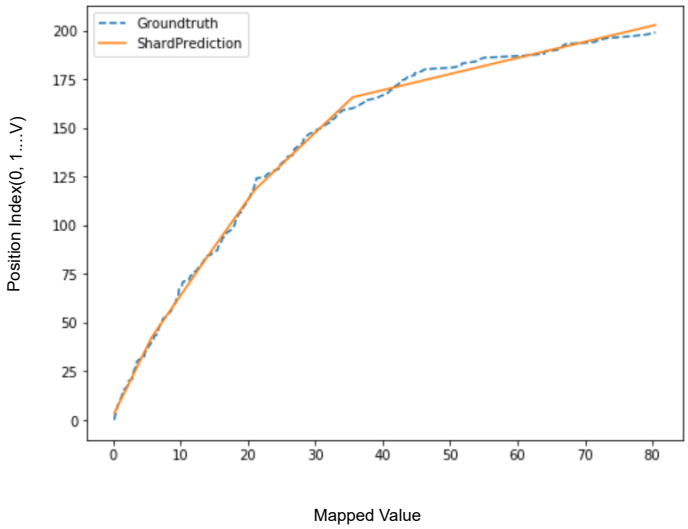


Figure 2.11.: Piecewise linear regression functions learnt by ShardTrainingAlgorithm, V+1 is the number of keys per mapped interval

inputs $\boldsymbol{x}$ and ground truth $\boldsymbol{y}$. For a given point with mapped value $m \in [m_{i-1}, m_i)$, its shard id is given by $\lceil \frac{f_i(m)}{\Psi} \rceil + i \times D$, i.e. $\mathcal{F}_i(x) = \frac{f_i(m)}{\Psi}$.

Example 2.9 In our previous example, in the interval $[0, 2]$, we have $\boldsymbol{x} = (1, 1.2, 2)$ and $\boldsymbol{y} = (0, 1, 2)$. Then for a point with the mapped value $m = 1.2$, the expected output will be $f_i(m) = 1$ and the shard id is given by $\lceil \frac{1}{1} \rceil + 0 \times 2 = 1$. Hence, the point with mapped value $m = 1.2$ will be allocated to the second shard with shard id 1. Then the problem is to train a continuous piecewise linear regression function in each interval. We constrain the piecewise linear regression function to be continuous so that it is guaranteed be monotonic as shown in Figure 2.11.

Formally, a piecewise linear function can be described as

$$f(x) = \begin{cases} b_0 + \alpha_0(x - \beta_0) & \beta_0 \leq x < \beta_1 \\ b_1 + \alpha_1(x - \beta_1) & \beta_1 \leq x < \beta_2 \\ \vdots & \\ b_\sigma + \alpha_\sigma(x - \beta_\sigma) & \beta_\sigma \leq x \end{cases} \tag{2.6}$$

In order to make this piecewise linear function continuous, the slopes and intercepts of each linear region depend on previous values. Formally, let $\bar{a} = b_0$, then Eq. (2.6) reduces to

$$f(x) = \begin{cases} \bar{\alpha} + \alpha_0(x - \beta_0) & \beta_0 \leq x < \beta_1 \\ \bar{\alpha} + \alpha_0(x - \beta_0) + \alpha_1(x - \beta_1) & \beta_1 \leq x < \beta_2 \\ \dots & \\ \bar{\alpha} + \alpha_0(x - \beta_0) + \alpha_1(x - \beta_1) + \dots + \alpha_\sigma(x - \beta_\sigma) & \beta_\sigma \leq x \end{cases} \tag{2.7}$$

Then to make Eq. (2.7) monotonically increasing, we only need to ensure that

$$\sum_{i=0}^{\eta} \alpha_i \geq 0, \forall 0 \leq \eta \leq \sigma$$

Let $\boldsymbol{\alpha} = (\bar{\alpha}, \alpha_0, \cdots, \alpha_\sigma)$, the square loss function $L(\boldsymbol{\alpha}, \boldsymbol{\beta}) = \sum_{i=1}^{V} (f(x_i) - y_i)^2$. We then optimise $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ iteratively.

Assume that $\boldsymbol{\beta} = \hat{\boldsymbol{\beta}} = (\hat{\beta}_0, \hat{\beta}_1, \cdots, \hat{\beta}_\sigma)$ is fixed, then $\boldsymbol{\alpha}$ can be regarded as the least square solution of the linear equation $\boldsymbol{A\alpha} = \boldsymbol{y}$, where

$$\boldsymbol{A} = \begin{bmatrix} 1 & x_0 - \hat{\beta}_0 & \left(x_0 - \hat{\beta}_1\right) 1_{x_0 \geq \hat{\beta}_1} & \cdots & \left(x_0 - \hat{\beta}_\sigma\right) 1_{x_0 \geq \hat{\beta}_\sigma} \\ 1 & x_1 - \hat{\beta}_0 & \left(x_1 - \hat{\beta}_1\right) 1_{x_1 \geq \hat{\beta}_1} & \cdots & \left(x_1 - \hat{\beta}_\sigma\right) 1_{x_1} \geq \hat{\beta}_\sigma \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_N - \hat{\beta}_0 & \left(x_V - \hat{\beta}_1\right) 1_{x_V \geq \hat{\beta}_2} & \cdots & \left(x_V - \hat{\beta}_\sigma\right) 1_{x_V \geq \hat{\beta}_\sigma} \end{bmatrix}$$

where $1_{x_0 \geq \hat{\beta}_1}$ equals to 1 if $x_0 \geq \hat{\beta}_1$, otherwise it equals to 0.
We have

$$\begin{aligned} L(\boldsymbol{\alpha}, \boldsymbol{\beta}) = (\boldsymbol{y} - \boldsymbol{A\alpha})^T (\boldsymbol{y} - \boldsymbol{A\alpha}) &= \boldsymbol{y}^T \boldsymbol{y} - \boldsymbol{\alpha}^T \boldsymbol{A}^T \boldsymbol{y} - \boldsymbol{y}^T \boldsymbol{A\alpha} + \boldsymbol{\alpha}^T \boldsymbol{A}^T \boldsymbol{A\alpha} \\ &= \boldsymbol{y}^T \boldsymbol{y} - 2\boldsymbol{\alpha}^T \boldsymbol{A}^T \boldsymbol{y} + \boldsymbol{\alpha}^T \boldsymbol{A}^T \boldsymbol{A\alpha} \end{aligned} \tag{2.8}$$

and if we let

$$\begin{aligned} \frac{\partial L(\boldsymbol{\alpha}, \boldsymbol{\beta})}{\boldsymbol{\alpha}} &= 2\boldsymbol{A}^T \boldsymbol{A\alpha} - 2\boldsymbol{A}^{\boldsymbol{T}} \boldsymbol{y} = 0 \\ &\implies \boldsymbol{\alpha} = (\boldsymbol{A}^T \boldsymbol{A})^{-1} \boldsymbol{Ay} \end{aligned} \tag{2.9}$$

we get the $\boldsymbol{\alpha}$ with the given fixed $\boldsymbol{\beta}$. Clearly, different $\boldsymbol{\beta}$ give rise to different optimal parameters. Let $\boldsymbol{\alpha}^\star(\boldsymbol{\beta})$ be the optimal $\boldsymbol{\alpha}$ for a particular $\boldsymbol{\beta}$, then we want to find $\boldsymbol{\beta}$ such that

$$L(\boldsymbol{\alpha}^\star(\boldsymbol{\beta}^\star), \boldsymbol{\beta}^\star) = \min\{L(\boldsymbol{\alpha}^\star(\boldsymbol{\beta}), \boldsymbol{\beta}) | \boldsymbol{\beta} \in \mathbb{R}^{\boldsymbol{\sigma+1}}\} \tag{2.10}$$

For $\boldsymbol{\beta}$, we define $\boldsymbol{r} = \boldsymbol{A\alpha} - \boldsymbol{y}$ and

$$\boldsymbol{K} = \text{diag}(\bar{\alpha}, \alpha_0, \cdots, \alpha_\sigma), \boldsymbol{G} = \begin{bmatrix} -1 & -1 & \cdots & -1 \\ p_0^{(0)} & p_0^{(1)} & \cdots & p_0^{(V)} \\ p_1^{(0)} & p_1^{(1)} & \cdots & p_1^{(V)} \\ \vdots & \vdots & \ddots & \vdots \\ p_\sigma^{(0)} & p_\sigma^{(1)} & \cdots & p_\sigma^{(V)} \end{bmatrix}$$

where $p_i^{(l)} = -1_{x_l \geq \beta_i}$. Then

$$\boldsymbol{KG} = \begin{bmatrix} -\bar{\alpha} & -\bar{\alpha} & \cdots & -\bar{\alpha} \\ 0 & \alpha_0 p_0^{(1)} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \alpha_\sigma p_\sigma^{(V)} \end{bmatrix}$$

then we have

$$g = \frac{\partial L(\boldsymbol{\alpha}, \boldsymbol{\beta})}{\partial \boldsymbol{\beta}} = 2\boldsymbol{KGr}, Y = \frac{\partial g}{\partial \boldsymbol{\beta}} = 2\boldsymbol{KGG}^T\boldsymbol{K}^T \tag{2.11}$$

Show how these are calculated

As $g = \nabla_{\boldsymbol{\beta}} L$, $-g$ specifies the steepest descent direction of $\boldsymbol{\beta}$ for L. However, the convergence rate of $-g$ is low as it does not consider the second order derivative of L. Hence, we use Newton's method to perform the update along the direction of second derivative, $s = -\boldsymbol{Y}^{-1}g$. Newton's method assumes that the loss L is twice differentiable and uses the approximation with Hessian The geometric interpretation of Newton's method is that at each iteration, it amounts to the fitting of a paraboloid to the surface of $L(\boldsymbol{\alpha}, \boldsymbol{\beta})$ at the trial value β_k, having the same slopes and curvature as the surface at that point, and then proceeding to the maximum or minimum of that paraboloid. Hessian matrix, Y in our case is positive semidefinite and hence can be inverted.

$$Y = \frac{\partial g}{\partial \boldsymbol{\beta}} = 2\boldsymbol{KGG}^T\boldsymbol{K}^T = 2(\boldsymbol{KG})(\boldsymbol{G}^T\boldsymbol{K}^T) = 2(\boldsymbol{G}^T\boldsymbol{K}^T)^T(\boldsymbol{G}^T\boldsymbol{K}^T) = 2(\boldsymbol{M}^T\boldsymbol{M}) \tag{2.12}$$

Show how these are calculated Y is a full rank matrix as columns of Y are linearly independent (all keys are independent of each other). To prove that Y is positive definite, we need to show that $x^T Y x > 0, \forall x \neq 0$.
$x^T Y x = x^T M^T M x = (Mx)^T(Mx) = \|Mx\|_2^2 \geq 0, \forall x \neq 0$

In the beginning, we set $\beta^{(0)} = x_0$ and $\beta_i^{(0)} = x_{\lfloor i \times \frac{V}{\Psi} \rfloor}, \forall i \in [1, \sigma]$. Then we can obtain $\boldsymbol{\alpha}$ by solving Eq. (2.9). Then at each step, we perform a grid search to find the step $lr^{(k)}$ such that the loss L is minimal. Then at the next iteration, we increase k by one and set

$$\boldsymbol{\beta}^{(k+1)} = \boldsymbol{\beta}^{(k)} + lr^{(k)} s^{(k)}$$

As described in Algorithm 9, we perform following operations during shard training, :

1. Divide the sorted mapped values into equal sized U intervals. We found empirically that training algorithm generalizes better if mapped intervals are aligned with grid cell boundaries. U is initialized to numbers of grid cells.

2. Suppose $V + 1$ is the number of mapped values in each interval and D is the number of shards learned per mapped interval.

3. For each interval, we want to build a monotonic regression model $\mathcal{F}_i$ whose domain is $[m_{i-1}, m_i]$

4. Each $\mathcal{F}_i$ generates D shards and every such shard contains $\Psi = \lfloor \frac{V+1}{D} \rfloor$ number of keys
5. $x = [x_0, \cdots, x_V]$ specifies the keys' mapped values in interval i, $[m_{i-1}, m_i]$
6. Given $V + 1$ sorted mapped values $x = [x_0, \cdots, x_V]$ and their indices $y = [0, \cdots, V]$, each $\mathcal{F}_i$ is built and trained with the procedure mentioned in the algorithm 9.

Algorithm 9: Shard Training Algorithm

input: M_p:sorted mapped value array,U: number of mapped intervals, D:number of shards per interval

```
Partition M_p into equal length U intervals M_p = [m_1, ..., m_U]
for i ← 0 to U do
    x = [x_0, ..., x_V] be the keys' mapped values in interval i
    y = [0, ..., V]
    Initialize β^(0) as β^(0) = x_0 and β_i^(0) = x_⌊i×D⌋, ∀i ∈ [1, σ]
    while k <iter do
        Initialize A^(k) according to (2.7)
        α^(k) = ((A^(k))^T A^(k))^-1 (A^(k))^T y
        Calculate g^(k), Y^(k)
        s^k = -(Y^(k))^-1 g^(k),
        Find update step lr^(k) such that
          L(α*(β^k + lr^(k) s^k), β^k + lr^(k) s^k) = min{L(α*(β^k + lr^(k) s^k), β^k + lr^(k) s^k)}
        β^(k+1) = β^k + lr^(k) s^k
    end
end
```

Local Models for Shards

Local models are not relevant to our implementation as full data-set is loaded in the main memory.

2.3. Queries

2.3.1. Point Query

A point query is a database operation that finds the records that exactly match our query conditions. In this project, we perform point query on 1-dimensional data and 2 dimensional data. We assign the database records into pages, predict the page index with the index models and then perform sequential search on the predicted page. In order to evaluate the errors that different index models are making, we focus on predicting the page indices and ignore the sequential search operation on a specific page.

Example 2.10 For example, assume we have an 1-dimensional array $[1, 2, 3, 4]$ and two pages such that $[1, 2] \in P_0$ and $[3, 4] \in P_1$. A point query for $x = 2$ is expected to return 0 as the page index.

Point Query with B-Tree

Searching in a B-tree is similar to searching in a binary search tree. In a binary search tree, we traverse the tree and make a binary decision at each node. Similarly in order to perform point query with a B-tree, we traverse the tree and make a **multi-way** decision at each node.

In our implementation, the point query method with B-tree takes the root node `x` of a subtree and a key `k` to be searched for in that subtree. If `k` is in that subtree, the method returns the node `y` that contains the key `k` and an index `i` such that $\texttt{y.key}_i$=k. Otherwise the method will return `-1`. The point query algorithm for a B-tree is illustrated in Algo. 10.

Algorithm 10: B-tree Point Query

input: `x`: The node of the subtree to be searched; `k`: The key to be searched
Result: `y`: The node that contains the query key in its keys; `i`: the index of the query key

```
1  i=1
2  while i ≤ x.n and k>x.keys_i do
3  |  i=i+1
4  |  if i ≤ x.n and k==x.keys_i then
5  |  |  return x, i
6  |  else if x.leaf then
7  |  |  return NULL, -1
8  |  else
9  |  |  return BTreeSearch(x.c_i, k)
10 end
```

In the point query algorithm of B-tree as illustrated in 10, the search is performed with the following steps:

1. From Line 1 to 3, we use linear search to find the smallest index i such that $\texttt{k} \leq \texttt{x.key}_i$. If there is no such i, we set i to be `x.n+1`.
2. Then we check whether we have found the key in this node on Line 4 to 5. If we have, then the method returns current node and the index of the query key.
3. Otherwise, we check if current node is a leaf node. If it is a leaf node, then we know there is no such query key in this subtree. Hence, this method returns a null node and -1 to indicate there is no such key.
4. If current node is not a leaf node, we then recursively search the appropriate subtree of `x`.

Example 2.11 For example if we were to search for 41 in the Fig. 2.1, we would first compare query key 41 and the keys in root node, which is 31. Hence we go to the second subtree, whose root node contains two values 51 and 71. By comparison, we should go the first subtree of this node. Then we reach the leaf node, which contains our query key 41 and hence the query will return this leaf node and the index 1 as output. If there is no such key, then the method will return `NULL` and -1.

Point Query with KD-Tree

Similar to search with binary search tree, we also need to traverse the tree in order to perform point query. However, we need to switch the dimensions when we compare the values between the query key and the values in the nodes.

Algorithm 11: Point Query with KD-Tree

Input : `t`: The node being searched; `x`: The query key; `cd`: Current dimension
Output: `n`: the node that contains the query key

```
1 DIM=2
2 if t==NULL then
3 |   return NULL
4 if x[0]==t.data[0] and x[1]==t.data[1] then
5 |   return t
6 else if x[cd]<t.data then
7 |   return pointSearch(t.left, x, (cd+1) % DIM)
8 else if x[cd]>t.data then
9 |   return pointSearch(t.right, x, (cd+1) % DIM)
```

The point query works in the following steps:

1. From Line 2 to 3, we first check if current node is `NULL`. If so, that means that we have already traversed all the possible nodes and found nothing. In this case, the query returns `NULL`.

2. From Line 4 to 5, we check if the current node contains the same key as the query key. If so, the current node is the node that we are looking for. Hence, we return the current node in this case.

3. Otherwise, from Line 6 to 9, we check if the current dimension of the query key is smaller, larger or equal to the current dimension of the data in the node.
   a) If it is smaller, then we search on the left subtree of current node, with the same query key and switched dimension.
   b) If it is larger, then we search on the right subtree of current node, with the same query key and switched dimension.

Example 2.12 In the previous figure 2.4, we showed an example KD-tree. If we want to search for $(50, 30)$ in this tree, we would follow the following steps:

1. We first check the root node and compares the x-coordinate. As $50 > 30$, we go to the right subtree of the root node.
2. Then in the subtree, we compare the y-coordinate. As $50 < 70$, we go to the left subtree of this node.
3. Then in the left subtree, the termination condition is reached, hence we return this node as result.

Point Query with Baseline Index Model

The point query with baseline model is the same with forward pass in the training process. As the baseline model is a two-layer fully connected neural network with `ReLU` activation functions, we calculate the output of a given input x with the equation below:

$$\hat{y} = \boldsymbol{w_3}\text{max}(\boldsymbol{w_2}\text{max}(\boldsymbol{w_1}x + \boldsymbol{b_1}, 0) + \boldsymbol{b_2}, 0) + \boldsymbol{b_3} \tag{2.13}$$

As we assumed, the baseline model is approximating the CDF of X. Hence, for a certain x, the output is the probability that $F(X \leq x)$. Since we are working with a static array without insertion and deletion, we can assume that we know the total number of records as N. We also define the page size to be S as a parameter. Then we can calculate the position of this key as $\hat{p} = \lfloor \hat{y} * N \rfloor$.

After knowing the position of the key in the static array, we then calculate the page where it should be allocated to as below

$$\hat{o} = \lfloor \frac{\hat{p}}{S} \rfloor = \lfloor \frac{\hat{y} * N}{S} \rfloor \tag{2.14}$$

Complexity Analysis

For any key, the computation complexities of $\hat{o}$ are the same, as there are only fixed number of computations needed. Hence, the time complexity of query with the baseline model is $\mathcal{O}(1)$, i.e. constant for any training data size.

Point Query with Recursive Model Index

The point query of recursive model is a top-down process. With a given x, the root model will first predict an output that represents the probability that $F(X \leq x)$. Then we map this output into the index of models in the next stage. Afterwards, we use that model to predict an output with the given x. We iterate these steps until the last stage in which we use the output as the

final output. The above process is described in Algorithm. 12

Algorithm 12: Point Query With Recursive Model Index

```
   input: x; models; num_of_stages
1  stage← 0
2  next_model← 0
3  while stage <num_of_stages do
4  |  model=models[stage][next_model]
5  |  output = model.predict(x)
6  |  if stage==num_of_stages-1 then
7  |  |  y = output
8  |  else
9  |  |  next_model=output*len(models[stage+1])
10 |  |  stage = stage+1
11 |  end
12 end
13 return y
```

In the query algorithm, we have three inputs: x as the query key, trained models and the number of stages.

On line 1−2, we first initialise the $stage$ and $next\_model$ to be 0, so that we use the root model at the very beginning. Then on line 3, we iterate over all stages. In each stage, we perform the following actions:

1. On line 4, we access the model at $stage$ whose index is $next\_model$.
2. On line 5, we perform the prediction with the query key x and the model selected by the previous step.
3. On line 6, we check if current stage is the last stage.
   a) If it is, then we get the final output, which equals to the output from line 5.
   b) If it is not the last stage, then we map the output from previous step into the index of the model in the next stage. As there are `len(models[stage+1])` models in the next stage and the output represents some probability (hence, `output` $\in [0, 1]$), we multiply them and find the `next_model`. In the meanwhile, we add 1 to the stage.
4. At the end, we return the final output, which is the output from the model in the last stage.

After calculating the output as described in the Algorithm. 12, we calculate the page index in a same way as we described in the baseline model.

Point Query with Lisa

Point query search in LISA is composed of following steps.

1. Find the cell to which point query belongs by comparing the query key value with first and last key in each cell. First key in the cell represents the lower corner of the cell, whereas last key in the cell represents the upper corner. This search will be linear in the number of cells.

2. Calculate mapped value of the query key as mentioned in the section 'Mapping Function' 12

3. During model training, 2 dimensional key space is mapped into a sorted one dimensional array. Find the mapped interval to which point query's mapped value belongs using binary search on this array.

4. Predict the shard id for calculated mapped interval. It is found empirically that predicted shard id can differ from ground-truth value by 1 for keys falling near the shard boundaries.

5. Search for the query key in the predicted shard by sequentially comparing against all the keys in the shard until a match is found. In case of no match, search in adjacent left and right shards as predicted shard id can have an error of 1.

2.3.2. Range Query

A range query is a database operation that retrieves all the records that lies in a range. In this project, we perform range query on 2-dimensional data only. In addition, we only consider a range query where the range is defined as a rectangle. Under these assumptions, a range query can be formalised as a query $\mathcal{Q}(\boldsymbol{l}, \boldsymbol{u})$ where $l, u \in \mathbb{R}^2$ and $split\_axis$ as $\mathcal{S}$.

Example 2.13 For example, assume we have the points

$$[(1,2),(3,4),(3.5,4),(5,6)]$$

and the range query $\mathcal{Q}((2,3),(5,5))$, as shown below:

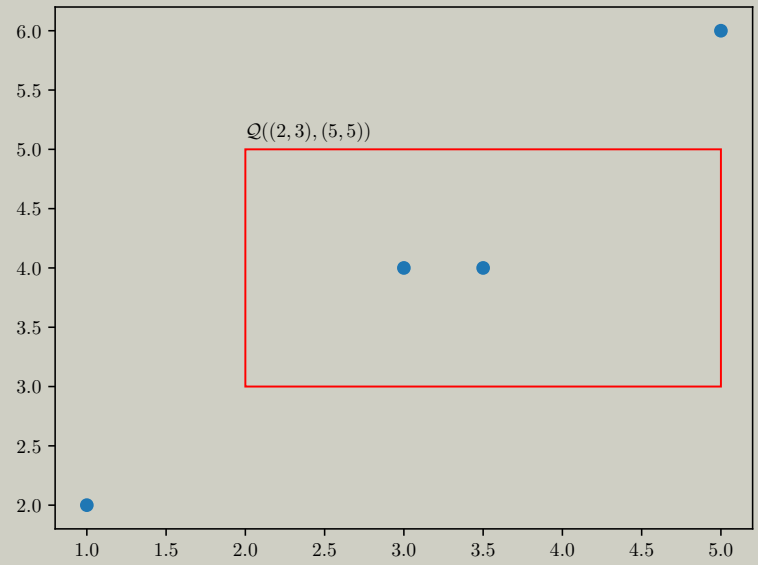
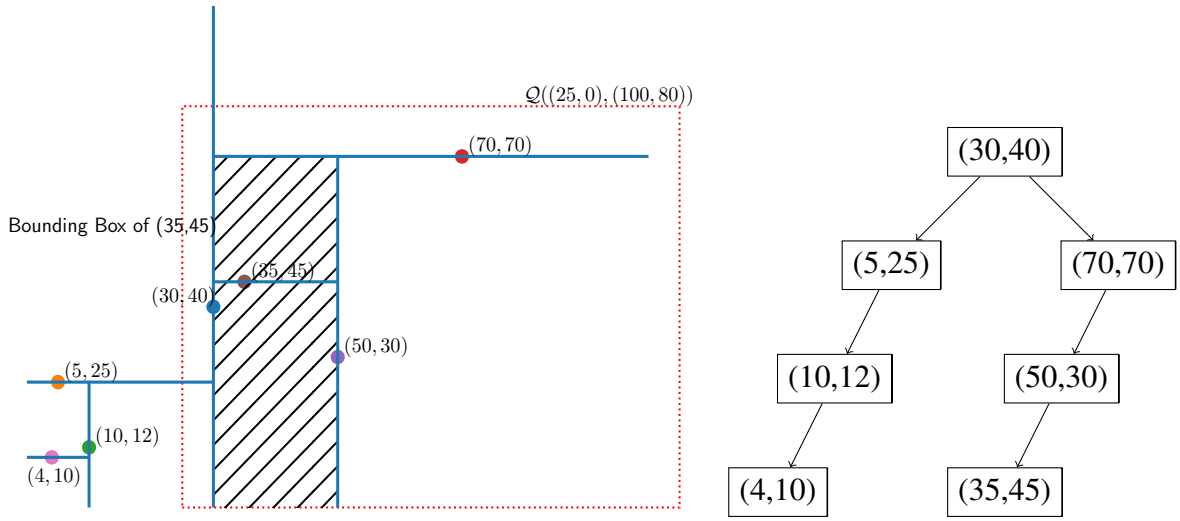


Figure 2.12.: A Range Query Example where $\mathcal{Q}(\boldsymbol{l}, \boldsymbol{u}) = \mathcal{Q}((2,3),(5,5))$
In this example, the range query should return the points that lies inside the red rectangle, i.e. $((3,4),(3.5,4))$.

Range Query with KD-Tree



(a) The 2D space and the partition of KD-tree **(b)** The tree structure of the KD-tree

Figure 2.13.: An example of KD-Tree

Performing range query in a KD-tree needs to traverse the whole tree, but we can apply some pruning strategy to avoid useless searching for some nodes. We first present the **bounding box** of subtree in a KD-tree.

Bounding Box

When we are traversing the KD-tree along the way, we are assured that a node is bounded in a rectangle region. Assume that a node $\mathtt{t}$ has k ancestors, then the node $\mathtt{t}$ is bounded in a rectangle in the following way:

1. We traverse from the root node whose coordinate is (x_r, y_r). If we go to the right subtree, then the node $\mathtt{t}$ is bounded in the right side of the root node. That means, the right subtree of the root node is bounded in a rectangle region determined by the lower bound $\boldsymbol{l} = (x_r, 0)$[1] and the upper bound $\boldsymbol{u} = (\infty, \infty)$. Similarly, we can determine the bounds of the left subtree as $\boldsymbol{l} = (0, 0)$ and $\boldsymbol{u} = (x_r, 0)$. We call the bounding box at this level as B_0^r and B_0^l for the right subtree and left subtree respectively.

2. We then traverse into the next level and determine the bounding box B_1^r and B_1^l of the subtrees rooted at the root's child node. At this time, we will need to switch the axis into the y-axis. If the child node is in the left subtree of the root node, the final bounding box is the intersection between the bounding box at this level and the bounding box of left subtree at the root level, i.e. $B_0^l \cap B_1^r$ and $B_0^l \cap B_1^l$. Similarly, if the child node is in the right subtree of the root node, the final bounding box are $B_0^r \cap B_1^r$ and $B_0^r \cap B_1^l$.

3. We traverse until the left node and determine the bounding box of each subtree and save this property into the root node of each subtree.

[1]For simplicity and clarity, we assume our keys are starting from $(0, 0)$ and are positive in both dimensions

Example 2.14 In the Fig. 2.13, we present the bounding box of the leaf node $(35, 45)$ as the hatched area. In this example we will demonstrate how we calculate this.

1. We first start with the root node and we go to the right subtree. Hence the bounding box of $(70, 70)$ will be $\boldsymbol{l} = (30, 0)$ and $\boldsymbol{u} = (\infty, \infty)$.
2. Then we traverse to the $(70, 70)$ and we go to the left subtree. Hence the bounding box of $(50, 30)$ will be $\boldsymbol{l} = (0, 0)$ and $\boldsymbol{u} = (0, 70)$. By intersecting with the bounding box from the first step, we get the final bounding box as $\boldsymbol{l} = (30, 0)$ and $\boldsymbol{u} = (0, 70)$, which refers to the right bottom area in the figure.
3. We then go to the left subtree and calculate the bounding box and get $\boldsymbol{l} = (0, 30)$, $\boldsymbol{u} = (50, 70)$, i.e. the hatched region in the figure.

With the bounding box, there are three conditions in our pruning strategy while traversing the tree:

- If the bounding box does not overlap with the query rectangle, we stop the recursion and traverse the subtree.
- If the bounding box is a subset of a query box, then we report all the points in current subtree.
- If the bounding box overlaps query box, then we recurse the left and right subtrees.

Formally, the algorithm for range query is illustrated as in Algo. 13.

Algorithm 13: KD-tree Range Query

input: Q: The query rectangle; T: The root node of a subtree to be range searched
Result: S: The set of all nodes that are in the query range

```
1  S=φ
2  if T==NULL then
3  |  return φ
4  if T.range ∩ Q==φ then
5  |  return NULL
6  if T.range ⊂ Q then
7  |  return AllNodesUnder(T)
8  if T.data ∈ Q then
9  |  S = S.union({T.data})
10 S = S.union(RangeQuery(Q, T.left))
11 S = S.union(RangeQuery(Q, T.right))
12 return S
```

In the above algorithm, we perform the range query with the following steps:

1. First we check if the node is NULL, if so, we simply return an empty set.

2. On Line 4-5, we check if the bounding box is overlapping with the query rectangle, by comparing the bounds of the query rectangle and the bounding box.

3. On Line 6-7, we check if the bounding box is a subset of the query rectangle. If it is, then we will traverse the subtree of `T` and simply return all nodes that are contained in the subtree.

4. On Line 8-11, we cannot apply any pruning strategy. Hence, we first check if the data is inside the query rectangle by comparing the coordinates with the query rectangle. If it is inside, then we put the point into our result set. Then we recurse to the left and right subtree and append the results into our result set `S`.

Example 2.15 In Fig. 2.13, we present an example query rectangle $\mathcal{Q}((25, 0), (80, 80))$. In this example, we show how we perform range query with this rectangle. We assume that our space is from 0 to 100 on both dimension so that there is no ∞ bounds.

1. First we start with the root node, whose bounding box is the whole space. Hence we check if $(30, 40) \in \mathcal{Q}$. Since it is inside, we add it to the result set $S = \{(30, 40)\}$.

2. We then look at the left subtree, whose bounding box is $(l) = (0, 0)$, $\boldsymbol{u} = (30, 100)$. As there is some overlapping with the query rectangle, we check if $(5, 25)$ is inside the query rectangle. Since it is not in the rectangle, we do not put it in the result set.

3. Then we go to $(10, 12)$ whose bounding box is $(l) = (0, 0)$, $\boldsymbol{u} = (30, 25)$, which is overlapping with the query rectangle. Hence, we need to check if it is inside the query rectangle. Since it is not in the rectangle, we do not put it in the result set.

4. **No Overlapping** We then move to $(4, 10)$ whose bounding box is $\boldsymbol{l} = (0, 0)$, $\boldsymbol{u} = (10, 25)$ which is not overlapping with the query rectangle. Hence, we prune the whole subtree rooted at $(4, 10)$.

5. We then move to the right subtree of the root node, whose bounding box is $(l) = (30, 0)$, $\boldsymbol{u} = (100, 100)$. As there is overlapping between the query rectangle and the bounding box, we then check if $(70, 70)$ is inside the query rectangle. We then put it in the result list as it is inside the query rectangle. $S = \{(30, 40), (70, 70)\}$.

6. **Subset** Then we go to the left subtree whose bounding box is $(l) = (30, 0)$, $\boldsymbol{u} = (100, 70)$. The bounding box is fully inside the query rectangle, and hence we add all the results under $(70, 70)$ in to the result list. Finally we have

$$S = \{(30, 40), (70, 70), (50, 30), (35, 45)\}$$

Range Query with LISA

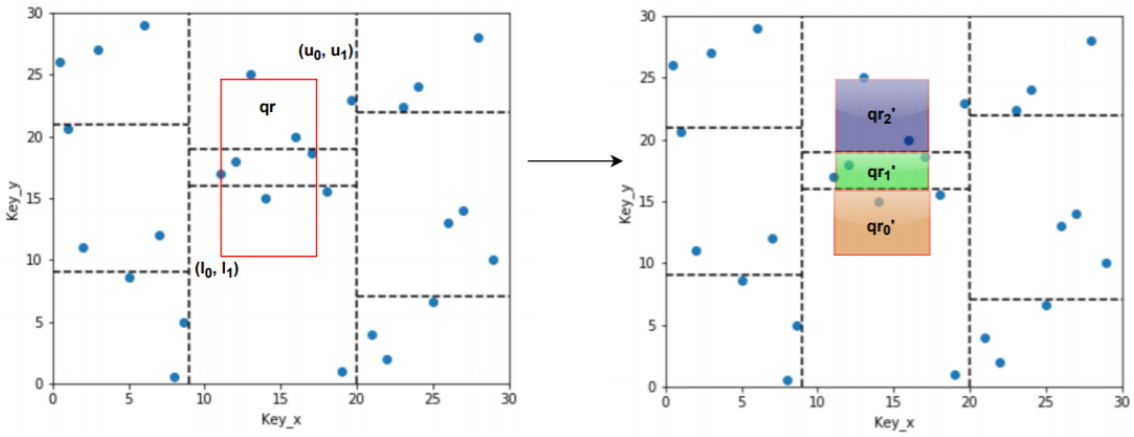


Figure 2.14.: Range Query Search in Lisa

For a range query $\mathcal{Q}(\boldsymbol{l}, \boldsymbol{u})$, we first find the cells that overlap with $\mathcal{Q}$. Then we decompose $\mathcal{Q}$ into the union of smaller query rectangles $\bigcup \mathcal{Q}_i$ such that each smaller query rectangles intersects only one cell, as shown in the Fig. 2.14.

Suppose that $\mathcal{Q} = \bigcup \mathcal{Q}_i$ where $\mathcal{Q}_i = [l_{i_0}, u_{i_o}) \times [l_{i_1}, u_{i_1})$, i.e. we have $\mathcal{Q}_i$ representing the ith smaller query rectangles of one cell C_j.

Then we can calculate the mapped values of $\mathcal{Q}_i$, i.e. $\mathcal{M}(l_{i_0}, l_{i_1})$ and $\mathcal{M}(u_{i_0}, u_{i_1})$. For simplicity, we use $m_l^{(i)}$ and $m_u^{(i)}$ to denote $\mathcal{M}(l_{i_0}, l_{i_1})$ and $\mathcal{M}(u_{i_0}, u_{i_1})$ respectively.

After creating corresponding mapped values, we then apply the shard prediction function $\mathcal{SP}(m_l^i)$ and $\mathcal{SP}(m_u^i)$ to predict the shard that could possibly contain keys that lie in the query rectangle $\mathcal{Q}_i$. Then in each shard, we perform a sequential search to find the desired keys.

2.3.3. KNN Query

K-Nearest Neighbours (KNN), as the name suggests, is the process of finding K nearest neighbours to a given query point. In this project, KNN query is only performed on 2-dimensional data. We use ℓ_2 norm as the distance metric. A KNN query will be formalised as $\mathcal{K}(\boldsymbol{X})$ where $\boldsymbol{X} \in \mathbb{R}^2$.

KNN query with KD-Tree

As a baseline, we first perform KNN query with KD-tree.
The main advantage of KD-Tree is that we can exploit the tree structure and prune points we don't think will have distance smaller than the ones we have already calculated. This improves the time complexity as compared to finding the distance of point with every other point in space to get the closest neighbours.

Algorithm 14: KNN Query Algorithm for KD-Tree

Input : K; `Number of nearest neighbour, List of TestPoints;` $\mathcal{P}(\boldsymbol{x}, \boldsymbol{y}); [x \in \mathbb{R}; y \in \mathbb{R}]$
Output: `List of` K `nearest points(ResultList)`

```
for i ← 0 to len(TestPoints) do
    Start at root
    Traverse subtree where P(x, y)_i can be added.
    Find the leaf; Calculate the distance and store it as D
    if len(ResultList) < K then
        if Perpendicular distance of Parent with P(x, y) <= D
         then
            Go on the other side of subtree
        else
            Go up another level
        end
    else
        return ResultList
    end
end
```

In algorithm 14,

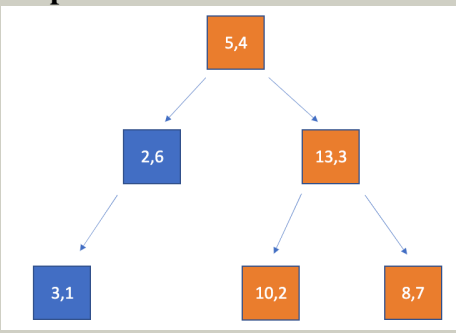
1. Start with the root to traverse tree until we reach the leaf. We find the subtree where the new $\mathcal{P}(\boldsymbol{x}, \boldsymbol{y})$ could be added and finally reach the leaf of this subtree.

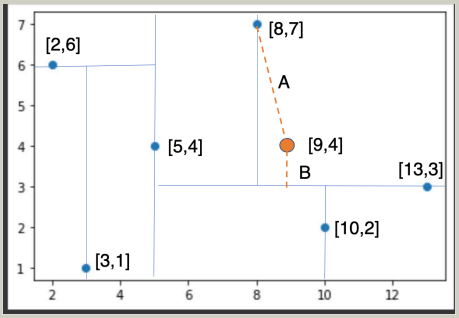
2. Calculate the square of the euclidean distance of this point from the $\mathcal{P}(\boldsymbol{x}, \boldsymbol{y})$. We add it to the list and push and pop values from the list depending on the distances we calculate while traversing the tree upwards from here.

3. From the leaf we could either go up another level or go the other side of the subtree to get a point that could have a distance smaller than the last best calculated distance in the list.

4. Once we make a decision in the above step, we can recursively traverse the tree upwards until we reach the root.

Example 2.16





For example, we have Point list as

$$((5,4),(2,6),(13,3),(8,7),(3,1),(10,2))]$$

Test point; $\mathcal{P}(\boldsymbol{x},\boldsymbol{y}) = (9,4)$

Below are the steps followed to get the 4 nearest neighbours:

1. Traverse to $(8,7)$ by searching for a location where $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$ could be added.
2. Add $(8,7)$ to result list.
3. Calculate the distance of $(8,7)$ and $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$. Save the distance as $\mathcal{D}$
4. Make a decision whether to traverse to the other side of the subtree to point $(10,2)$ by checking the perpendicular distance of $(13,3)$ with $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$ and compare this with $\mathcal{D}$.(We do this to verify if there is even a possibility to find a point smaller than the last best distance on the other side of the subtree.)
5. Since the perpendicular distance is smaller than the best calculated $\mathcal{D}$ $(A > B)$, we will check the distance of $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$ and $(10,2)$. This distance in our case is indeed smaller than the best calculated distance of $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$ with $(8,7)$ so far.
6. Add $(10,2)$ to result list.
7. Similarly, we traverse until we have 4 nearest neighbour to $\mathcal{P}(\boldsymbol{x},\boldsymbol{y})$ in the list.

KNN Query with LISA

It is difficult to apply traditional KNN query pruning strategies applicable for KD-Trees, to LISA model as it doesn't maintain a tree like structure with all nodes and entries based on MBRs (minimum bounding rectangle) and parent-children relationships. Shard boundaries are learned per mapped interval and no data structure is maintained to refer to shards in adjacent

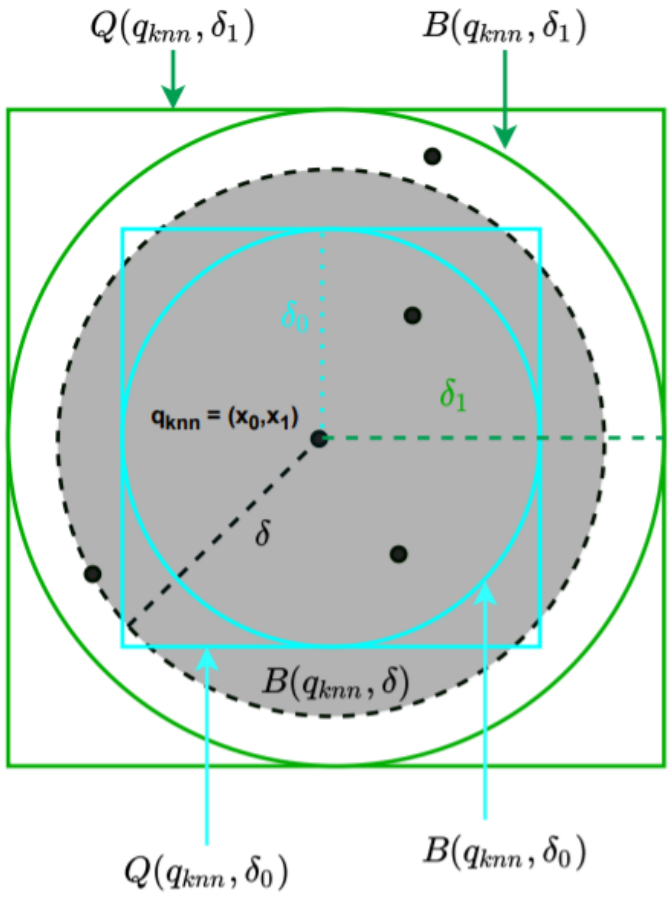


Figure 2.15.: KNN Query Implementation in Lisa(K=3)
1)q_{knn} represents the query point, $\mathcal{Q}(x, \delta) \triangleq [x_0 - \delta, x_0 + \delta) \times [x_1 - \delta, x_1 + \delta)$, represents query rectangle and $\mathcal{B}(x, \delta)$ represents the key space at distance δ containing K nearest keys.
2)KNN query can be solved by range query if we can estimate an appropriate distance bound δ for every query point

mapped intervals. The key idea in the KNN query is to convert it into a range query by estimating an appropriate query range. LISA paper suggests a learning model to learn an appropriate distance bound from underlying training data for every query point and specific value of K. However, we used empirically estimates to learn this distance bound for different values of K. This distance bound is used to convert the KNN query to range query.The query range is augmented if less than K neighbors are found in a range query.

Consider a query point $q_{knn} = (x_0, x_1)$, let $x^{'} \in V$ be the Kth nearest key to x in database at a distance value $\delta = \|x^{'} - q_{knn}\|_2$. Lets define $\mathcal{Q}(q_{knn}, \delta) \triangleq [x_0 - \delta, x_0 + \delta) \times [x_1 - \delta, x_1 + \delta)$ and $\mathcal{B}(q_{knn}, \delta) \triangleq \{p \in V \mid \|q_{knn} - p\|_2 \leq \delta\}$. We can create a query rectangle $qr = \mathcal{Q}(q_{knn}, \delta + \epsilon)$ where $\epsilon \to 0$. As shown in Fig. 2.15, K nearest keys to q_{knn} are all in $\mathcal{B}(q_{knn}, \delta)$ and thus in $\mathcal{Q}$. KNN query can be solved using the range query if we can estimate an appropriate distance bound δ for every query point.

In our experiments, we find the δ empirically. We try with different values of δ and choose

the one for which we get the best results.

3. Evaluation

Summary In this chapter, we describe how we evaluate the database indexes that we have implemented in previous chapter. For both one and two dimensional data, we use manually synthesised dataset that are generated from a certain distribution as our dataset. This chapter is organised into two sections, where the first section describes the experiment settings and results for one-dimensional data and indexes and the second section describes the two-dimensional data.

3.1. One Dimensional Data and Indexes

For one dimensional data, the evaluation covers the following tasks:

- Find a structure for recursive model index empirically.
- Compares the performance between baseline model, recursive model and traditional B-Tree.

3.1.1. Dataset

For one dimensional case, we manually generate two columns of the data:

- The first column contains the keys X, which is randomly sampled from a given distribution.
- Then we assign the keys into different pages according to a preset parameter N_{page} for page size. Specifically, the first N_{page} keys will be assigned into the first page, the second N_{page} keys will be assigned into the second page and so on so forth. After the assignments, we set the second column Y to be the page index of the corresponding x.

3.1.2. Small Lognormal Data

We first generate $10,000$ data points where X is from a lognormal distribution Lognormal$(0, 4)$. In the Fig 3.1, we illustrate the $x-y$ relations where X is randomly sampled from a lognormal distribution.

We use three groups to find the best recursive model for lognormal data.

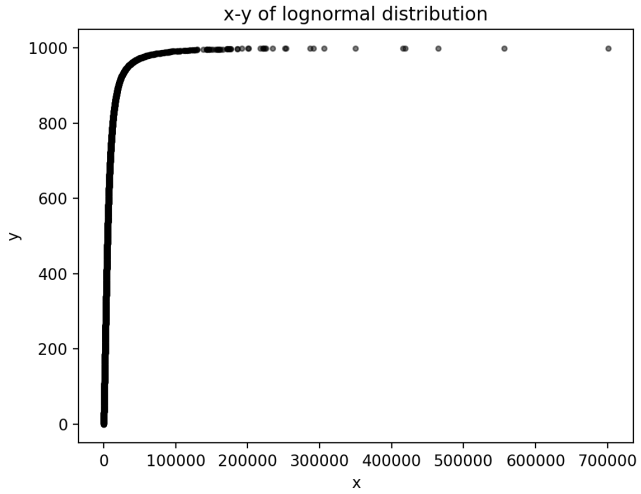
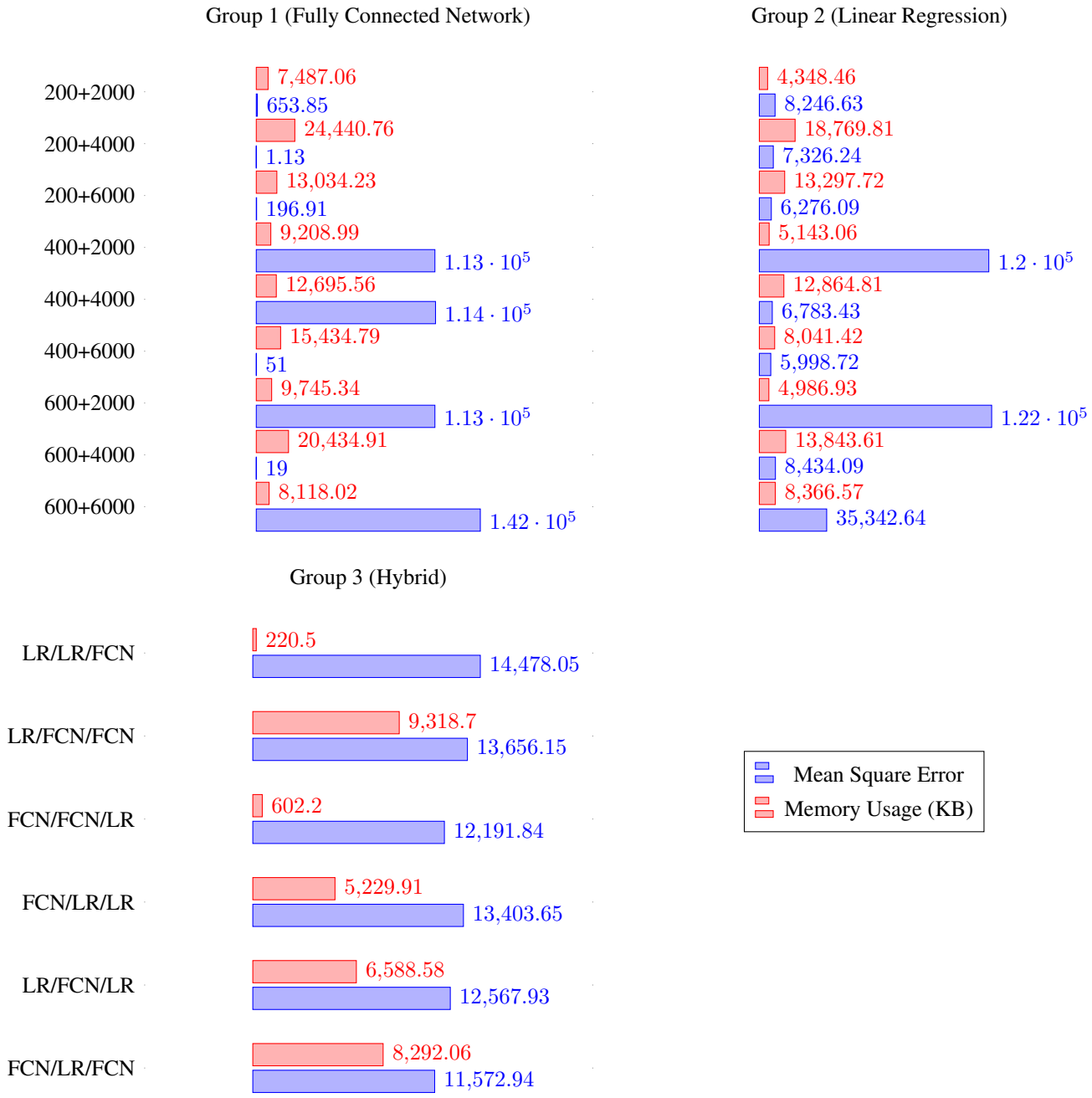


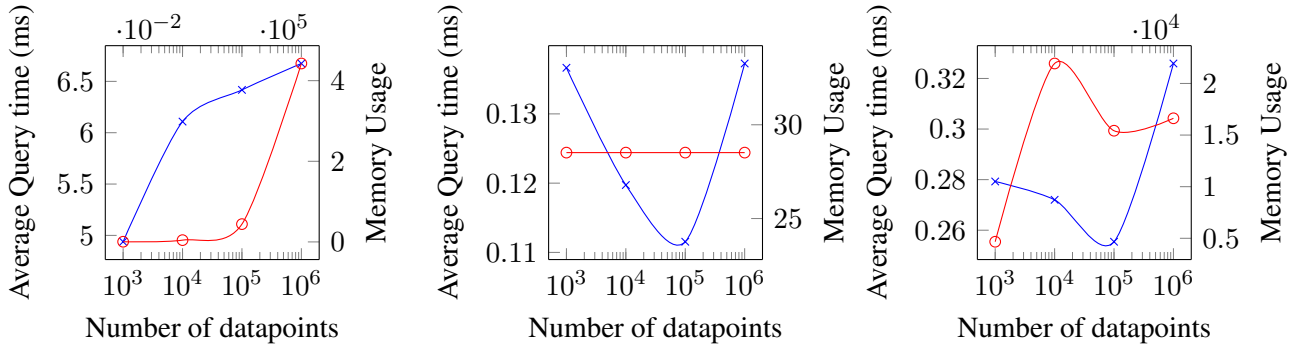
Figure 3.1.: The x-y graph where x is randomly sampled from a lognormal distribution

- All models are fully connected neural networks. The number of second-level models are $200, 400,$ and 600 respectively. The number of third-level models are $2000, 4000$ and 6000 for each number of second-level models.
- All models are linear regression models. The number of second-level models are $200, 400,$ and 600 respectively. The number of third-level models are $2000, 4000$ and 6000 for each number of second-level models.
- Models are combinations of fully connected neural networks and linear regression models. The numbers of second-level and third-level models are determined by the best settings in previous two group.

From the experiment results, we found that the second setting in group 1 (1 FCN model as root, 200 FCN models as second level models and 4000 FCN models as third level models) is the best regarding the mean square error. We also have the following findings in this searching process.

- Generally, the average error in group 1, where all models are fully connected neural networks is less than the error in group 2. Fully connected neural networks have a potential to be more accurate, i.e. it could achieve a small error if we tuned the models parameters properly.
- Tuning a model is tedious and can be costly. There are lots of hyper-parameters to choose from, such as the number of models in each level, types of models in each level, number of levels, and the internal hyper-parameters in each model. Using grid search, as we did in this experiment can be costly and time-consuming.


Group 1 (Fully Connected Network)
200+2000
200+4000
200+6000
400+2000
400+4000
400+6000
600+2000
600+4000
600+6000
7,487.06
653.85
24,440.76
1.13
13,034.23
196.91
9,208.99
1.13 · 10^5
12,695.56
1.14 · 10^5
15,434.79
51
9,745.34
1.13 · 10^5
20,434.91
19
8,118.02
1.42 · 10^5
Group 2 (Linear Regression)
4,348.46
8,246.63
18,769.81
7,326.24
13,297.72
6,276.09
5,143.06
1.2 · 10^5
12,864.81
6,783.43
8,041.42
5,998.72
4,986.93
1.22 · 10^5
13,843.61
8,434.09
8,366.57
35,342.64
Group 3 (Hybrid)
LR/LR/FCN
LR/FCN/FCN
FCN/FCN/LR
FCN/LR/LR
LR/FCN/LR
FCN/LR/FCN
220.5
14,478.05
9,318.7
13,656.15
602.2
12,191.84
5,229.91
13,403.65
6,588.58
12,567.93
8,292.06
11,572.94
Mean Square Error
Memory Usage (KB)



(a) B-Tree **(b)** FCN **(c)** Recursive Model

Figure 3.2.: The relations between the number of data points, average query time and the memory usage among three different indexes. The blue line represents the average query time and the red line represents the memory usage

3.1.3. Various Distributions and Sizes

After the search process for a recursive model, we then conduct experiments on several different distributions and sizes datasets. During this process, we use the following settings:

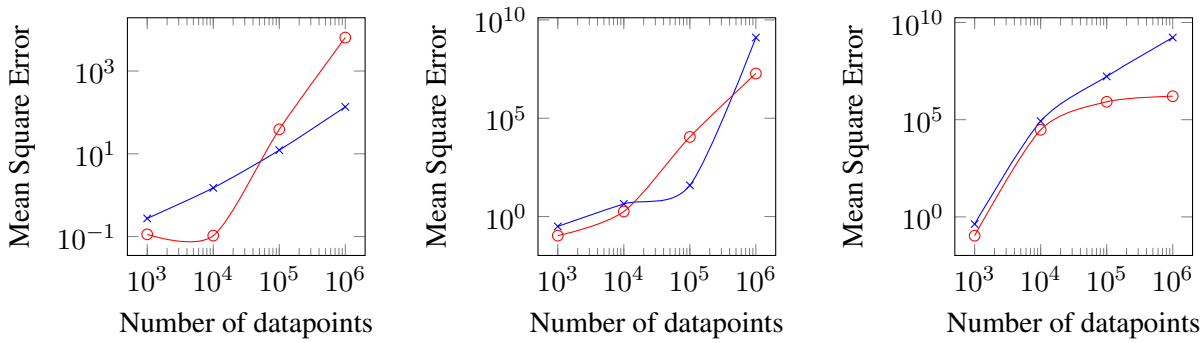
- The $\boldsymbol{X}$ is generated from *uniform*, *normal* and *lognormal* distribution.
- For each distribution, we generate 1 thousand, 10 thousands, 100 thousands and 1 million data points. We then assign the generated data points into pages where $N_{page} = 10$.
- We use a B-Tree with degree=20, a fully connected neural network with two layers and 32 nodes per layer, and a recursive model with 200 second-layer models and 4000 third-layer models.

We compare the following performance metrics:

- The query time per key and the memory usage among three index models.
- The mean square error caused by fully connected network and recursive models, across different distributions.
- The construction time among three index models.

Conclusion 3.1 From Fig 3.2, we analysed the time complexities for query and the space complexity for storing three different index models.

1. From Fig 3.2a, we verified that the average query time per key for a B-Tree is growing as the number of data points is increasing. It grows with a complexity of $\mathcal{O}(\log n)$, i.e. it grows slower when there are more data points.



(a) Uniform **(b)** Normal **(c)** Lognormal

Figure 3.3.: The relations between the number of data points and the mean square error in three different distributions. The blue line represents the fully connected network and the red line represents the recursive model

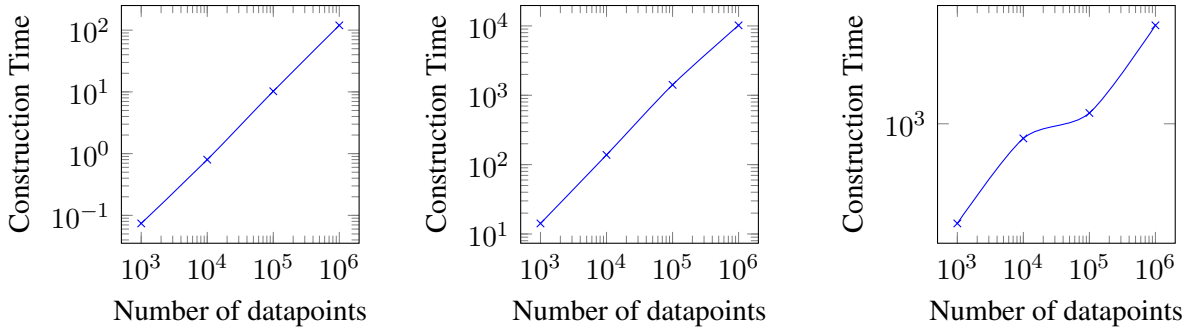
2. From Fig 3.2b, we found that the memory usage of a fully connected neural network is significantly less than the memory usage of B-Tree. Meanwhile, the fully connected neural network takes constant memory usage, as there are fixed number of nodes in the neural network. Similarly, the average query time is also a constant in theory. In the experiments, the average query time is changing, but very likely caused by turbulence.

3. From Fig 3.2c, we found that the memory usage of a recursive model is significantly higher than the memory usage of a fully connected neural network, but still less than a B-Tree, which is because the recursive model consists of thousands fully connected network. The memory usage of a recursive model is fluctuating, as the actually used number of fully connected network varies. The query time is higher than B-Tree and single fully connected network, but still a constant in theory, as there are only fixed number of computations.

Conclusion 3.2 From Fig 3.3, we analysed the errors of fully connected neural network and recursive model on different distributed dataset.

1. From Fig 3.3a, we found that both fully connected neural network and recursive model are capable of modelling uniformly distributed dataset with a rather low error. In the mean while, fully connected neural network could achieve less error, especially when there is large amount of data.

2. From Fig 3.3b, we found that the error is increasing exponentially as the number of data points is increasing. The error in fully connected neural network is significantly higher than recursive model.



(a) B-Tree **(b)** FCN **(c)** Recursive Model

Figure 3.4.: The relations between the number of data points and the construction time among three different index models.

3. From Fig 3.3c, we found that the error from recursive model is significantly less than the error in fully connected neural network. Combined with 3.3b and 3.3a, we conclude that the recursive model could surpass fully connected network when the data is not uniformly distributed. That means, the fully connected network is suitable for uniformly distributed data. We will analyse this property in more detail in the chapter *Insights and Findings*.

Conclusion 3.3 In 3.4, we analysed the construction time of different models.

1. As shown in 3.4a and 3.4b, the construction time of both B-Tree and fully connected neural network is increasing almost linearly as the number of datapoints is increasing. Theoretically, the construction time for B-Tree is $\mathcal{O}(n \log n)$ and $\mathcal{O}(n)$ for fully connected neural network.

2. In 3.4c, we found that the construction time of recursive model is increasing as well. The time in construction varies by two factors:
   - The number of data points will affect the construction time.
   - As we need to iterate over all possible models in each layer to assign training set, the number of models in each layer will affect the construction time as well.

3.1.4. 190M Lognormal Distributed Data

The last and largest dataset that we used is a large dataset that contains 190 million key value pairs that are distributed under lognormal distribution. There are two challenges in this task:

1. The training set is too large to be trained and tuned. As our implementation only supports single process, it would take a tediously long time to train the recursive model.

2. It takes super long time (several days in our settings) to evaluate on the very large dataset, as only one CPU thread will be used.

To tackle these challenges, we take the following strategies:

Training on Sampled Dataset We first randomly and uniformed sample from the whole training dataset. By sampling uniformly, we could keep the shape of the distribution unchanged. Assume we sampled S data pairs from the whole training dataset which contains N pairs, then we define the sampling ratio as $R = \frac{S}{N}$. We then map the output $\tilde{y}$ from our index model to its approximate position by $\hat{y} = \frac{\tilde{y}}{R}$. An example is illustrated in Example 3.1.

Example 3.1 Assume the **X** in training set is exponentially distributed as

$$[1, 2, 4, 8, 16, 32, 64, 128]$$

and we use a sample size $S = 4$. As we know the size of the fully training dataset is $N = 8$, we have $R = \frac{S}{N} = 0.5$. We uniformly sample from the training set and we will get $[1, 4, 16, 64]$. Then we train an index model based on

$$[(1, 0), (4, 1), (16, 2), (64, 3)]$$

For the key 32 as an example, ideally, we want our index model $\mathcal{F}$ to have an output such that $\tilde{y} = \mathcal{F}(32) = 2.5$. Then the original index of the key 32 can be calculated as $\hat{y} = \frac{\tilde{y}}{R} = \frac{2.5}{0.5} = 5$, which is exactly the index of 32 in the original full training dataset.

Evaluation with Multiple Processes To evaluate our models on the full training set would take several days to complete because there is only one process working on it. As the query is independent from each other, we utilise multiple processes to work on it by taking the following steps:

1. We first train our model on the sampled dataset with $S = 100,000$.
2. Then we split the full training set into 10 pieces such that each piece contains only 19 million pairs.
3. Afterwards, we perform the point query with the trained model on each piece in parallel.
4. Finally, we collect the query time from 10 pieces and sum them to get the total query time of the full training set. Then we divide it by the number of pairs in total, i.e. 19 million and get the average query time per key. For the mean square error, we take the average of errors from each piece.

With these two approaches, we achieved the results as shown below:

[1]The memory usage of each node is larger than previous experiments. It is because the tools for measuring memory usage (`pympler`) requires extra memory, and caused the program to be killed when there is not enough memory. Hence we use a different tool (`top`) to measure an approximate memory usage.

Model	Construction Time (s)	Avery Query Time (ms)	Memory Usage (MB)
B-Tree (degree=20)	26356 (1.00x)	**0.3489 (1.00x)**	96912 [1]
Recursive Model	**334 (0.013x)**	2.6505 (7.60x)	**8.836**

Table 3.1.: The construction time, average query time and memory usage of a B-Tree (with a degree=20) and a recursive model.

Conclusion 3.4 From Table 3.1, we have the following conclusions:

1. The construction time of recursive model can be significantly less than the construction of B-Tree, for two reasons:
   - We sampled from the training dataset, and avoid iterating over all the data points. In contrast, B-Tree has to iterate all the data points and insert them one-by-one.
   - The recursive model trains relatively fast as it can converge in one to a few passes over the data points.
2. Then query time for recursive model is higher than B-Tree, but not significantly higher. The computation costs is mainly on the calculation in fully connected neural networks. The query time for recursive model can be improved by either using a well-established library, such as PyTorch, that provides faster matrix computation, or using faster hardware, such as GPU to improve the query.
3. The memory usage of B-Tree is significantly higher than the recursive model. As we showed above, the memory usage of B-Tree is $\mathcal{O}(n)$ and hence growing linearly. For recursive model, the memory usage is mainly depends on how many models in each layer. Therefore, the memory usage of recursive model has an upper bound (if all models are used), and then does not grow as the number of data points is growing.

3.2. Two Dimensional Data and Indexes

For two dimensional data, the evaluation covers the following tasks:

- Find hyper-parameters for the LISA Baseline model empirically.
- Find hyper-parameters for the LISA model empirically.
- Compares the performance between KD-tree, LISA Baseline and LISA models for point query.
- Compare the performance between KD-tree, LISA Baseline and LISA models for range query.

- Compare the performance between KD-tree and LISA models for KNN query. KNN Query has not been implemented for LISA Baseline as there is no description of KNN Query for Baseline model in the paper.

3.2.1. Dataset

For two dimensional case, we manually generate three columns of the data:

- The first two columns contain the 2 dimensional keys $\boldsymbol{X} \in \mathbb{R}^2$, which are independently sampled from Lognormal Distributed Data. contains 190 million key value pairs that are distributed under lognormal distribution.
- Then we assign the keys into different pages according to a preset parameter N_{page} for page size. Specifically, the first N_{page} keys will be assigned into the first page, the second N_{page} keys will be assigned into the second page and so on so forth. After the assignments, we set the second column Y to be the page index of the corresponding x.

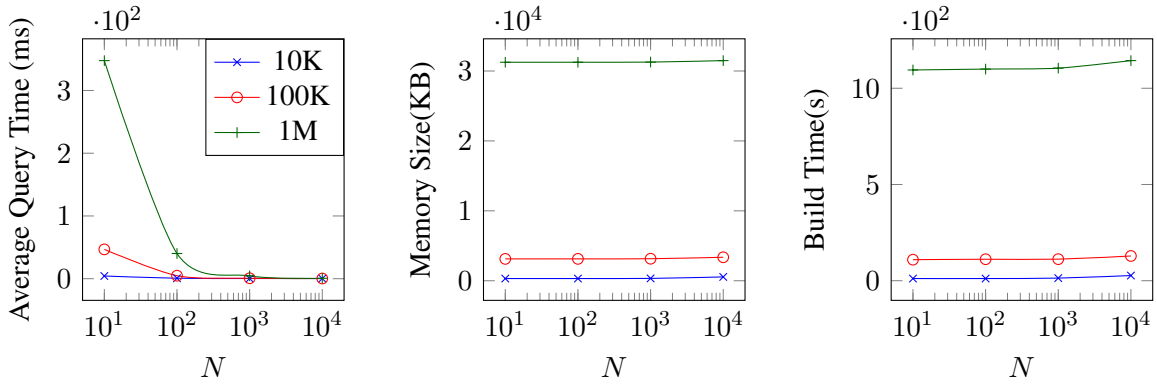
Our final data-set consists of 190 million key value pairs that are distributed under log-normal distribution As discussed in previous section, there are multiple challenges in using the complete data-set for training and hyper-parameters tuning. Even on google cloud server, running experiments with the full data take considerable long times (Lisa model took 26 hours to build), we had limited cloud server budget and a large number of experiments to run. Therefore, for two dimensional indexes evaluation, we have used sampling to generate smaller training datasets.

3.2.2. Hyper-parameters Search

After generating dataset as mentioned in previous section, we sample a smaller subset from it. We repeat our experiments for 3 different sample sizes of 10000, 100000 and 1000000 points. Test data is a copy of training data for all our experiments. For Baseline and Lisa models, final prediction is given by linear search through a range of values (identified as a Cell for Baseline and Shard for LISA model) and mean square error (MSE) is zero as test points are already learned during training. This is where Learned Index models differ from traditional machine learning models where model performance is evaluated on unseen data.

Hyper-parameter search for the LISA Baseline implementation

Baseline model has one hyper-parameter: N (Number of cells specifying the number of equal length intervals into which mapped values are divided). The point query search consists of two parts, first is binary search to locate the cell into which the query key is located, followed by sequentially comparison of the query key value with keys in the found cell until a match is found. The time complexity of first search is $log_2 N_1$, where N_1 is the number of cells. The time complexity of second search is $\lceil N_2/2 \rceil$, where N_2 is the number of keys per cell.



(a) Average Query Time (ms) **(b)** Memory Size (KB) **(c)** Build Time (s)

Figure 3.5.: Hyper-parameter search in LISA Baseline for training sizes $10K$, $100K$ and $1M$.

Conclusion 3.5 Following conclusions can be drawn from experimental results shown in table A.1 and Fig. 3.5

1. Optimum value of hyper-parameter N will be equal to number of points in the training data-set, resulting in 1 key per cell and search query time of O($log_2 N$).
2. Average Query Time : Average Query Time decreases with increase in value of N as number of keys per cell decreases.
3. Build time : Build time increases with increase in value of N, as metadata for additional cells needs to be calculated.
4. Memory Size : Memory requirements of the model increases with increase in value of N, as metadata for additional cells needs to be stored. Increase in memory size is not significant with increase in N as we maintain only two values per cell, mapped value of first key in the cell and mapped value of last key in the cell.

Hyper-parameter search for the LISA implementation

For LISA model, we have 3 hyper parameters:

1. G : The size of the grid cell. Number of grid cells into which the key space is divided. In our implementation, we use a square grid cell, and total number of cells is given by $G \times G$.
2. N : Number of equal length intervals into which mapped value range is divided. During our experiments, we found that shard prediction algorithm gives better performance if mapped interval boundaries are aligned to grid cell boundaries. That's why this parameter is always initialised to N=$G \times G$

3. S : Number of shards to learn per mapped interval.

Conclusion 3.6 Following conclusions can be drawn from experiments results shown in tables A.3, A.4 and A.5.

1. For a particular value of G, average query time decreases and memory size increases with increase in value of S. This is expected as increasing S, will result in lesser number of keys per shard, thereby reducing the sequential search cost of scanning the query key through the Shard.
2. Average query time decreases and memory size increases with increase in values of G and S.
3. We need to choose S such that there are at least 40 keys per shard. We may see mean square errors(mse) if number of keys per shard are less than 45 for following reasons.
   a) For point query search, we first predict a shard and then sequentially compare the query point key values with all the keys in the predicted shard until a match is found
   b) For query points near the shard boundaries, there can be a mismatch in ground truth shardId and predicted shardId.If the query point is not found in the predicted shard, we continue our search in adjacent left and right shards in an empirically found range.

   During test experiments, we found that if shard size is less than 40 keys, then sometimes shard prediction error can be greater than 1 and point query search can fail resulting in MSE errors.

3.2.3. Comparisons Across Models

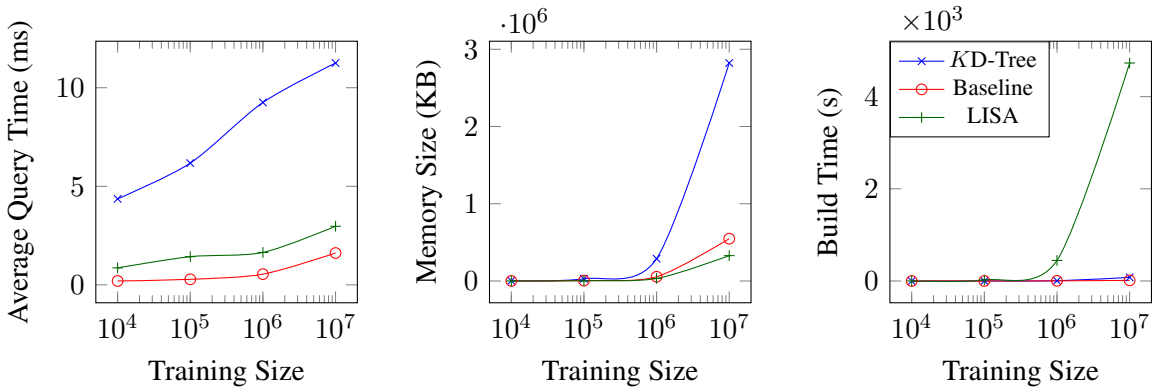
During following experiments, for each training data size, we have used hyper-parameters optimized for that particular data set size.

Point Query Comparison

Table A.6 and Fig. 3.6 shows the performance evaluation for KD-Tree, LISA-Baseline and LISA Models for different training data sizes. For a given training set, we perform point query evaluation for every point in the data-set and take the average.

Conclusion 3.7 The following conclusions can be concluded:

1. LISA outperforms KD-tree in terms of average query time. Search complexity of KD-Tree and LISA baseline is $O(N)$, and O($log_2 N$) respectively where N is the



(a) Average Query Time (ms) **(b)** Memory Size (KB) **(c)** Build Time (s)

Figure 3.6.: Point Query experimental results for KD-Tree, Baseline and LISA models.

number of points in the training data-set. On the other hand point query search cost in LISA is a combination of 3 costs.

a) Search cost to find the grid cell to which point query belongs. This cost increase linearly with increase in number of grid cells.

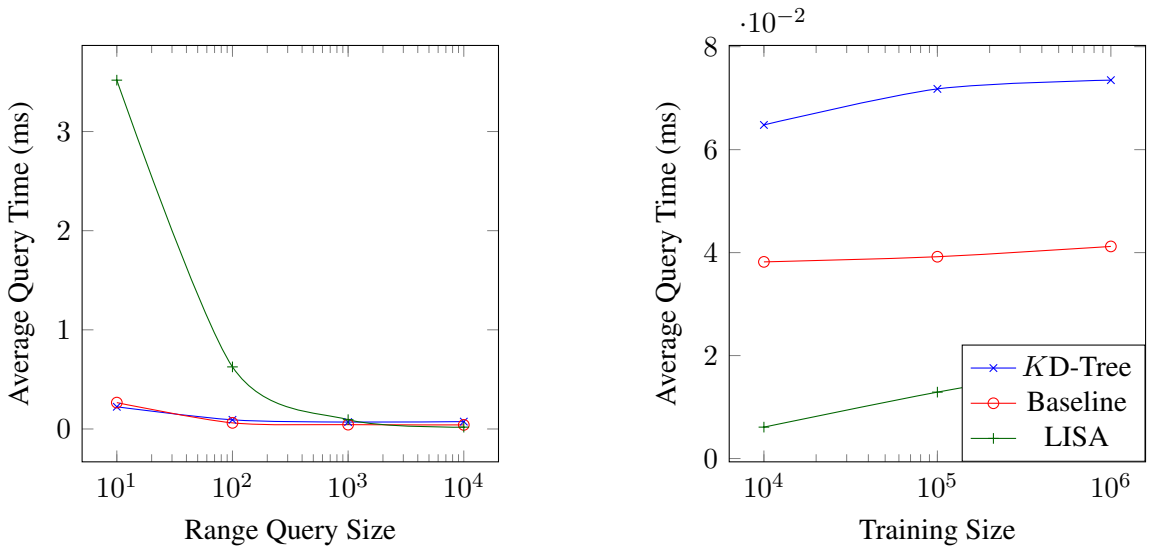
b) Find the shard Id to which point query belongs. This cost is constant as shard prediction function weights are already learned during the build process.

c) Once the shard Id is found, search sequentially in the shard interval by comparing query point key value with all the keys in the shard until a match is found. This cost is relatively constant with respect to increase in training data-size as we try initialize our hyper-parameters in such a way that number of keys per shard remain close to 50.

2. LISA outperforms KD-tree in terms of memory size requirements, however its build time is significantly higher than KD-Tree and LISA Baseline. The storage consumption of LISA is considerably smaller than KD-Tree that has to construct a tree with all nodes and entries based on MBRs (minimum bounding rectangle) and parent-children relationships. In contrast, LISA only keeps the parameters of M and SP. Specifically,M's parameters contain several numbers and a small list only, and SP is composed of a series of piecewise linear functions whose parameters are a number of coefficients.

Range Query Experiments

Table A.7 shows evaluation results for LISA,Baseline and KD-tree models for range sizes of 10, 100, 1000 for different training sizes. For a given range query size, we perform 20 trials and take the average. For each trial, we sample a random point from the test set and find the range from sampled point to the range query size. Average query time for each range is further divided by the range size to compare the query time across various ranges. As shown in the Fig. 3.7, LISA outperforms KD-tree for range query size of 10000 for all training sizes,



(a) Range Query Size

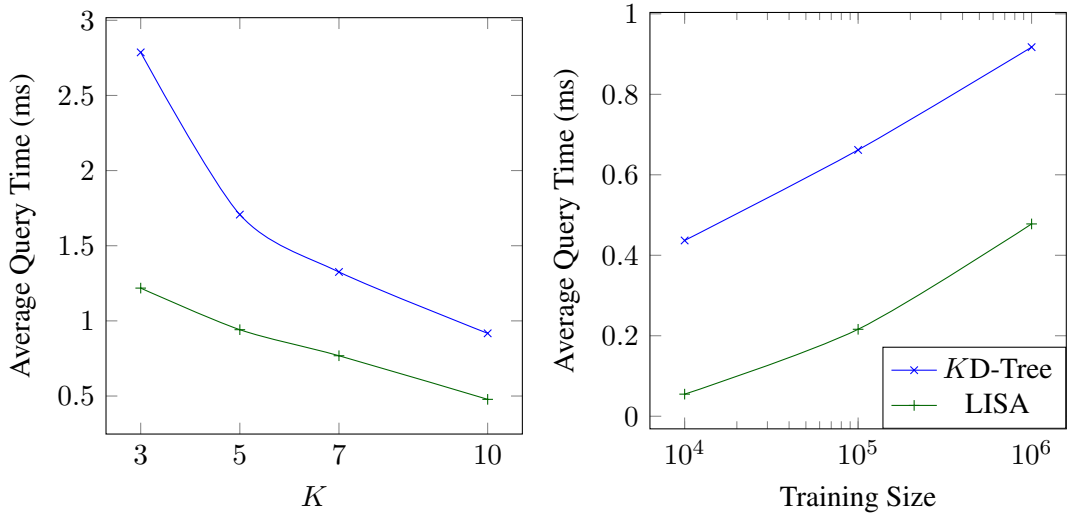
(b) Training Size

Figure 3.7.: Range Query experimental results for KD-Tree, Baseline and LISA models.
a) Plot A shows average range query time for a fixed training size of 1M points.
b) Plot B shows average range query time for a fixed range query of size 10000 for various training sizes.

however its range query time for smaller range sizes is significantly higher than KD-Tree.

KNN Query Experiments

Table A.8 shows evaluation results for LISA and KD-tree models for KNN Queries for various value of K and training sizes. For a given K value, we perform 20 trials and take the average of query time. For each trial, we sample a random point from the test set and find K neighbours around that point. Average query Time is further divided by K to compare the Query time across various values of K.As shown in the Fig. 3.8, LISA outperforms KD-tree for different training sizes and K values.



(a) Range Query Size

(b) Training Size

Figure 3.8.: KNN Query experimental results for KD-Tree and LISA models.
a) Plot A shows average KNN query time for a fixed training size of $1M$ points for different values of K.
b) Plot B shows average KNN query time for various training sizes with K = 10.

4. Insights and Findings

4.1. General Discussions

Limitations

Though the learned index model, especially the recursive model has a potential to greatly reduce the memory usage and cost less time in making the query. It is still limited in several perspective.

- **Read-only Database**. Current recursive model index assumes that the data is a static, read-only array. Only when this assumption is hold, we can regard the database index as the CDF. However, in reality, we usually need to insert and delete the data in the array and violates this assumption.
- **Sorted Keys**. The recursive model and baseline model assume that the keys are sorted in ascending order, so that the CDF assumption applies.
- **In-Memory Database**. In our implementations, we only consider the case where all the keys are stored in the memory.

To apply the learned indexes into a general-purpose database, we will need to overcome these limitations. For example, the model needs to be trained again in order to support the read-and-write database.

4.2. One Dimensional Learned Index

4.2.1. Baseline Learned Index

Activation Functions

- If we use identity activation function, i.e.$z^{(i)}(x) = x$, then no matter how many layers are there, the fully connected neural network falls back to a linear regression.

  Proof: The output of the first layer, with identity activation function, will be $z^{(1)}(w^{(1)}x + b^{(1)}) = w^{(1)}x + b^{(1)}$. Then the output will be the input of the next layer, and hence the output of the second layer will be $z^{(2)}(w^{(2)}(w^{(1)}x + b^{(1)}) + b^{(2)}) = w^{(2)}w^{(1)}x + w^{(2)}b^{(1)} + b^{(2)}$. Similar induction can be obtained for multiple layers. Hence if we use identity activation, the trained neural network will fall back to a linear regression.

- With ReLU (Rectified Linear Unit) as activation function i.e. $z^{(i)}(x) = \max(0, x)$, then the fully connected neural network falls back to a piecewise linear function.

  Proof: The output with ReLU activation function, will be $z^{(1)}(w^{(1)}x+b^{(1)}) = \max(w^{(1)}x+b^{(1)}, 0)$. Then the output will be the input of the next layer, and hence the output of the second layer will be $z^{(2)}(w^{(2)}(w^{(1)}x+b^{(1)})+b^{(2)}) = \max(w^{(2)}w^{(1)}x+w^{(2)}b^{(1)}+b^{(2)}, 0)$. Similar induction can be obtained for multiple layers. Hence if we use identity activation, the trained neural network will fall back to a piecewise linear function. The visualization below shows our lemma is correct.

4.3. Two Dimensional Learned Index

LISA Baseline model search optimization for smaller values of N

In case of high dimensional key values, key with in a cell can not be searched with mapped value, as a large number of keys can have the same mapped value. However for the 2 dimensional scenario, we can get considerable savings in search cost by replacing sequential scan based on keys values to binary search based on mapped value. As in the original method, search process will consist of two parts.

1. Find the cell which contains the query key based on mapped value using binary search.
2. With in the cell, replace sequential search based on query key value with the binary search based on query key mapped value. Once mapped value is found, do a lookup in the neighbourhood of the found key based on query key 2 dimensional value.

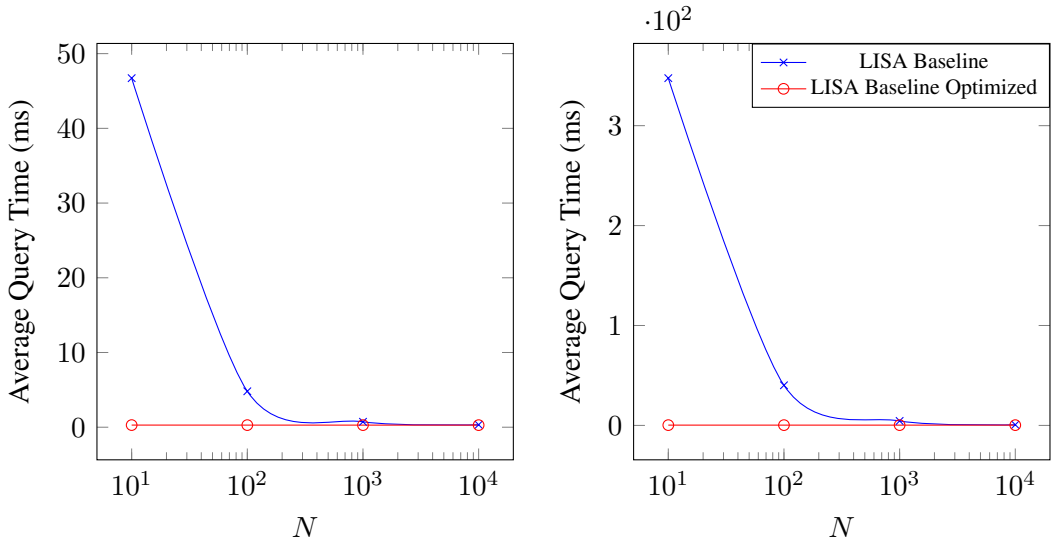
As shown in Fig. 4.1, we get significant savings in the query time with this approach for smaller values of N. As the value of N increases, number of Keys per cell decreases, and savings in avoiding sequential search gets normalized.

4.4. Future Work

Future work

In current work, we have implemented RMI and LISA, two novel learned index structures for one and two dimensional data respectively. This work opens up several directions for future research on learned indexes for database systems. We are listing some of them here.

1. Read only and in-memory database are two major constraints applicable to our LISA implementation that are supported by the original paper. Adding support for insertion, deletion and disk resident training data can be taken in next phase for both one dimensional and spatial databases.
2. LISA paper suggests Lattice Regression model to learn an appropriate distance bound from underlying training data for every query point and specific value of K. This distance bound is used to convert the KNN query to range query. It will be interesting



(a) Training Size 100K **(b)** Training Size 1M

Figure 4.1.: Point query results comparison between LISA Baseline and Optimized Model for different training sizes.

to try different learning models like Lattice Regression, Neural Network and Bayesian Neural Network to learn this distance bound from underlying data.

3. It will be interesting to study other query types (e.g., spatial joins and closest pairs) using LISA

4. Our results show that learned index models outperform traditional databases by utilizing the distribution of data being indexed.. It will be interesting to develop functional databases using learned index models and investigate their performance on real data

Conclusion

In this work, we have implemented RMI and LISA, two novel learned index structures and B-Tree and KD-Tree two traditional database indexes for one and two dimensional data respectively. We have conducted a number of experiments using real and synthetic datasets. The experimental results demonstrate that learned index models outperforms traditional indexes in terms of storage and IO costs for point, range and KNN queries. Some of our learnings are listed below:

1. The key idea in our work has been to map the key space into a sorted one dimensional array and use learned models to approximate the cumulative distribution function (CDF).While RMI uses a hierarchy of linear regression models, LISA makes use of piecewise linear models to learn the cdf.

5. Convolution and CNN for Learned Indexes

From the previous discussion, we summarise that both one-dimensional and two-dimensional indexes requires to learn a function from a one-dimensional array.

1. In one dimensional data, the learned function is used directly as an approximation to the CDF. We use a fully connected neural network or a recursive model to learn such function.

2. In two dimensional data, the learned function is used to predict the corresponding shard. We use a piecewise linear function to achieve this task.

These models in our previous chapters have their shortcomings:

1. The fully connected neural network (with ReLU as activation functions) is essentially a continuous piecewise linear function. The training of such neural network is unstable and highly dependent on the initial values, well-tuned hyper-parameters, etc. Meanwhile, it requires more work if we want to ensure the monotonicity.

2. The recursive model takes more memory than a single neural network, and there are many more parameters to tune than neural network.

3. The training method for a piecewise linear function is an iteration-based method. If we choose a large number of break points, then the training time will be long.

In fact, in order to train the piecewise linear function, we only need to know either the slope of each segments or the position of the breakpoints. If we know any one of them, we can learn the other in a closed form, as we shown in the shard prediction section. In this chapter, we present a method to learn the position of breakpoints.

Learning the position of breakpoints can be regarded as a binary point-wise classification problem. That means, for each point in our X, we want to learn to classify it to be 1 if it is a breakpoint, otherwise we want it to be 0. Then we classify all the points in our X and each point is classified to be 1 with a confidence. Afterwards, we only need to filter the top-K points to be the breakpoints.

This task is similar to the image segmentation in computer vision, which essentially tries to classify every pixel in the image. One successful technique in image segmentation is by using the convolution and convolution transpose network [LSD15]. Inspired by this, we propose a similar network to perform binary point-wise classification. In this chapter, we describe the steps of using convolutional neural network to find breakpoints in a one-dimensional array.

5.1. Problem Formation

Assume that we have the keys X and their corresponding pages Y, the problem can be formulated and divided into the following subproblems:

1. How do we prepare the training labels L that represents the break points?
2. What kind of neural networks is capable of classifying each points in the training input X and Y?
3. After predicting the break points, how do we proceed to train linear function on each segment?

5.2. Training

5.2.1. Dataset

The dataset we used in the convolutional neural network is manually synthesised as well. We use the following steps to generate the training dataset:

1. Similar to the dataset we used in recursive model, we first generate X by randomly sampling from a certain distribution. Then we assign the keys into different pages according to a preset parameter N_{page}. We call the generated pages as Y. After this step, we get a two-dimensional matrix.
2. Then we calculate the positions of breakpoints by the iteration-based approach described in the *Shard Prediction* section.
3. Afterwards, we iterate over all the calculated breakpoints and find the closest point to it in X. We call the set of closest points as B and we can generate the training labels as

$$l = \begin{cases} 1 & x \in B \\ 0 & \text{otherwise} \end{cases} \tag{5.1}$$

In addition to the above steps, we could also generate several dataset from several different distributions, and then concatenate them such that the training dataset contains samples from different distributions.

After these steps, we get the training input as $[X, Y]$ and the training label as L. Assume there are N keys in total, then the training input is a $N \times 2$ matrix and the training label is a $N \times 1$ vector.

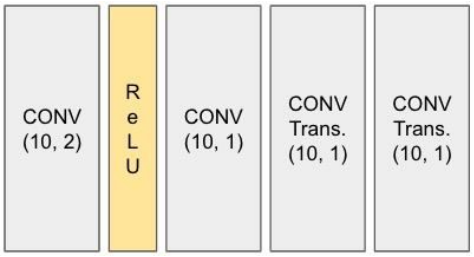


Figure 5.1.: Illustration of the structure of fully convolutional network, in which the yellow rectangle represents the activation function and other grey rectangles represents convolution and convolution transpose operations. The $(10, 2)$ and $(10, 1)$ represent the kernel size of the convolution operation

5.2.2. Fully Convolutional Network

Convolution is an operation that makes the input smaller, which makes it impossible to perform point-wise classification. Hence, we use the convolution transpose (also called deconvolution) to make the input larger. We manually set up the hyper-parameters (e.g. the kernel size of convolution operation) in the neural network such that the output has a shape of $N \times 1$. In our experiments, we use the neural network illustrated as Fig. 5.1.

With this neural network, we can get an output of the shape $N \times 1$. The expected output represents the probability that this position is a breakpoint.

We can train the neural network with standard gradient descent approach. During the training process, we try to minimise the mean square distance between the predicted output $\hat{L}$ and the labels L.

5.2.3. Training of Linear Functions

After getting the predicted output, we then find the largest $K+1$ positions from the predicted output $\hat{L}$. We call these K elements as $\boldsymbol{\beta} = (\beta_0, \beta_1, \cdots, \beta_K)$. Then we want to train a piecewise linear function described as

$$y = \begin{cases} \overline{\alpha} + \alpha_0(x - \beta_0) & \beta_0 \leq x < \beta_1 \\ \overline{\alpha} + \alpha_0(x - \beta_0) + \alpha_1(x - \beta_1) & \beta_1 \leq x < \beta_2 \\ \cdots & \\ \overline{\alpha} + \alpha_0(x - \beta_0) + \alpha_1(x - \beta_1) + \cdots + \alpha_K(x - \beta_K) & \beta_K \leq x \end{cases} \tag{5.2}$$

Since $\boldsymbol{\beta}$ is fixed, we only need to calculate $\boldsymbol{\alpha} = (\overline{\alpha}, \alpha_1, \alpha_2, \cdots, \alpha_K)$, which can be considered as the solution of the linear equation $\boldsymbol{A\alpha} = \boldsymbol{y}$, where

$$\boldsymbol{A} = \begin{bmatrix} 1 & x_0 - \beta_0 & (x_0 - \beta_1)\,1_{x_0 \geq \beta_1} & \cdots & (x_0 - \beta_K)\,1_{x_0 \geq \beta_K} \\ 1 & x_1 - \beta_0 & (x_1 - \beta_1)\,1_{x_1 \geq \beta_1} & \cdots & (x_1 - \beta_K)\,1_{x_1 \geq \beta_K} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 1 & x_N - \beta_0 & (x_N - \beta_1)\,1_{x_N \geq \beta_1} & \cdots & (x_N - \beta_K)\,1_{x_N \geq \beta_K} \end{bmatrix} \tag{5.3}$$

where $1_{x_i \geq \beta_j}$ equals to 1 if $x_i \geq \beta_j$. Otherwise it equals to 0.
The by applying least square method, we get

$$\boldsymbol{\alpha} = (\boldsymbol{A}^T \boldsymbol{A})^{-1} \boldsymbol{A} \boldsymbol{y} \tag{5.4}$$

The calculated $\boldsymbol{\alpha}$ and $\boldsymbol{\beta}$ are what we need to define the piecewise linear functions. With these steps, we could calculate them within a fixed number of computations.

5.3. Experiment

We first present the break points that we found with the fully convolutional network as in Fig. 5.2. We found that it works better with normally distributed data, especially after 0.4. However, the current model cannot be applied directly to lognormal distributed data.

Then we perform an evaluation on 10 thousands normal distributed keys. The results are shown in Table 5.1. From the table, we have the following analysis:

1. The convolutional model outperformed other models in the construction time, which is due to the fact that we only train linear models on the predicted break points. As we can reuse the pre-trained convolutional models to find the break points, the time for training convolutional models is not included in this construction time.

2. The query time for convolutional model is larger than B-Tree and baseline model. It is because we need to iterate over

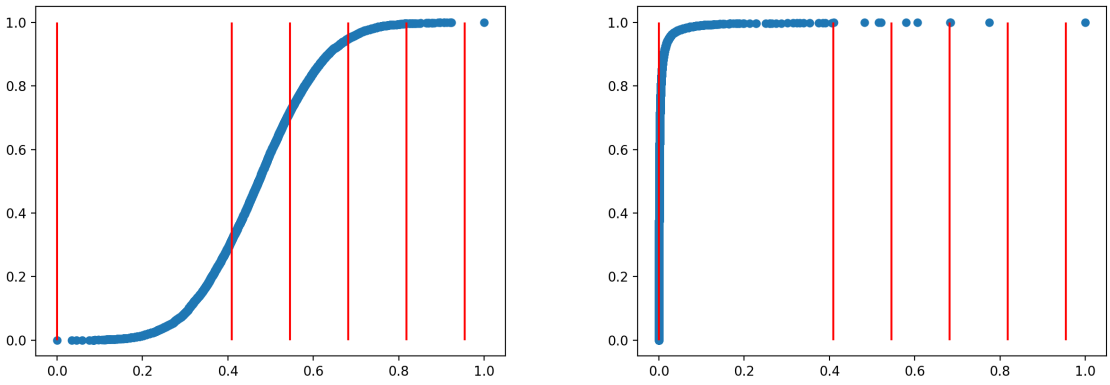
Model	Build (s)	Query (ms)	MSE	Memory (KB)
B-Tree (degree=20)	1.0311	*0.1395*	*0*	4056.05
Baseline	1045.25	**0.3136**	3.8825	**11.0859**
Recursive Model	503.72	0.7066	2.1483	15531.7
Convolution (breaks=32)	**0.01811**	0.48522	**0.6762**	240.484

Table 5.1.: The construction time, average query time (Lookup), mean square error and memory usage of a B-Tree (with degree=20), a baseline model, a recursive model and a fully convolutional model (with 32 breakpoints). The experiment is performed on 10 thousand normally distributed keys.

5.4. Applications and Future Work

The approach we described above can be used in both one-dimensional and two-dimensional data. In one-dimensional case, the learned piecewise function can be used directly as the approximation for the CDF. In the two-dimensional case, this approach can be used to improve the training speed of shard prediction function.

In future, there might be some possibilities in exploring in the following directions:



(a) Normal Distribution **(b)** Lognormal Distribution

Figure 5.2.: The break points found by the fully convolutional neural network

1. Concatenate more distributions and explore if the convolutional model has actually learned the patterns for break points.
2. Investigate the hyper-parameters in the fully convolutional neural network.
3. We can find the break points not only for linear piecewise functions, but also polynomials etc. It might be possible for the convolutional neural network to learn the patterns of break points under different functions for each segment. That means, we may extend the binary classification task into a multi-categories classification task where each category represents a type of functions.

6. Conclusion

In this project, we reviewed and implemented two classic tree structures, **B-Tree** and K**D-Tree**, used as database indexes. The tree structures are capable of finding elements precisely as it will traverse all possible nodes. The shortcomings of these tree structures also come from this property: the tree needs to save and traverse the possible nodes, which yields a space complexity that are proportional to the number of records. In the meanwhile, it yields a query time complexity that has a positive correlation with the number of records. As the volume of data is increasing rapidly, the time and space complexity becomes huge and becomes a bottleneck of applications.

We then implement two kinds of learned indexes: the **recursive model index** for one-dimensional data and the **LISA** model for two-dimensional data. We conclude that the recursive model and its baseline model have a bounded time and space complexity for performing queries and storing the model.

Having said these advantages of learned indexes, they all have their shortcomings.

1. Even though the learned indexes have a constant time complexity for queries, the constant is relatively large. Therefore, if the number of records is not huge, learned index will not output classic tree structures.

2. The recursive model, baseline model and the convolutional model are prone to error. It may not be a big issue with in-memory database, but will cost much more time when it needs to search different disk pages, especially with traditional hard disk drive (HDD).

Acknowledgement

We would like to express our sincere gratitude to Prof. Dr. Michael Böhlen, and Mr. Qing Chen for their commitment in supervising this project. Our appreciation extends to Dr. Sven Helmer in reading our report and arranging discussion and presentation of this project.

Appendices

A. Appendix

Training/Test Data Size	Model	N	Build Time (ms)	Avg Query Time (ms)	Memory Size (KB)
10,000	Lisa Baseline	10	11.17	4.3426	313
10,000	LISA Baseline	100	11.25	0.7189	315
10,000	LISA Baseline	1000	13.54	0.3283	336
10,000	LISA Baseline	10000	26.83	0.2415	547
100,000	LISA Baseline	10	109.28	46.7173	3126
100,000	LISA Baseline	100	111.59	4.8086	3128
100,000	LISA Baseline	1000	111.97	0.7271	3149
100,000	LISA Baseline	10000	128.49	0.3301	3360
100,000	LISA Baseline	100000	272.93	0.2381	5469
1,000,000	LISA Baseline	10	1094.85	347.5613	31251
1,000,000	LISA Baseline	100	1099.38	40.1451	31253
1,000,000	LISA Baseline	1000	1104.65	4.4732	31274
1,000,000	LISA Baseline	10000	1143.65	0.6697	31485
1,000,000	LISA Baseline	100000	1273.56	0.2944	33594
1,000,000	LISA Baseline	1000000	2717.65	0.2436	54688

Table A.1.: Hyper-parameters Search LISA Baseline Model for training sizes $10K$, $100K$ and $1M$

Training/Test Data Size	Model	N	Build Time(ms)	Avg Query Time(ms)	Memory Size(KB)
10,000	LISA Baseline Optimized	10	11.1208	0.2841	313
10,000	LISA Baseline Optimized	100	12.0108	0.2779	315
10,000	LISA Baseline Optimized	1000	12.7589	0.2765	336
10,000	LISA Baseline Optimized	10000	25.8732	0.2752	547
100,000	LISA Baseline Optimized	10	112.973	0.2855	3126
100,000	LISA Baseline Optimized	100	114.318	0.2823	3128
100,000	LISA Baseline Optimized	1000	116.699	0.2806	3149
100,000	LISA Baseline Optimized	10000	129.514	0.2794	3360
1,000,000	LISA Baseline Optimized	10	1116.51	0.2905	31251
1,000,000	LISA Baseline Optimized	100	1118.85	0.2858	31253
1,000,000	LISA Baseline Optimized	1000	1134.88	0.2844	31274
1,000,000	LISA Baseline Optimized	10000	1134.88	0.2831	31485

Table A.2.: Experimental results for LISA Baseline model with search optimization

Training/Test Data Size	Model	G	S	Build Time(s)	Avg Query Time(ms)	Memory Size(KB)	mse
10,000	LISA	4*4=16	5	4.335	1.13135	324.72	0
10,000	LISA	4*4=16	10	3.370	0.96036	329.07	0
10,000	LISA	4*4=16	20	1.127	0.86184	337.85	0
10,000	LISA	4*4=16	30	3.478	0.74339	346.63	5729

Table A.3.: Hyper-parameters Search LISA Model: Training Size:10,000 Points.
a) For the last row, Numbers of keys= 10000
b) Keys per cell= $10000 \setminus (4 \times 4) = 625$
c) Keys per shard = $625 \setminus 30 = 20$ keys per shard, resulting in mse errors

Training/Test Data Size	Model	GridCellSize	No of Shards	Build Time(s)	Avg Query Time(ms)	Memory Size(KB)	mse
100,000	LISA	4*4=16	50	122.64	1.51173	3176.6	0
100,000	Lisa	4*4=16	100	30.211	1.44084	3220.3	0
100,000	LISA	4*4=16	150	142.13	1.15491	3264.1	297234
100,000	Lisa	6*6=36	50	66.375	1.55903	3238.1	0
100,000	LISA	6*6=36	75	72.491	1.43043	3287.2	0
100,000	Lisa	6*6=36	100	60.929	1.64881	3336.4	5.6e+07
100,000	LISA	8*8=64	20	35.638	1.54029	3218.7	0
100,000	LISA	8*8=64	50	45.014	1.52117	3323.6	0

Table A.4.: Hyper-parameters Search LISA Model: Training Size:100,000 Points

Training/Test Data Size	Model	GridCellSize	No of Shards	Build Time(s)	Avg Query Time(ms)	Memory Size(KB)	mse
1,000,000	Lisa	10*10=100	50	743.29	1.77751	31558.9	0
1,000,000	Lisa	10*10=100	100	1077.89	1.63397	31832.3	0
1,000,000	Lisa	20*20=400	25	365.49	2.53317	31930.8	0
1,000,000	Lisa	20*20=400	50	609.32	1.44526	32477.6	0
1,000,000	Lisa	25*25=625	25	240.22	1.56227	32779.8	0
1,000,000	Lisa	30*30=900	25	205.18	1.79839	33010.3	0

Table A.5.: Hyper-parameters Search LISA Model: Training Size:1,000,000 Points

Training/Test Data Size	Model	Build Time (s)	Avg Query Time (ms)	Memory Size (KB)
10,000	KD-Tree	0.023	4.363	2890
10,000	Baseline	0.026	0.198	547
10,000	LISA	1.127	0.861	337
100,000	KD-Tree	0.340	6.176	28906
100,000	Baseline	0.324	0.241	5469
100,000	LISA	22.491	1.43	3169
1,000,000	KD-Tree	4.124	9.254	289062
1,000,000	Baseline	2.718	0.343	54688
1,000,000	LISA	445.324	1.445	32477

Table A.6.: Point Query experimental results for KDTree, Baseline and LISA models

Training/Test Data Size	Range Query Size	Avg Query Time (ms) (KD-tree)	Avg Query Time (ms) (Baseline)	Avg Query Time (ms) (LISA)
10,000	10	0.1361	0.1113	0.8204
10,000	100	0.0533	0.0451	0.1201
10,000	1000	0.0438	0.0399	0.0294
10,000	10000	0.0648	0.0382	0.0061
100,000	10	0.1392	0.1298	2.8961
100,000	100	0.0539	0.0505	0.2792
100,000	1000	0.043	0.0428	0.0563
100,000	10000	0.0718	0.0392	0.0129
1,000,000	10	0.2238	0.2661	3.5181
1,000,000	100	0.0922	0.0617	0.6263
1,000,000	1000	0.0744	0.0437	0.0939
1,000,000	10000	0.0735	0.0412	0.0186

Table A.7.: Range Query experimental results for KD-tree, Baseline and LISA models

Training/Test Data Size	K	Avg Query Time(ms)(KD-tree)	Avg Query Time(ms)(LISA)
10,000	3	1.4069	0.2020
10,000	5	0.8753	0.1181
10,000	7	0.6333	0.0811
10,000	10	0.4368	0.0549
100,000	3	2.0325	0.5867
100,000	5	1.2004	0.3549
100,000	7	0.8812	0.2779
100,000	10	0.6618	0.2161
1,000,000	3	2.7865	1.218
1,000,000	5	1.7072	0.9414
1,000,000	7	1.3255	0.7681
1,000,000	10	0.9172	0.5779

Table A.8.: KNN Query experimental results for KD-tree and LISA model

# id	Distributions	root model	second model	third models	Build Time (s)	Query Time (ms)	Evaluation Error (MSE)	Memory Size (KB)
1	log_normal	fcn	200 fcn	2000 fcn	418.9493798	0.970932583	653.8536667	7487.059896
2		fcn	200 fcn	4000 fcn	1141.521194	0.9675528	**1.134166667**	24440.75523
3		fcn	200 fcn	6000 fcn	688.8004486	1.07512705	196.9116667	13034.22656
4		fcn	400 fcn	2000 fcn	483.1734781	1.158343717	113246.196	9208.992183
5		fcn	400 fcn	4000 fcn	636.8463397	1.339095933	113652.3212	12695.55731
6		fcn	400 fcn	6000 fcn	742.0712694	1.243333667	51.00183333	15434.78905
7		fcn	600 fcn	2000 fcn	504.959355	1.06512235	113246.2647	9745.335942
8		fcn	600 fcn	4000 fcn	879.6010201	0.973031833	18.99766667	20434.90626
9		fcn	600 fcn	6000 fcn	373.6126809	1.11725315	142041.6877	8118.023442
10		lr	200 lr	2000 lr	262.5089284	1.280502367	8246.633985	4348.463542
11		lr	200 lr	4000 lr	869.7494701	1.304096217	7326.238372	18769.81252
12		lr	200 lr	6000 lr	655.0431077	1.318176683	6276.09111	13297.72135
13		lr	400 lr	2000 lr	275.3925674	1.31789575	120427.9247	5143.059892
14		lr	400 lr	4000 lr	601.7362665	1.453903583	6783.428749	12864.80731
15		lr	400 lr	6000 lr	388.5866734	1.623972083	5998.720313	8041.416654
16		lr	600 lr	2000 lr	267.8966881	1.861582733	121932.5051	4986.927088
17		lr	600 lr	4000 lr	558.531068	1.52717965	8434.091306	13843.60678
18		lr	600 lr	6000 lr	337.0881814	1.28034995	35342.6365	8366.570317
19		lr	200 lr	4000 fcn	34.86059083	1.63086885	14478.05283	**220.4973958**
20		lr	200 fcn	4000 fcn	410.2378013	1.653916983	13656.1507	9318.697933
21		fcn	200 fcn	4000 lr	38.131223	1.667702583	12191.8397	602.2005208
22		fcn	200 lr	4000 lr	238.9569197	1.663567483	13403.64758	5229.914058
23		lr	200 fcn	4000 lr	290.6430138	1.657428583	12567.93278	6588.58335
24		fcn	200 lr	4000 fcn	352.6849412	1.909310833	11572.93555	8292.059883

Table 6.9.

Bibliography

[KBC+18] Tim Kraska, Alex Beutel, Ed H Chi, Jeffrey Dean, and Neoklis Polyzotis. The case for learned index structures. In *Proceedings of the 2018 International Conference on Management of Data*, pages 489–504, 2018.

[LLZ+20] Pengfei Li, Hua Lu, Qian Zheng, Long Yang, and Gang Pan. Lisa: A learned index structure for spatial data. In *Proceedings of the 2020 ACM SIGMOD International Conference on Management of Data*, pages 2119–2133, 2020.

[LSD15] Jonathan Long, Evan Shelhamer, and Trevor Darrell. Fully convolutional networks for semantic segmentation. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 3431–3440, 2015.