Computer Vision: Foundations

Lecture Notes

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Week 1 Introduction

Computer Vision

- useful in consumer devices (e. g. fingerprint login on smartphone)
- is used as machine vision in quality control (e. g. check that all pixels of a screen work → rather easy task, that there are no scratches → rather hard task)
- makes life-and-death decisions (e. g. in autonomous emergency braking, cyclist and pedestrian detection → needs extremely high accuracy)
  - Example procedure: Take last n frames (e. g. $n = 11$) and decide based on them wether or not to brake
  - Need extremely low false positive rate (do not want to brake if it is not necessary)
  - Need low false negative rate
  - Need to process the data in real-time, i. e., need to process $\sim$ 30 MB input/s

Computer Vision is a compute-intensive endeavor and only two hand ful of algorithms are sufficiently efficient, i. e., work at high scale and will make it into consumer devices. We will therefore study these two hand ful of algorithms in-depth. They can then be combined in complicated pipelines. Although we will study some of these pipelines we will mainly focus on the building blocks (see Table 1.1).

Input	Output	Task
Image	0/1	Image classification
Image	One class per pixel	Semantic/pixel segmentation
Image	Which pixel belong to which instance	Instance segmentation
Image	Pose of one or more humans	Pose estimation
Video	Tracks of all targets	tracking

Table 1.1: Example tasks in computer vision {tab:ex:tas

Lecture 1.1 Linear Filters: Convolution[1]

Convolution is useful for

- Smoothing (Not SOTA)
- Edge/Blob detection
- General: Feature extraction

Has been mainstay of image analysis since it's very cheap (still matters now) and is well-understood.

1D Convolution

Consider the mean square estimator for $\{y_i\} \in \mathbb{R}$

$$\hat{y} = \arg\min_y \sum_{i=1}^{n} (y_i - y)^2$$

that is given by (can be seen by letting the derivative of the sum above be zero)

$$\hat{y} = \frac{1}{n} \sum_{i=1}^{n} y_i \,.$$

Using the same idea but introducing weights $w_i \geq 0$, i. e.,

$$\hat{y}_w = \arg\min_y \sum_{i=1}^{n} w_i (y_i - y)^2$$

yields

$$\hat{y} = \frac{\sum_i w_i y_i}{\sum_i w_i} \,.$$

If, in addition, the weights depend on the distance from x only, this can be rewritten as (note that this no is a function of x)

$$\hat{y}_w(x) = \arg\min_y \sum_{i=1}^{n} w_i (x - x_i)(y_i - y)^2$$

[1] See also Appendix B

with solution

$$\hat{y}(x) = \frac{\sum_i w_i(x - x_i)y_i}{\sum_i w_i(x - x_i)}$$

and in the case of equidistant observations this simplifies to

$$\hat{y}_l = \frac{1}{\sum_i w_{l-i}} \sum_i w_{l-i} y_i \,,$$

which can be interpreted as the convolution of the signal y and a weight function w. The Figure below demonstrates the results of smoothing a perturbed signal using two different weight functions, one being a NN kernel (that corresponds to a characteristic function of an interval) and one being a Epanechnikov kernel (that corresponds to a parabola that has been cut off at its roots).

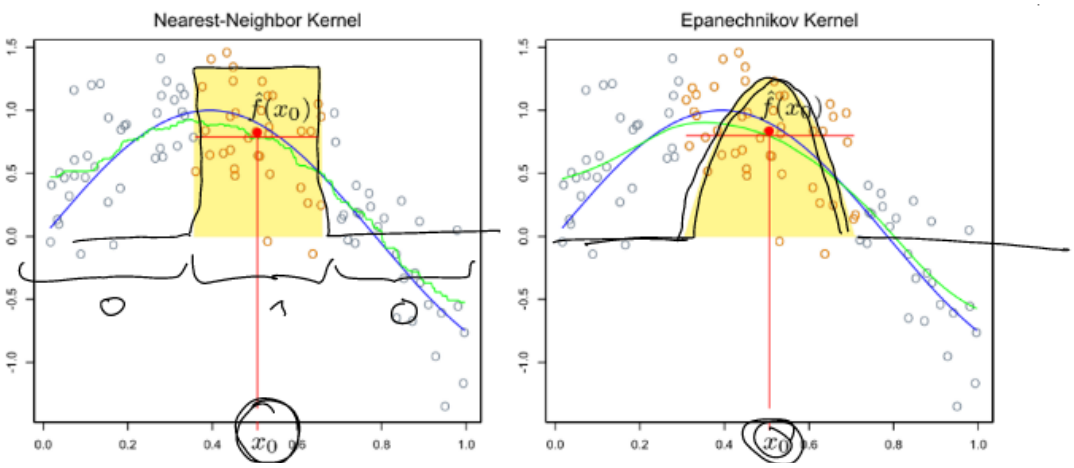


Figure 1.1: Box kernel and Epanechnikov kernel {fig:conv:k

Different filters can produce very different results ($\rightsquigarrow$ filter optimazation). This is one instance of *discrete convolution*

$$\sum_{i=0}^{n-1} f_{l-1} g_i =: (f * g)_l$$

Properties:

- Convolution is **commutative**: $f * g = g * f$
- Convolution is **associative**: $f * g * h = f * (g * h) = (f * g) * h$
  - Important in practice, especially for image analysis
- Convolution is **distributive**: $f * (g + h) = f * g + f * h$

Important convolution filters include

- $f_i \geq 0$ smoothing (see above)
- $_i = \delta_{i-s}$ shifting
- $f = 1/2(1\ 0\ -1)$ central finite difference (analogously non-central FD)
- $f = [1 \quad -1] * [1 \quad -1] = [1 \quad -2 \quad 1]$ second derivative ?

Note: 1D convolution can be written as matrix multiplication with a *Töplitz matrix*

$$\sum_i f_{l-1} g_i \qquad \text{vs.} \qquad \sum_i M_{li} v_i = [M \cdot v]_r$$

Example: Consider the convolution

What is the r in the sub of matrix mult?

$$\begin{aligned}
&[1 \quad 0 \quad -1] * [g_0 \quad g_1 \quad g_2 \quad g_3 \quad g_4] \\
&= \begin{bmatrix} 0 & 1 & & & -1 \\ -1 & 0 & 1 & & \\ & -1 & 0 & 1 & \\ & & -1 & 0 & 1 \\ 1 & & & -1 & 0 \end{bmatrix} \cdot \begin{bmatrix} g_0 \\ g_1 \\ g_2 \\ g_3 \\ g_4 \end{bmatrix},
\end{aligned}$$

where the terms in the corners arise from periodic boundary conditions (i. e., the "-1-th" term is the last term and the "$n+1$-st" term is the first term).

2D Convolution

Convolution in higher dimensions can be defined analogously. Here, we have

$$\sum_i \sum_j f_{i,j} g_{u-i,v-j} =: (f * g)(u, v)\,.$$

In image analysis f is often small (e. g. 3×3) and g large (e. g. 3840×2160).

Some filters are **seperable** which means they can be written as an outer product $f_{i,j} = a_i \cdot b_j$ This allows for storage reduction (instead of storing the full matrix it suffices to store the vectors a and b)[2]. In practice you would use libraries because with the right memory layout, clever use

[2] Aside: Some filters are not seperable but of low rank and using singular value decomposition we can find a suitable represantation such as $f_{i,j} = \sum_{k=1}^{r} a_i^k b_j^k$ with r small.

of co-processors and GPUs the speed can be drastically increased. If the filter is separable into a and b as above, we can write

$$\underbrace{\sum_i a_i \underbrace{\sum_j b_j g_{u-i,v-j}}_{\text{1D convolution of rows}}}_{\text{1D convolution of columns}}$$

There are different options to extrapolate at the boundary of the image.

Week 2 Sensing, Subsampling and interpolation

{chap:02}

Lecture 2.2 On Downsampling

To deal with very large images one often needs to downsample the imaage so that it fits into the memory of the GPU. The *wrong* appproach would be to take the first pixels, then leave out a fixed number, then take the next pixel and repeat.

Add Example images

The effect of this naïve approach can be explained as follows. Subsampling is a linear operation and can thus be written as a matrix multiplication. If we denote by a preceding downwars arrow the signal after subsampling, we can write

$$\downarrow g = h = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 \end{bmatrix} \cdot \begin{bmatrix} g_0 \\ g_1 \\ \vdots \\ g_7 \end{bmatrix} .$$

Every other sample is completely lost! Idea: Average two adjacent samples. This can be written as a convolution of a blur with the signal

$$\downarrow (b * g) = h' = \frac{1}{2} \begin{bmatrix} 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 \end{bmatrix} \cdot \begin{bmatrix} g_0 \\ g_1 \\ \vdots \\ g_7 \end{bmatrix} = \begin{bmatrix} \frac{1}{2}g_0 + \frac{1}{2}g_1 \\ \frac{1}{2}g_2 + \frac{1}{2}g_3 \\ \vdots \\ \frac{1}{2}g_6 + \frac{1}{2}g_7 \end{bmatrix} .$$

All observations contribute to the result, i. e., less information is lost. There are also other approaches. Are there optimal filters? In general, these filters will be data-dependent (this essentially is PCA), i. e., different filters for different data sets. To obtain a generally appllicable filter which is not data-dependent, we need to make some assumptions. A typical choice would be to assume the signal to be mostly low-pass (such filters will predominantly preserve low frequencies). A perfect low-pass filter

- eliminates all frequencies above the new Nyquist limit (highest frequency that can be represented by sampling a signal uniformly), and
- leaves frequencies below the Nyquist limit completely untouched.

The optimal choice is (no proof given)

$$\operatorname{sinc} x = \frac{\sin \pi x}{\pi x}$$

Finish this lecture

Lecture 2.3 Upsampling/ Interpolating an Image

Finish this lecture

Week 3 CNNs: Deep Learning

{chap:03}

Lecture 3.1 Shallow and Deep Learning

Example: Pixel classification/ semantic segmentation. State of the art before 2000:

1. Take image
2. Compute features
3. Construct decision rule **by hand** (e. g. select foreground and background)
4. Mark pixels according to decision rule

State of the art 2000–2012:

1. Take image
2. Put into filter bank that produced lots of images that summarise local contexts (i. e., produce features)
3. Take all of the images and classify using a shallow classifier (Support vector machine, random forest)

The second step is done by the user, i. e., the features are selected by hand. After 2012: Deep learning. Take the image and repeatedly apply a set of filters + non-liearity (the "layers"). At the very end use a shallow classifier (in NN: perceptron/ logistic regression). The layers are trained jointly!

Week 4 CNN architectures

{chap:04}

Week 5 Instance segmentation

{chap:05}

Week 6 Shortest Paths

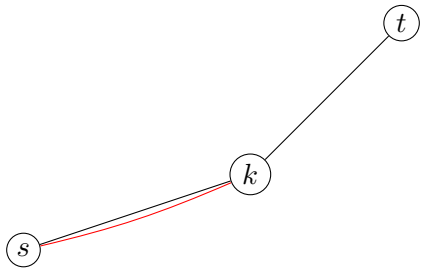
{chap:06}

Examples where shortest path algorithms are used in computer vision

- Intelligent scissors (GIMP)/ Magnetic lasso (Photoshop)
- Geodesic matting/ seeded segmentation
- segmented least squares (estimate piecewise constant best approximation, but a cost is imposed on jumps in the resulting function)

Basic approach to tackle shortest path problems: **dynamic programming**. Generally problems where dynamic programming techniques are applied are required to have the *optimal subproblem* property, which means that the optimal solution to a partial problem has to be part of the overall optimal solution.

Example (Shortest path)**.** Consider the following graph:



We do not know if the shortest path from s to t will go through k; if it does go through k, however, the the shortest path $s \to k$ must be part of the globally optimal shortest path $s \to t$ (red path).

It only makes sense to use dynamic programming if the solutions of the subproblems can be re-used multiple times. In methods where the paths are acyclic, the dynamic programming approach grows only linearly with the problem size which is the best possible complexity one can expect.

Lecture 6.2 Shortest path algorithms

{sec:shortp

In the following, the length of a path is defined to be the sum of the edge weights.

Dijkstra and Viterbi with example from lecture

Lecture 6.3 Scanline optimization/ Stereo disperity estimation

Setting: Two cameras, slighlty shifted or rotated and rectified, take two pictures of the same scene. We want to estimate the "depth" of the elements in the scene. As illustrated in the image below, the two pictures are evaluated along a horizontal scanline (the example is taken from `http://lunokhod.org/?p=1356`).

Figure 6.1: Original rectified stereo images

For each pixel along that line, each possible disparity result is evaluated. The cost of each pixel along a scanline can then be stacked into a matrix; the cost for each pixel on the scanline in the example image versus each possible disparity value is shown in the Figure below. The solution for the disparity along this scanline is then the path through this matrix (image) that has minimum costs (dark areas) with some smoothness constraint imposed (i. e., , the shortest path). The process is repeated for every horizontal scanline; the resulting disparity map is given in Figure 6.3. Since each scanline is treated individually, the result might be not very smooth in the y-direction and one can apply different smoothing techniques to obtain a disparity map this is smooth in both the x- and y-direction.

Figure 6.2: All possible disparities along one scanline

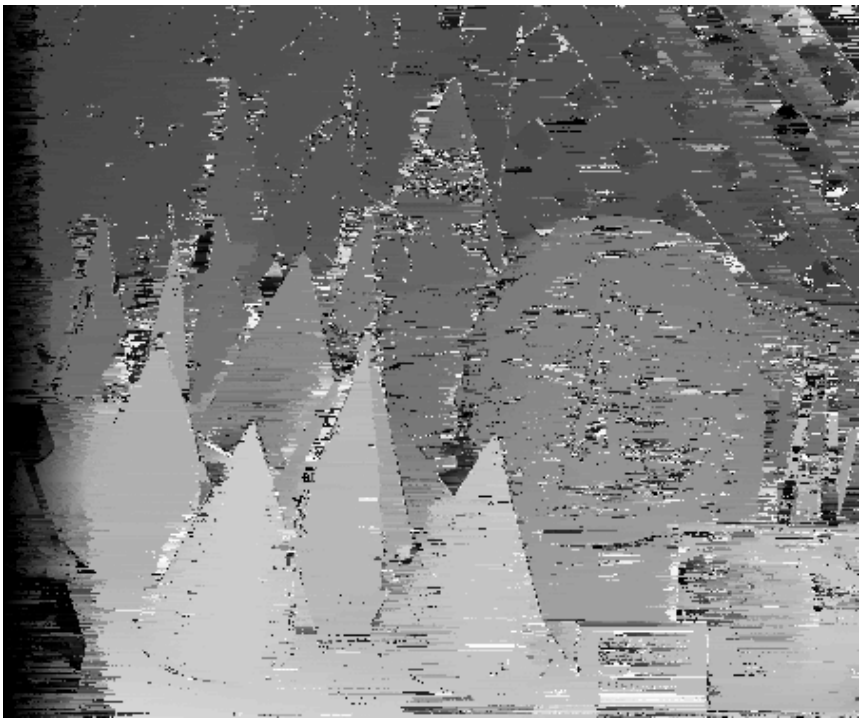


Figure 6.3: Disparity map for the example above {fig:disper

MAP – maximum a posteriori estimation

The problem above can be rewritten as: Find

$$\begin{aligned}\min_{z_1,\dots,z_n} e(z) &= \min_{z_1,\dots,z_n} \sum_{i=1}^{n-1} \psi_{i,i+1}(z_i, z_{i+1}) \\ &= \min_{z_1,\dots,z_n} \psi_{n-1,n}(z_{n-1}, z_n) + \cdots + \psi_{2,3}(z_2, z_3) + \psi_{0,1}(z_0, z_1) \\ &= \min_{z_n} \left(\min_{z_{n-1}} \psi_{n-1,n}(z_{n-1}, z_n) + \cdots + \min_{z_2} \Big(\psi_{2,3}(z_2, z_3) + \underbrace{\min_{z_1} \psi_{1,2}(z_1, z_2)}_{m_{1\to 2}(z_2)} \Big) \cdots \right),\end{aligned}$$

where the vectors z_i denote the "state" at time i (i. e., , the ith column of the graph). Note that the components of these vectors are either one or zero, and they have to sum up to one. In other words, these state vectors denote in the end which of the respective nodes of the graph lie in the shortest path (see also the Figure below).

Lecture 6.4 Segmented least squares

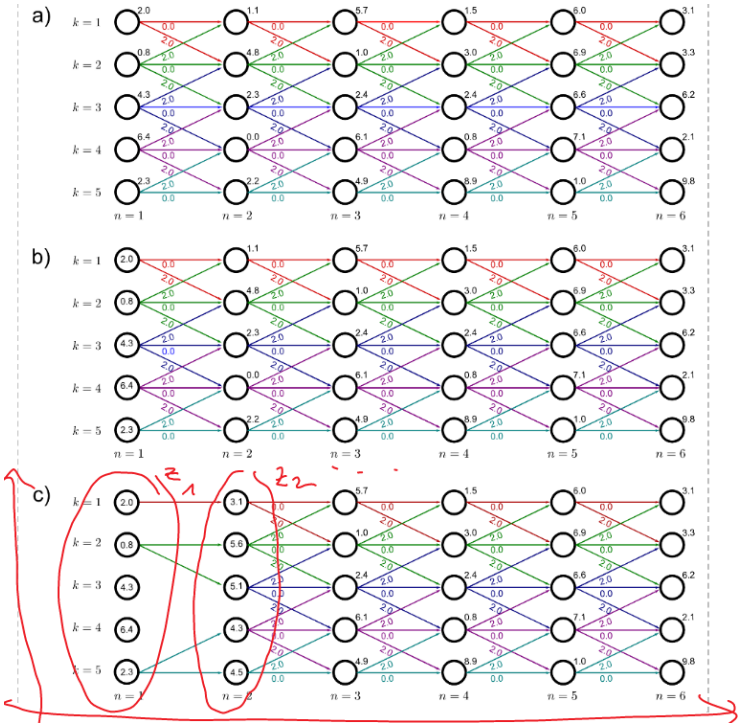


Figure 6.4: State vectors

Week 7 Message passing

{chap:07}

Lecture 7.1 Why dynamic programming on trees?

In many applications in computer vision we want to model connectivity. Consider the segmentation of blood vessels in a lung. These vessels form a tree and thus it is natural to pose a connectivity constraint in a segmentation task. For example, this leads to the connections of previously unconnected regions which in turn reduces the noise in the computed segmentation.

Trees are also a very natural choice for modeling hierachies. For instance, in cell segmentation, one can represent the segmented cells in a tree structure where children correspond to the individual parts of a "clumped" cell, see also the Figure below.

We can also model (simple) constellations; applications are facial feature detection in images. Here, the parts of a face (eyes, nose, mouth etc.) are modeled in a tree structure where the edges can be interpredted as springs in a star configuration to the nose, see the Figure below. Extending these springs or posing them in certain positions that do not make sense has a high cost, and thus, plausible configurations that correspond to realistic facial features correspond to low costs.

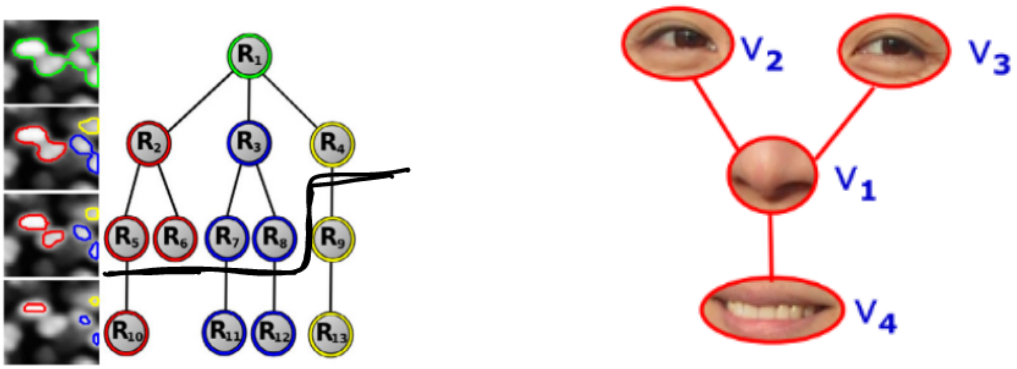


Figure 7.1: Two example of how trees can be used to model hierachies and simple constellations in computer vision applications.

Week 8 Widest paths

{chap:08}

Lecture 8.2 Shortest vs. widest paths

In the "classical" shortest path algorithms discussed so far the length of a path was given by the **sum** of the edge weights. In this chapter we discuss widest path (bottleneck shortest path/ maximum capacity path/ minimax path) methods. Here, the length of a path is given by the **single largest** (smallest) edge weight.

1D example from lecture

Lecture 8.3 Minimax paths and Prim's algorithm

Recall Disjkstra's Algorithm from a previous lecture. At each iteration we do the following: take the node v from the list of nodes that have not yet been visited with the smallest distance from the starting node. Denote by $e = (v, u)$ the edge from v to u. In the "classical" Dijkstra algorithm (where we want to compute the shortest path from the starting vertex to each of the other nodes) we now do the following: For each edge $e(v, u)$, u in the forward-star (i. e., the set of edges connecting "outgoing" nodes) of v, update the distance to the node u according to

$$d(u) = \min\{d(u), d(v) + w(e)\}\,,$$

where $w(e)$ is the edge weight of e. If we want to compute the minimax path, we can still use the same idea; however, we instead update $d(u)$ by

$$d(u) = \min\{d(u), \max\{d(v), w(e)\}\}\,,$$

since we are only interested in the single most expensive edge on the way from the starting node to u. This change essentially leads to a related algorithm, called (eager) Prim's algorithm. Instead of finding the shortest path we now build a spanning tree, i. e., a minimal tree that contains every node of the graph. We see that the shortest path problem and the minimax problem are in essence the same problem only with different definition of what we mean by the distance between two nodes. In other words: both a shortest path problems with a different notion of what it means to be short. Algebraic graph theory, which is discussed in the next chapter, provides a unified framework to better understand this relationship.

Lecture 8.4 All-pairs minimax paths and the minimum spanning tree

A minimum spanning tree (MST) is a subgraph with the shape of a tree (i. e., it contains no loops) that is spanning (i. e., each node can be reached from any other in the subgraph) whose sum of edge weights is minimal. Every edge not in the MST is at least as large/ heavy/ costly as all other edges in the loop induced by adding that edge to a MST ("cycle property"), see Figure 8.1.

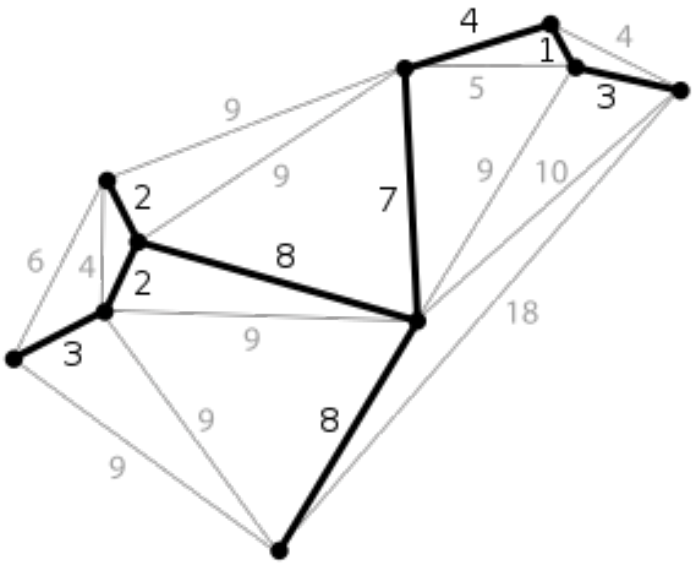


Figure 8.1: A minimum spanning tree. {fig:mst}

It turns out that the path from some node u to some other node v in the MST of an undirected graph is a minimax path between u and v in that graph. The converse is not true in general: the union of the minimax paths between all nodes is not necessarily a tree and hence in particular it need not be the MST.

Further, in an undirected graph with non-negative edge weights, the minimax distance between pairs of vertices defines an **ultrametric**.

Definition. An ultrametric d_{uv} is a metric with the following additional property

$$d_{uv} \leq \max\{d_{uw}, d_{wv}\}\,,$$

the so called *strong triangle inequality* (or ultrametric inequality).

Note that the ultrametric inequality implies that there exists a permutation (i, j, k) of three vertices (u, v, w) such that

$$d_{ij} \leq d_{ik} = d_{kj} \,.$$

This, in trurn, implies that a set of points in an ultrametric space can always be represented as leaves in a binary rooted tree that all have the same distance from the root (a so called *ultramteric tree*). Consider again the MST from Figure 8.1. We can build the corresponding ultrametric tree as follows. Start with the nodes that have the smallest distance, draw them as leaves of a tree and connect them to the same parent that is located at the "height" that corresponds to their distance (see Figure below; we start with the two nodes on the top right that are connected by an edge with weight one). Then we take the node that is next closest and connect the subtree from the previous step to this node (in the Figure 8.2, now all vertices within the green ellipse are processed). We then repeat this process until no more nodes are left. The ultrametric distance between two nodes is then given by the height of their least common ancestor in the ultrametric tree. Note that there exist data structures such that finding the least common ancestor of two nodes is an $\mathcal{O}(1)$ operation.

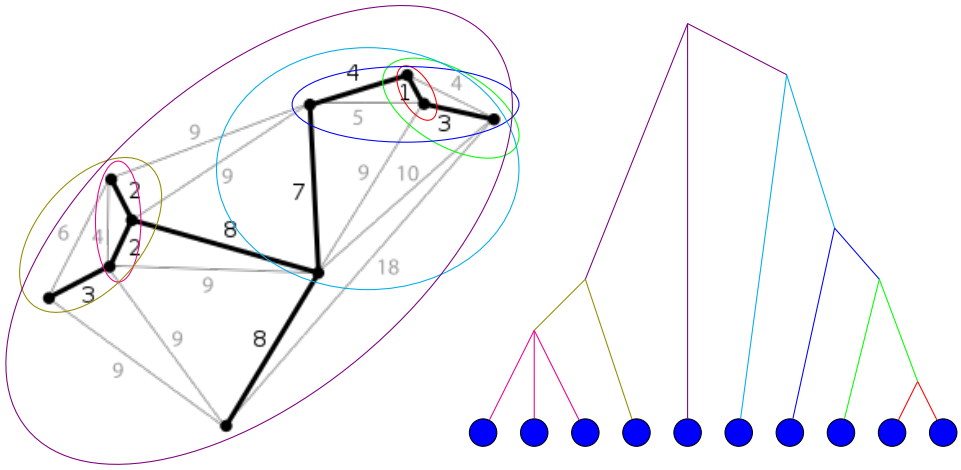


Figure 8.2: Minimum spanning tree and corresponding ultrametric tree. The ultrametric tree is built by repeatedly finding the nodes that have the smallest distance to the nodes already processed (indicated by the ellipses). {fig:ultram

Lecture 8.5 Seeded watershed segmenation

Finish lecture

Lecture 8.6 Learned watershed

Finish lecture

Week 9 Algebraic graph theory

{chap:09}

Summary In this lecture we discuss a unified framework that allows to us to understand many different path problems (shortest paths, widest paths, existence of paths etc.) in a single context. This will be done by generalising the notion of matrix multiplications which will allow us to write shortest path, widest path and path existence problems in terms of matrix powers.

Lecture 9.1 Generic single source shortest paths

Recall again Dijkstra's algorithm. In the inner loop we look at each edge $e = (v, u)$ in the forward star of the current looked-at node v. We discussed two different types of Dijkstra's algorithm that only differ in the way the distance $d(u)$ from the starting vertix is updated (sum of all edge weights in shortest path; single most expensive edge weight in minimax path). We now discuss a third variant. Here, we want to answer the question whether or not there is a path at all. However, this is a special case of the above discussed methods where we encode the edges of the original path as 0 if there is a connection between the nodes and ∞ if there is no edge between two vertices. Alternatively, we can formulate this problem as follows. Consider a fully connected graph with edge weights $\{\texttt{FALSE}, \texttt{TRUE}\}$. In the initialisation phase of Dijkstra's algorithm, we set

$$d(s) = \texttt{TRUE} \quad \text{and} \quad d(u \in V \setminus \{s\}) = \texttt{FALSE}\,.$$

The update of the "distance" $d(u)$ then looks as follows

$$d(u) = \texttt{OR}(d(u),\, \texttt{AND}(d(v), w(e)))\,.$$

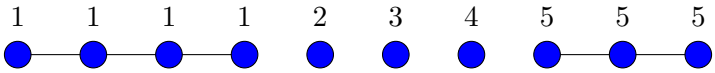
In other words: along a path, each single edge weight has to be `TRUE` (this is the inner `AND`) while of many different paths only one has to be `TRUE` (this is the outer `OR`) for $d(u)$ to be set to `TRUE`. Example applications for this problem are

- In computer vision this is often used when training a network that is supposed to detect some feature and one wants to collect all pixels that are connected (and lie above a certain threshold). This is usually not done using the approach introduced above but it the problem itself can still be solved by an algorithm that falls in this general framework discussed in the following.
- Other problems include: reachability, percolation (simulate if water will reach the bottom when flowing through a certain network), connectedness or maze solving.

We see that all the different kinds of Dijkstra's algorithm are only certain special cases of a generic single-source generalized-shortest-distance algorithm that can find shortest and widest path as well as determine whether or not there is a path at all etc. Note, however, that these algorithms need not be the most efficient ones solving the particular problem (e. g. for the problem of finding if there exists a path one would implement the algorithm using a disjoint-set/ union-find data structure where each node is mapped to an index such that nodes with same index are connected).

In 1D there is simple $\mathcal{O}(N)$ algorithm to determine whether or not two nodes are connected. Consider the following simple graph.

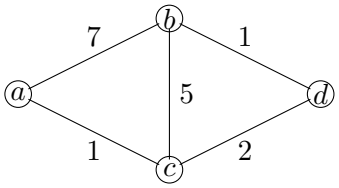
We now start from the left and assign an arbitrary label to the first node. If the next node is connected to the current node then we assign to it the same label. Otherwise we choose a different label. Using numbers as labels, our graph from above might then look like this. Checking if two



nodes are connected is now simply achieved by checking whether or not their assigned node labels are the same. Assigning the node labels is obviously in $\mathcal{O}(N)$, where N is the number of nodes and checking two nodes is in $\mathcal{O}(1)$.

Lecture 9.2 All-pairs shortest paths and the distance product

Consider the following graph and its associated adjency matrix. where the entries (a, d) and (d, a)



$$A = \begin{array}{c} \\ a \\ b \\ c \\ d \end{array} \begin{array}{c} \begin{array}{cccc} a & b & c & d \end{array} \\ \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} \end{array}$$

are set to ∞ since there is no connection between these two vertices. Now, recall that usual matrix

multiplication formula. If we multiply two matrices $C = AB$, we have

$$[C]_{ij} = \sum_k [A]_{ik} \cdot [B]_{kj} \,.$$

We will now define different kinds of "matrix multiplications" where we replace at least one of the sum (green) and product (red). We start by replacing the sum by taking a minimum and replacing the product by a sum. The resulting operation looks as follows.

$$[C]_{ij} = \min_k [A]_{ik} + [B]_{kj} \,.$$

If we compute the "matrix product" $A \cdot A$ for the adjancy matrix from the example above using this formula we obtain

$$A^2 = \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 6 & 1 & 3 \\ 6 & 0 & 3 & 1 \\ 1 & 3 & 0 & 2 \\ 3 & 1 & 2 & 0 \end{bmatrix} .$$

The matrix A obviously contains the cost to go from one node to another with at most one hop. The matrix A^2, computed using the min sum matrix product now contains the cost of the shortest path from all nodes to all other nodes with at most two hops! The entries with the yellow background in the matrix above correspond to paths where in two hops we found a shorter path as compared to using just one hop.[1]

If we now multiply this result again by A, i. e., if we compute $A \cdot A^2$, we obtain the cheapest cost from all nodes to all other nodes while taking at most three hops. The result is as follows

$$AA^2 = \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} \begin{bmatrix} 0 & 6 & 1 & 3 \\ 6 & 0 & 3 & 1 \\ 1 & 3 & 0 & 2 \\ 3 & 1 & 2 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 4 & 1 & 3 \\ 4 & 0 & 3 & 1 \\ 1 & 3 & 0 & 2 \\ 3 & 1 & 2 & 0 \end{bmatrix} .$$

We again highlighted the costs that have changed. If repeat this process another time, the matrix no longer changes since in a graph with four nodes, we can only do three hops before arriving at nodes that have been visited on the path. Depending on the graph, this "convergence" might happen earlier.

We can use this iterated generalised matrix multiplication to also solve minimax path and path-existence problems that we have discussed earlier. For the minimax path we define the matrix

[1] This is in essence a matrix formulation of the Floyd-Warshal algorithm.

product as

$$[C]_{ij} = \min_k \max \left\{ [A]_{ik}[B]_{kj} \right\}.$$

Again using the example from the beginning of the section, after two hops we have

$$A^2 = \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} = \begin{bmatrix} 0 & 5 & 1 & 2 \\ 5 & 0 & 2 & 1 \\ 1 & 2 & 0 & 2 \\ 2 & 1 & 2 & 0 \end{bmatrix},$$

and after three hops

$$AA^2 = \begin{bmatrix} 0 & 7 & 1 & \infty \\ 7 & 0 & 5 & 1 \\ 1 & 5 & 0 & 2 \\ \infty & 1 & 2 & 0 \end{bmatrix} \begin{bmatrix} 0 & 5 & 1 & 2 \\ 5 & 0 & 2 & 1 \\ 1 & 2 & 0 & 2 \\ 2 & 1 & 2 & 0 \end{bmatrix}, = \begin{bmatrix} 0 & 2 & 1 & 2 \\ 2 & 0 & 1 & 2 \\ 1 & 2 & 0 & 2 \\ 2 & 1 & 2 & 0 \end{bmatrix}.$$

Again, the result after four hops is the same as after three. Lastly, for the path existence problem we let

$$[C]_{ij} = \underset{k}{\texttt{OR}} \left\{ [A]_{ik} \ \texttt{AND} \ [B]_{kj} \right\}.$$

As mentioned above, the edge weights are now either `T` = `TRUE` or `F` = `FALSE` depending on whether or not an edge connects the two nodes in consideration. Thus the matrix after one hop is given by

$$A = \begin{bmatrix} \texttt{T} & \texttt{T} & \texttt{T} & \texttt{F} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{F} & \texttt{T} & \texttt{T} & \texttt{T} \end{bmatrix}.$$

The result after two hops is then given by

$$A^2 = \begin{bmatrix} \texttt{T} & \texttt{T} & \texttt{T} & \texttt{F} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{F} & \texttt{T} & \texttt{T} & \texttt{T} \end{bmatrix} \begin{bmatrix} \texttt{T} & \texttt{T} & \texttt{T} & \texttt{F} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{F} & \texttt{T} & \texttt{T} & \texttt{T} \end{bmatrix} = \begin{bmatrix} \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \\ \texttt{T} & \texttt{T} & \texttt{T} & \texttt{T} \end{bmatrix},$$

after which the result obviously does not change anymore. Note that we can speed the method up by using the fact that after we have computed $A^2 = A \cdot A$ we can use this to compute $A^4 = A^2 \cdot A^2$ etc. In practice one would also use optimized matrix multiplication algorithms and/ or use approximations of the matrices (e. g. one might only use randomly selected rows and columns).

Note that we did consider all-pairs path problems. In practice one does often not have enough memory to store this matrix and thus, instead of applying these algorithms to the original image, they are applied to patches or superpixels.

Lecture 9.3 The algebraic path problem

We have just seen that single source (generalised Bellmann-Ford) and all pairs shortest paths (generalised Floyd-Warshall, distance matrix product) algorithms can be seen as special cases of one basic algorithm. More precisely, they can be seen as multiple incarnations of matrix multiplications on different *commutative semirings*. We start with a short recap on monoids.

Definition. A *monoid* $(\mathbb{K}, \cdot, \overline{e})$ is a set $\mathbb{K}$ with a binary operation $\cdot : \mathbb{K} \times \mathbb{K} \to \mathbb{K}$ such that for all $a, b, c \in \mathbb{K}$, the equation

$$(a \cdot b) \cdot c = a \cdot (b \cdot c)$$

holds and an identity element $\overline{e}$ which satisfies

$$a \cdot \overline{e} = \overline{e} \cdot a\,, \quad \text{for all } a \in \mathbb{K}\,.$$

If additionally we have $a \cdot b = b \cdot a$ for all $a, b \in \mathbb{K}$ we call the monoid *commutative*.

We can now define a semiring.

Definition. A semiring is a system $(\mathbb{K}, \oplus, \otimes, \overline{0}, \overline{1})$ such that

1. $(\mathbb{K}, \oplus, \overline{0})$ is a commutative monoid,
2. $(\mathbb{K}, \otimes, \overline{1})$ is a monoid (not necessarily commutative),
3. $\otimes$ distributes over $\oplus$, i. e., for all $a, b, c \in \mathbb{K}$ we have

$$\begin{aligned}(a \oplus b) \otimes c &= (a \otimes c) \oplus (b \otimes c)\\ c \otimes (a \oplus b) &= (c \otimes a) \oplus (c \otimes b)\,,\end{aligned}$$

   and
4. $\overline{0}$ is an annihilator for $\otimes$, i. e., $a \otimes \overline{0} = \overline{0} \otimes a = \overline{0}$ for all $a \in \mathbb{K}$.

The semiring is said to be commutative is $\otimes$ is commutative.

Given a semiring, one can define the associated matrix semiring $M_n(\mathbb{K})$ of $n \times n$ matrices with entries in $\mathbb{K}$. Note that commutativity does not necessarily transfer from $\mathbb{K}$ to $M_n(\mathbb{K})$. This is what we essentially used in the previous section where we discussed different matrix semirings such as the minmax semiring.

We now consider the algebraic path problem. We begin with the following equation that defines the entries of a distance matrix $[D]_{st}$ from a source s to a target t as

$$[D]_{st} = \bigoplus_{P \in \mathcal{P}_{st}} \bigotimes_{e \in P} w_e \,,$$

where $\mathcal{P}_{st}$ is the set of all paths P from s to t and $\otimes$ is taken over all edges within P. Here $\otimes$ is the semiring multiplication and is applied along the path whereas the semiring addition $\oplus$ is done between paths. For instance, when we solve the shortest path problem, we can interpret this as solving the algebraic path problem in the $(\min, \mathrm{sum})$ semiring.

Lecture 9.4 Infimal convolution, morphology and the Euclidean distance transform

We discussed earlier that convolution can be written as a matrix multiplication with a Toeplitz matrix. We can now define a generalised notion of convolution similar to how we generalised matrix multiplication in the previous section. There, we defined matrix multiplication over a semiring as

$$[AB]_{ij} = \bigoplus_k [A]_{ik} \otimes [B]_{kj} \,.$$

Analogously, one can define a generalised inner product

$$\langle a, b \rangle = \bigoplus_k a_k \otimes b_k \,.$$

With the same approach, we can define convolution on different semirings, e. g. on the sum-product semiring

$$f \star g(x) = \sum_y f(x - y) \cdot g(y) \,,$$

which results in the "standard" convolution that we have seen earlier or on the min-sum semiring

$$f \star g(x) = \inf_y \left(f(x - y) + g(y) \right) \,,$$

which results in the important generalisation of the *infimal* or *tropical convolution*.

Week 10 Tracking

{chap:10}

Appendices

Week A Machine Learning primer

This overview is based on the chapter `https://www.deeplearningbook.org/contents/ml.html`.

Lecture A.1 Learning Algorithms

What does the *learning* mean in machine learning? Popular definition is due to Mitchell:

> A Computer program is said to learn from experience E with respect to some class of tasks T and performance measure P if its performance at tasks in T, as measured by P, improves with experience E.

In the following, we give intuitive descriptions and examples of what T, P and E might be in practice.

The Task T

Task is not the process of learning itself. Learning is our means of attaining the ability to perform the task (Example: If we want the robot to walk, walking is the task). Usually, tasks are described in terms of how the machine should process an **example**. An example conists of **features** that have been quantitatively measurred from something that we want the machine learning system to process. Typically, we represent an example as $\mathbf{x} \in \mathbb{R}^n$ where each x_i is another feature (features of images $\hat{=}$ values of the pixels).

Some of the most common ML tasks are

- **Classification.** Here, the system is asked to put the input into one of k categories. Typically, this is modelled as a function $f : \mathbb{R}^n \to \{1, \dots, k\}$. Other variants are possible, where f outputs a probability distribution over the different classes. A popular example is object recognition.
- **Regression.** Predict a numerical value given some input, i. e., output a function $f : \mathbb{R}^n \to \mathbb{R}$.
- **Transcription.** Here, the system is asked to observe a relatively unstructred representation of some data and transcribe into textual form (Example: transform photograph of text into sequence of ASCII characters; Speech recognition).

- **Machine translation.** Convert sequence of symbols from one language into sequence of characters of another language.
- **Structured output.** Broad category, involving any task that outputs a vector with important relationships between different elements. Examples from above also fall in this category; other examples are formation of sentences that describe what is shown in an image (here the words in the output have the relationship that they must form a correct sentence).
- **Anomaly detection.** Flag some events or objects from some set as being unusual (example: credit card fraud detection).

Add the missing tasks (not that important?)

These tasks are only examples; many other types of tasks are possible.

The Performance Measure P

To quantitatively measure the learning process we need to be able to evaluate the algorithm's performance. To that end, a performance measure is required that is usually specific to the task. For tasks as classification we often measure the **accuracy** of the model (= the proportion of examples for which the model produces the correct output). Alternatively, we can measure the proportion of examples that result in incorrect output (**error rate**). We often refer to the error rate as the expected 0-1 loss (0 if an example is correctly classified, 1 if it is not). For continuous examples we need a continuous performance metric (e. g. , the average log-probability the model assigns to some examples). It is often difficult to define a performance measure that corresponds well to the desired behavior of the system (What should be measured? What if measuring is impractical or even intractable? How can alternative criteria be designed?).

We are usually interested in the perfomance of the ML algorithm on data it has never seen before; thus the performance is measured on a **test set**. This set is different from the training data.

The Experience E

ML methods can be broadly categorized as **unsupervised** and **supervised**. They differ in the kind of experience they are allowed to have during the training. Most of the algorithms we consider have access to an entire dataset, i. e., a collection of many examples which themselves consist of features. Sometimes these examples are called data points. Examples for supervised learning algorithms have additional **labels** or **targets**. Note, that unsupervised learning and supervised learning are not formally defined and the lines between them are often blurred.

A common way of describing a dataset is with a **design matrix** that contains in each of its rows a different example. The columns correspond to the features. Of course, this implicitly requires each example to be a vector of the same size which is not always possible (e. g. , photographs with different widths and heights). In these cases, design matrices are not the right choice of representation. In the case of supervised learning, where each example contains a label or target, we work with a design matrix of observations $\boldsymbol{X}$ and a vector of labels $\mathbf{y}$, with y_i providing the label for example i (Of course, the label can be more than just a single number).

Week B Convolution primer

{chap:appen

This overview is mainly based on the paper `https://arxiv.org/pdf/1603.07285.pdf` and the chapter `https://www.deeplearningbook.org/contents/convnets.html`.

Lecture B.1 Intro

Generally, a discrete convolution is a linear transformation that preserves ordering in the signal (such as width and height axis in images, time axis in sound clips). The figure below shows an example of a discrete convolution. The light blue grid is called the *input feature map* (multiple feature maps are possible, e. g. when convoluting the different color channels of an image). The shaded are is referred to as the *kernel*. The results (in green) are the *output feature maps*.

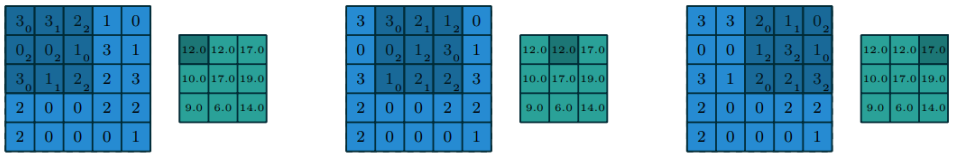


Figure B.1: Discrete convolution

{fig:conv:e

The figure is an instance of a 2-D convolution but it can be generalised to N-D convolutions. The output size o_j of a convolutional layer along an axis j is affected by

- i_j: input size along the axis
- k_j: kernel size along the axis
- s_j: stride along the axis (distance between to consecutive positions of the kernel)
- p_j: zero padding along the axis

For instance, Figure B.2 shows a 3×3 kernel applied to a 5×5 input padded with a 1×1 border of zeros using 2×2 strides. Note that strides can be interpreted also as follows. Moving the kernel by, e. g. , hops of two is the same thing as moving it by hops of ibe but retaining only odd output elements.

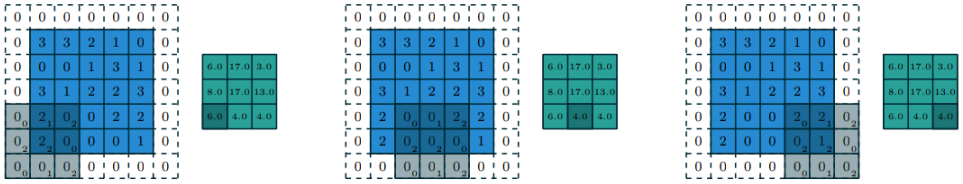


Figure B.2: Different discrete convolution

{fig:conv:e

Lecture B.2 The Convolution Operation

In the most general form, convolution is an operation of two functions of a real-valued argument. Take this example: Suppose we track a spaceship using a laser sensor that provides a single output $x(t)$, the position of the spaceship at time t, where both x and t are real-valued. Now suppose this sensor is somewhat noisy. To obtain less noisy estimates of the position, we want to average over severale measurements. We would like to have a method that weighs more recent measurements more heavy. To that end, we define a weighting function $w(a)$, where a is the age of the measurement. If we apply such a weighted average operation at every moment, we obtain a new function s providing a smoothed estimate of the position of the spaceship

$$s(t) = \int x(a)w(t-a)\,\mathrm{d}a\,.$$

This operation is called **convolution** and is typically denoted with an asterisk, i. e., $s(t) = (x * w)(t)$.

In a machine learning context, the first argument (x, in this example) is usually called the **input**, and the second argument (w) is referred to as the **kernel**. The output is called the **(output) feature map**.

In most of our examples, we will encounter discrete time steps and thus deal with *discrete convolution*

$$s(t) = (x * w)(t) = \sum_{a=-\infty}^{\infty} x(a)w(t-a)\,.$$

The inputs and kernels are tensors that are represented as multi-dimensional arrays (e. g. images $\hat{=}$ matrices). We assume that only for a finite set of points are these functions not zero because otherwise they could not be implemented on a computer with finite storage. The summations then reduce to summation over a finite number of array elements.

Often, we use convolutions over more than one axis at a time. For example, if the input is an

image I the kernel K will probably also be 2D

$$S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(m,n)K(i-m, j-n)\,.$$

Since convolution is commutative, we can equivalently write

$$S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i-m, j-n)K(m,n)\,,$$

which is often more straightforward to implement. Convolution is commutative because the kernel is flipped (i. e., as m increases the index into the input increases whereas the index into the kernel decreases). Since the commutative property is often not an important property in a neural network implementation, many libraries implement a related function called the **cross-correlation** and often call this also convolution

$$S(i,j) = (I * K)(i,j) = \sum_m \sum_n I(i+m, j+n)K(m,n)\,.$$

Discrete convolution can be viewed as matrix multiplication. For example, univariate discrete convolutions are equivalent to multiplication by a **Toeplitz** matrix (each row is a shifted version of the row above). In 2D, convoltion corresponds to a **doubly block circulant matrix**. In most cases, these matrices are sparse.In the most general form, convolution is an operation of two functions of a real-valued argument. Take this example: Suppose we track a spaceship using a laser sensor that provides a single output $x(t)$, the position of the spaceship at time t, where both x and t are real-valued. Now suppose this sensor is somewhat noisy. To obtain less noisy estimates of the position, we want to average over severale measurements. We would like to have a method that weighs more recent measurements more heavy. To that end, we define a weighting function $w(a)$, where a is the age of the measurement. If we apply such a weighted average operation at every moment, we obtain a new function s providing a smoothed estimate of the position of the spaceship

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