Convolutional Layers: Space and Time

In our introductory examples

- The non-feature dimension of output $\mathbf{y}_{(l)}$
- Is identical to the non-feature dimension of input $\mathbf{y}_{(l-1)}$

There are different choices we can make when "sliding" the kernel over the input.

These choices impact

- The size of the non-feature dimension of the output
- And, in turn, the time requirements of subsequent layers (because of the size)

Let's do some quick calculations and then show choices for controlling the space consumed by $y_{(l)}$.

CNN Math: Time versus number of parameters

In designing a Neural Network we are confronted with choices

- how many layers
- width (number of features) at each layer

When Convolutional layers are included, there are additional choices

- size f of filter
- increment with which we slide the kernel over the non-feature dimensions locations

In the absence of a science defined optimal values for the choices

- we resort to empirical studies
- treat the choices as hyper-parameters
- establish a Performance Metric and a set of Benchmark examples
- examine the trade-off between Performance Metric and hyper-parameter choice.

One element in the trade-off involves external costs

- amount of space (memory)
- amount of time

We explore these costs in this section.

Consider input layer $(l-1)$ with

- N non-feature dimensions
- $n_{(l-1)}$ feature maps/channels

  $||\mathbf{y}_{(l-1)}|| = (d_{(l-1),1} \times d_{(l-1),2} \times \ldots d_{(l-1),N} \times n_{(l-1)})$

Layer l will apply a Convolution that preserves the non-feature dimensions

$$||\mathbf{y}_{(l)}|| = (d_{(l-1),1} \times d_{(l-1),2} \times \ldots d_{(l-1),N} \times n_{(l)})$$

For simplicity of presentation: consider the case when $N = 2$.

How many weights/parameters does layer l consume (i.e, what is size of $\mathbf{W}_{(l)}$) ?

- Each kernel $\mathbf{k}_{(l),j}$
    - Has non-feature dimension $(f_{(l)} \times f_{(l)})$
    - And "depth" $n_{(l-1)}$ (to match the number of input feature maps/channels)
- There are $n_{(l)}$ kernels in layer l

So the size of $W_{(l)}$ (ignoring the optional bias term per output feature map)

$$||\mathbf{W}_{(l)}|| = n_{(l)} * (n_{(l-1)} * f_{(l)} * f_{(l)})$$

The part of the product that most concerns us is $(n_{(l)} * n_{(l-1)})$

- Values for $n_{(l)}, n_{(l-1)}$ in $\{32, 64, 256\}$ are not uncommon !
- Hence $||\mathbf{W}_{(l)}||$ is often easily several thousand
- State of the art image recognition models use *several hundred million* weights !

How many multiplications (in the dot product) are required for layer l?

- We will ignore additions (the part of the dot product that reduces pair-wise products to a scalar, and for the bias)
- Each kernel $\mathbf{k}_{(l),j}$ of dimension
$$(f_{(l)} \times f_{(l)} \times n_{(l-1)})$$
- Applied over each location in the $(d_{(l-1),1} \times d_{(l-1),2})$ non-featuer dimension of the input layer $(l-1)$
- There are $n_{(l)}$ kernels in layer l

So the number of multiplications

$$n_{(l)} * (d_{(l-1),1} * d_{(l-1),2}) * (n_{(l-1)} * f_{(l)} * f_{(l)})$$

Consider a grey-scale image of size $(d_{(l-1),1} * d_{(l-1),2}) = (1024 \times 1024)$

- Lower than your cell-phones camera !
- Easily several *million* multiplications

Expect the time to train a Neural Network with Convolutional layers to be long !

- That's why GPU's are important in training
- But GPU's have limited memory so space is important too
    - Can control with batch size

All of this ignores the final layer L

- Often a Fully Connected layer implementing Regression or Classification
- With n_L output features
    - e.g., For Classification over classes in set C, $\mathbf{y}_{(L)}$ is a One Hot Vector of length $n_L = ||C||$

Suppose layer $(L-1)$ has dimension

$$||\mathbf{y}_{(L-1)}|| = (d_{(L-1),1} \times d_{(L-1),2} \times n_{(L-1)})$$

Before we can use it as input to the Fully Connected Layer L we flatten it to a vector of length

$$(d_{(L-1),1} * d_{(L-1),2} * n_{(L-1)})$$

The number of weights (ignoring biases) and multiplications is

$$||W_L|| = n_{(L)} * (d_{(L-1),1} * d_{(L-1),2} * n_{(L-1)})$$

- $n_{(L)} * n_{(L-1)}$ on the order of several thousand
- $(d_{(L-1),1} * d_{(L-1),2})$ on the order of several million, for images

This may not even be feasible !

Thus, controlling the size of each layer $\mathbf{y}_{(l)}$ is of great *practical* importance.

Controlling the size of the non-feature dimensions

Padding

In our examples thus far

- When a location in a non-feature dimensions of the input
- Is such that, when the kernel is placed there, it extends beyond the input
- We have added "padding"

This is not strictly necessary

- But has advantage that the size of the non-feature dimension of output $\mathbf{y}_{(l)}$ is the same as the input $\mathbf{y}_{(l-1)}$
- One can simply *not* produce an output for such locations
- It just means the output non-feature dimension shrinks in each dimension by $f_{(l)} - 1$
    - Assuming $f_{(l)}$ is odd
    - The number of locations in which the kernel extends over the border
    - Is Half of the filter size $(f_{(l)} - 1)/2$ times two (for each edge)

Stride

Thus far, we have placed the kernel over *each* location in the non-feature dimensions of the input layer.

This, along with padding, ensures that the non-feature dimension of the input and output layers are identical.

In the diagram below

- $N = 1$ non-feature dimensions; length $d_1 = 5$
- $n = 1$ feature
- $f = 3$ kernel size
- we slide the kernel over just the first two locations (for brevity)

Consider two adjacent locations in the non-feature dimension of the input layer

- The values of the input layer that appear in each dot product overlap

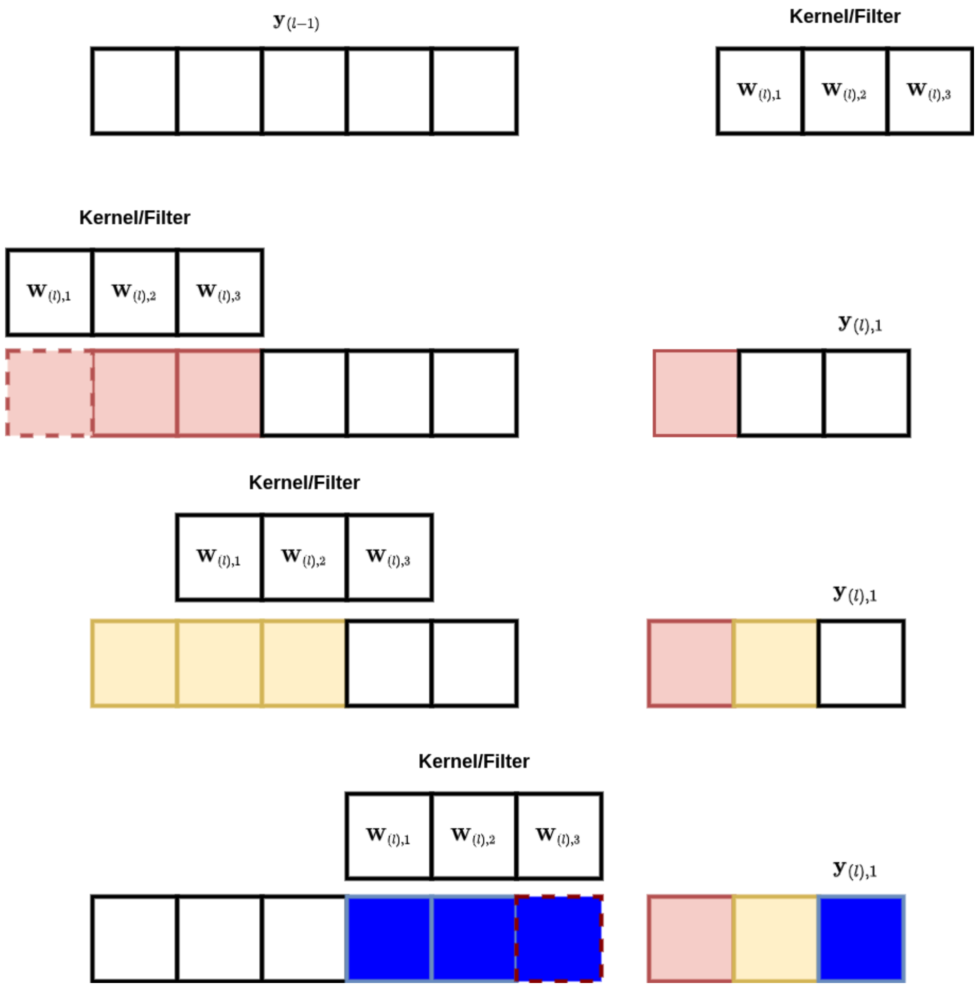
By placing the kernel over *every other* location of the non-feature dimension of the input layer

- We may still be able to recognize features
- And reduce the size of the non-feature dimension of the output layer by a factor of 2 for each dimension.

In the diagram below

- we use stride $S = 2$
- center the kernel over *every other* location
- reducing the size of the output non-feature dimension $d'_1 = \frac{d_1}{2}$

Sliding the kernel with stride $S = 2$



In general, we can choose to choose to pass over $(S-1)$ locations in the non-feature dimension of the input layer

- S is called the *stride*
- Up until now: $S = 1$
- But you are free to choose

When the number N of non-feature dimensions is greater than 1

- we apply the stride S to each dimension

Size of output

We can combine choices of Padding and Stride to control the size of the non-feature dimension of the output layer l:

Let

- $d_{(l-1),j}$ denote the number of elements in non-feature dimension j of layer $(l-1)$
- P denote the number of elements added as padding on each border
- S denote the stride
- $f_{(l)}$ be the size of the filter (for each non-feature dimension)

Then the number of elements in non-feature dimension j of output layer (l) is

$$d_{(l),j} = \frac{d_{(l-1),j} + 2P - f_{(l)}}{S} + 1$$

You can see that increasing the stride has the biggest impact on reducing the size of the non-feature dimension of the output.

Pooling layer

There is a layer type with the specific purpose of changing the size of the non-feature dimension of the output.

This is called a Pooling Layer.

A Pooling Layer combines the information from adjacent locations in the non-feature dimension of the input layer.

- The "combining" operation may be average or maximum
- Sacrificing the exact location in the non-feature dimension
- Often in exchange for reduced space

Pooling:

- Selects an N-dimensional region in the non-feature dimensions
    - where each dimension is of length $f_{(l)}$
- Centered at each location in the non-feature dimension
    - Of a **single feature map j** of the input layer $(l-1)$: $\mathbf{y}_{(l-1),\ldots,j}$

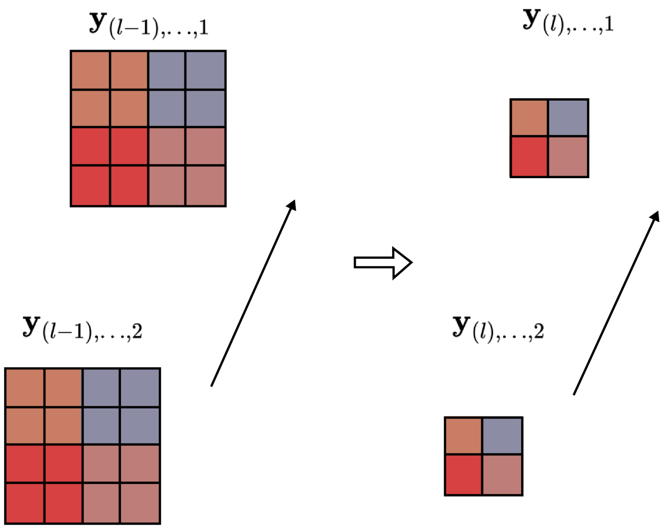
and produces a value in the corresponding location of output layer l

- That *summarizes* the selected region by applying
    - *pooling operation* $p_{(l)}$ to the selected region
    - typical pooling operations: maximum, average

Here is an illustration of Pooling

- $N = 2$ non-feature dimensions; $d_1 = d_2 = 4$
- $n = 2$ features
- $f_{(l)} = 2$
- with **stride** $S = 2$

Conv 2D: Pooling (Max/Average)



/

A Pooling Layer is similar in *some* respects to a Convolution.

Recall that the One Dimensional Convolutional Layer (Conv1d) with a single input feature computes the following for output feature/channel j:

$$\mathbf{y}_{(l),j} = \begin{pmatrix} a_{(l)} \left(N(\mathbf{y}_{(l-1)}, \mathbf{W}_{(l),j}, 1) \cdot \mathbf{W}_{(l)} \right) \\ a_{(l)} \left(N(\mathbf{y}_{(l-1)}, \mathbf{W}_{(l),j}, 2) \cdot \mathbf{W}_{(l)} \right) \\ \vdots \\ a_{(l)} \left(N(\mathbf{y}_{(l-1)}, \mathbf{W}_{(l),j}, n_{(l-1)}) \cdot \mathbf{W}_{(l)} \right) \end{pmatrix}$$

The analogous One Dimensional Pooling Layer (Pooling1D) computes

$$\mathbf{y}_{(l),j} = \begin{pmatrix} \boldsymbol{p}_{(l)}\left(\, \boldsymbol{N}'(\mathbf{y}_{(l-1)}, \boldsymbol{f}_{(l)}, \mathbf{1})\,\right) \\ \boldsymbol{p}_{(l)}\left(\, \boldsymbol{N}'(\mathbf{y}_{(l-1)}, \boldsymbol{f}_{(l)}, \mathbf{2})\,\right) \\ \vdots \\ \boldsymbol{p}_{(l)}\left(\, \boldsymbol{N}'(\mathbf{y}_{(l-1)}, \boldsymbol{f}_{(l)}, \boldsymbol{n}_{(l-1)})\right) \end{pmatrix}$$

where $\boldsymbol{N'}(\, \mathbf{y}_{(l-1)}, \boldsymbol{f}_{(l)}, \boldsymbol{j} \,)$

- selects a subsequence of $\mathbf{y}_{(l-1)}$ centered at $\mathbf{y}_{(l-1),\ldots,j}$
- of length $\boldsymbol{f}_{(l)}$

and $\boldsymbol{p}_{(l)}$ is a *pooling operation*

That is, similar to a Convolutional Layer, the Pooling Layer

- Selects a region of length $f_{(l)}$
- Centered at each location in the non-feature dimension of the input layer $(l-1)$

and produces a value in the corresponding location of output layer l

- That *summarizes* the selected region

Observe that

- **There are *no* weights**
- **No dot product**
- **Just a pooling operation**

Similar to Convolution, we can extend pooling to higher non-feature dimension ($N > 1$) and higher number of input channels $n_{(l-1)} > 1$.

Suppose the input $\mathbf{y}_{(l-1)}$ is $(N+1)$ dimensional of shape

$$||\mathbf{y}_{(l-1)}|| = (d_{(l-1),1} \times d_{(l-1),2} \times \ldots d_{(l-1),N} \times n_{(l-1)})$$

Pooling with a stride $S > 1$

- "Down samples" the non-feature dimension
- Sacrificing some information about locality

It effectively asks the question

- Does the feature exist in a broader neighborhood of the non-feature dimension

The key difference between Pooling and Convolution (other than the absence of the dot product and kernel weights)

- **The pooling operation is applied to each input feature map *separately***
- **Versus *all the input feature maps* at a given location in the non-feature dimension of the input**

Pooling operations

- Max pooling
    - Maximum over the selected region
    - Good for answering the question: "Does the feature exist" in the neighborhood
- Average pooling
    - average over the selected region
    - "blurs" the location in the non-feature dimension when it is unimportant or highly variable

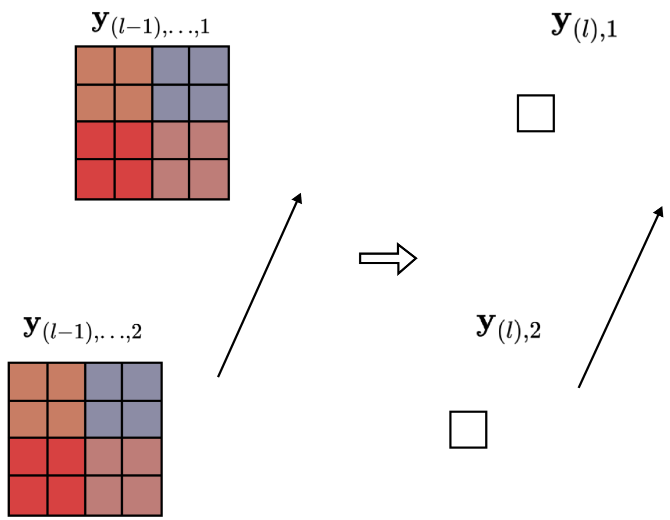
Global Pooling

Each feature map j of the input layer $(\mathbf{y}_{(l-1),\ldots,j})$

- Is summarized by a single value produced by Max Pooling operation $p'_{(l)}$
- *eliminating* the non-feature dimensions
- preserving the number of features

$$\mathbf{y}_{(l),j} = p'_{(l)}(\mathbf{y}_{(l-1),\ldots,j})$$

Conv 2D: Global Pooling (Max/Average)



Notice that each input feature map has been reduced to a single value in the output.

- No non-feature dimension in $\mathbf{y}_{(l)}$ (hence no "$\mathbf{...}$")

The Global Pooling operation effectively asks the question

- Does the feature occur *anywhere* in the feature map ?
- Losing information about the exact location in the non-feature dimensions

Global pooling operations

- Global average pooling
  - Maximum over the feature map
- K-Max pooling
  - replace one dimension of the volume with the K largest elements of the dimension

Review

Let's summarize our knowledge of controlling the size of $\mathbf{y}_{(l-1)}$:

- Controlling the size of non-feature dimensions
    - Increase stride
    - Pooling
        - Global average pooling often used in final Convolutional Layer
- Control number of feature maps per layer
    - Choice of $n_{(l),1}$
    - Kernel size $f_{(l)} = 1$
        - preserve non-feature dimension
        - change number of feature maps from $n_{(l-1),1}$ to $n_{(l),1}$

Striding and Pooling

- increase receptive field
- typically small values (e.g., $S = 2$)
  - limited reduction

Kernel size $f_{(l)} = 1$

- reduction depends on the ratio of $n_{(l),1}$ to $n_{(l-1),1}$
  - unlimited reduction possible

Kernel size 1

A less obvious way to control the size of $\mathbf{y}_{(l)}$ is to use a kernel with $\boldsymbol{f}_{(l)} = \mathbf{1}$

Why might that be ?

Recall that a Convolutional Layer

- Preserves the non-feature dimension
- Replaces the channel/feature dimension (number of feature maps)

That is\

$$
\begin{aligned}
||\mathbf{y}_{(l-1)}|| &= (\boldsymbol{d}_{(l-1),1} \times \boldsymbol{d}_{(l-1),2} \times \ldots \boldsymbol{d}_{(l-1),N} \times \mathbf{n}_{(\mathrm{l}-1)}) \\
||\mathbf{y}_{(l)}|| &= (\boldsymbol{d}_{(l-1),1} \times \boldsymbol{d}_{(l-1),2} \times \ldots \boldsymbol{d}_{(l-1),N} \times \mathbf{n}_{(\mathrm{l})})
\end{aligned}
$$

So a kernel of size $f_{(l)} = 1$ in all N non-feature dimensions

- With "depth" $n_{(l-1)}$
- Is just a way to resize $\mathbf{y}_{(l-1)}$from $n_{(l-1)}$feature maps to a *single* feature map
    - That sums, across feature maps, the elements in each feature map at the same location

In other words:

- Yet another way to reduce the size of $\mathbf{y}_{(l)}$.

Receptive field

The filter size $\mathbf{f}_{(l)}$ also plays a role in the space and time requirements of a Convolutional Layer.

It turns out that

- We can achieve the effect of a large $\mathbf{f}_{(l)}$
- With a smaller $\mathbf{f}_{(l)}$ in conjunction with *more* Convolutional Layers

Let's demonstrate this by examining the concept of [Receptive field (CNN_Receptive_Field.ipynb)](CNN_Receptive_Field.ipynb)

CNN advantages/disadvantages

Advantages

- Translational invariance
    - feature can be anywhere
- Locality
    - feature depends on nearby features, not the entire set of features
    - reduced number of parameters compared to a Fully Connected layer

Disadvantages

- Output feature map is roughly same size as input
    - lots of computation to compute a single output feature
        - one per feature of input map
    - higher computation cost
        - training and inference
- Translational invariance not always a positive

How many feature maps to use (What value to choose for $n_{(l)}$)

[Bag of Tricks for Image Classification with CNNs (https://arxiv.org/abs/1812.01187)](https://arxiv.org/abs/1812.01187)

Remember that a larger value for $n_{(l)}$ will increase space and time requirements.

One rule of thumb:

- For $N = 2$
- With filter size $f_{(l)}$
- The number of elements in the non-feature dimension of input $\mathbf{y}_{(l-1)}$ involved in the dot product is
$$e = (n_{(l-1)} * f_{(l)} * f_{(l)})$$
- It may not make sense to create *more* than e output features $n_{(l)} > e$
    - We would generate more features than input elements

Inverting convolution

The typical flow for multiple layers of Convolutions

- Is for the non-feature dimension of successive layers to get smaller
- By using stride $S > 1$
- By using Pooling Layers

This brings up the question: Can we invert the process ?

- That is, go from a smaller non-featue dimension back to the non-feature dimension of input layer 0

The answer is yes.

This process is sometimes called *Deconvolution* or *Transposed Convolution*.

- In a Deeper Dive, we relate Convolution to Matrix Multiplication
- So the inverting matrix's *dimensions* are the transpose of the matrix implementing the convolution

We will revisit this in the lecture addressing "What is a CNN looking for ?"

Technical points

Convolution versus Cross Correlation

- math definition of convolution
    - dot product of input and *reversed* filter
    - we are doing [cross correlation (https://en.wikipedia.org/wiki/Convolution)](https://en.wikipedia.org/wiki/Convolution)

In [4]:

```
print("Done")
```

Done