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Solution:

1. True. If we use reconstruction model for outlier detection.
2. True. Distances between any two vertices are of one length in a fully connected graph.
3. Data samples that are far away from each other are outliers, the samples that are close to each other are less likely to be outliers.
4. Sparse interactions / Parameter sharing / Translational equivalent / less computational expensive.
5. Translational equivalent means the model can produce the same output no matter where the input is placed, and it is achieved by parameter sharing (convolution).
Translational invariance means the model can produce the same output when the input is translated and it is achieved by pooling operation.
6. Dropout layer can be seen as a regularization on the model itself to force the model to be more robust to noise, and to learn more generalizable features.
7. $A : 0, B : \frac{1}{3}, C : \frac{1}{3}, D : \frac{2}{3}, E : \frac{4}{15}, F : 1, G : 1, H : \frac{2}{3}$, result: $\frac{8}{15}$

Solution:

- 2.A.** Numerator is the number of samples o' "near" the sample o , denominator is the number of samples in D , thus LHS is the ratio of samples from D that is close to o .

Therefore this ratio is less than $\pi \Leftrightarrow$ few samples from D is close to $o \Leftrightarrow o$ is a distance-based outlier.

- 2.B.**

$$\begin{aligned} \frac{\|o' | dist(o, o') \leq r\|}{\|D\|} &\leq \pi \\ \Leftrightarrow \|o' | dist(o, o') \leq r\| &\leq \|D\|\pi \\ \Leftrightarrow \|o' | dist(o, o') \leq r\| &< \lceil \pi \|D\| \rceil \\ \Leftrightarrow \|o' | dist(o, o') > r\| &> \lceil \pi \|D\| \rceil \\ \Leftrightarrow \|o' | dist(o, o') > r\| &> k \end{aligned}$$

Therefore if $dist(o, o_k) > r \forall o_k$, then $\|o' | dist(o, o') > r\| > k$, thus o is an outlier. ■

- 2.C.** Denote $f(o) = \frac{\|o' | dist(o, o') \leq r\|}{\|D\|}$, then

$f(-4.5) = 0.3 > \pi$, -4.5 is not an outlier.

$f(-4) = 0.3 > \pi$, -4 is not an outlier.

$f(-3) = 0.3 > \pi$, -3 is not an outlier.

$f(-2.5) = 0.3 > \pi$, -2.5 is not an outlier.

$f(3) = 0.4 > \pi$, 3 is not an outlier.

$f(3.5) = 0.4 > \pi$, 3.5 is not an outlier.

$f(4) = 0.4 > \pi$, 4 is not an outlier.

$f(4.5) = 0.4 > \pi$, 4.5 is not an outlier.

$f(5) = 0.4 > \pi$, 5 is not an outlier.

$f(0) = 0.0 \leq \pi$, 0 is an outlier.

Solution:

- 3.A.** Distance-based approach defines the outlier samples with the property that there are not enough neighbouring data samples around. Density-based approach defines the outlier samples with the property that the data sample density is significant lower than its neighbours.

3.B.
$$lrd_k(o) = \frac{\|N_k(o)\|}{\sum_{o' \in N_k(o)} reachdist_k(o' \leftarrow o)}$$

3.B.i. We have
$$\frac{\sum_{o' \in N_k(o)} reachdist_k(o' \leftarrow o)}{\|N_k(o)\|} = \frac{\sum_{o' \in N_k(o)} \max\{dist_k(o'), dist(o', o)\}}{k}$$

Which is the average reachability distance from o to $o' \in N_k(o)$.

- 3.B.ii.** Intuitively, when the density of o is small, in other words, if $o \notin dist_k(o')$, then $reachdist_k(o', o)$ will be larger and the average reachability distance from o to $o' \in N_k(o)$ will increase and $lrd_k(o)$ will decrease. Therefore, if the sample o is closer to a cluster, which can be interpreted as $o \in dist_k(o')$ for most $o' \in dist_k(o)$, then $lrd_k(o)$ will increase.

3.C.
$$LOF_k(o) = \frac{\sum_{o' \in N_k(o)} \frac{lrd_k(o')}{lrd_k(o)}}{\|N_k(o)\|}$$

By calculating the division, we can compare the density of o and o' , $LOF_k(o)$ is then defined as the average density ratio of the density of o 's k nearest neighbours and the density of o .

MY_LOF_k is not directly comparable. $MY_LOF_k(o)$ will be inherently bigger than $MY_LOF_k(o')$ when $\|N_k(o)\| > \|N_k(o')\|$

Solution:

4.A. a: local maximal; b: saddle point; c: cliff; d: local minimal

4.B. We have $\frac{\partial O}{\partial I} = O(1 - O)$

4.B.i.

$$\begin{aligned}\delta_k &= \frac{\partial L_k}{\partial I_k} \\ &= -(T - O_k) \frac{\partial O_k}{\partial I_k} \\ &= O_k(1 - O_k)(O_k - T) \blacksquare\end{aligned}$$

4.B.ii.

$$\begin{aligned}\delta_i &= \frac{\partial L_i}{\partial I_i} \\ &= \frac{\partial(\frac{1}{m} \sum_j^m w_{ij} L_j)}{\partial I_i} \\ &= \frac{\partial O_i}{\partial I_i} \sum_j^m w_{ij} \delta_j \\ &= O_k(1 - O_k) \sum_j^m w_{ij} \delta_j \blacksquare\end{aligned}$$

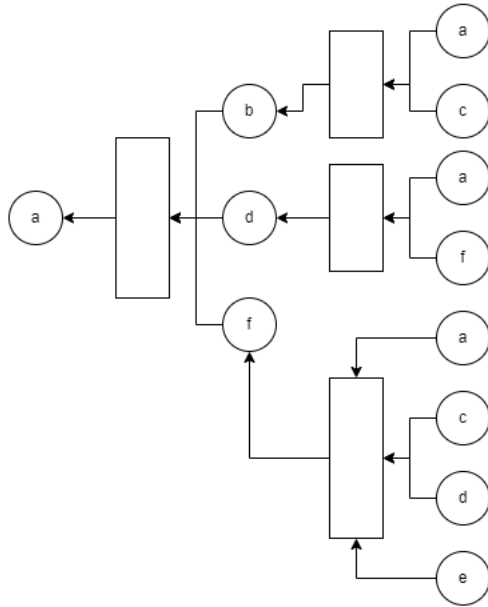
4.B.iii.

$$\begin{aligned}\delta'_k &= \frac{\partial L'_k}{\partial I_k} \\ &= \frac{\partial(-T \log O_k - (1 - T) \log(1 - O_k))}{\partial I_k} \\ &= \frac{\partial O_k}{\partial I_k} \frac{T - O_k}{O_k(1 - O_k)} \\ &= O_k(1 - O_k) \frac{T - O_k}{O_k(1 - O_k)} = T - O_k \blacksquare\end{aligned}$$

4.B.iv. When output unit is saturated, we have $\text{MSE} = O_k(1 - O_k)(O_k - T) \approx 0$ as well, where as for Cross-Entropy loss does not have this issue.

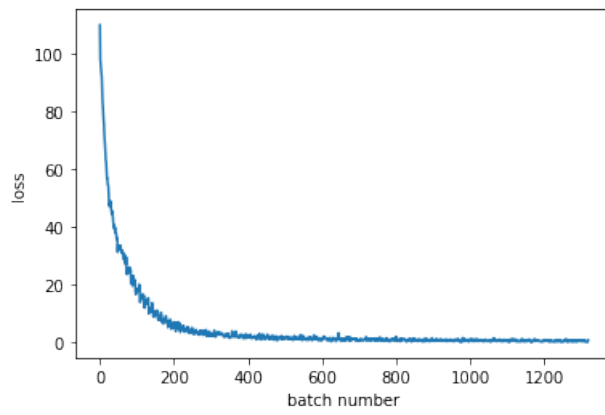
Solution:

- 5.A. Conv with K_1 : $[[0, 2, 1, 0], [1, 1, 0, 2], [2, 0, 2, 1], [1, 2, 0, 1]]$.
 Conv with K_2 : $[[2, 1, 1, 2], [1, 2, 1, 2], [1, 2, 1, 2], [3, 1, 1, 1]]$.
- 5.B. Avg Pooling on feature map with K_1 : $[[1.0, 0.75], [1.25, 1.0]]$.
 Avg Pooling on feature map with K_2 : $[[1.5, 1.5], [1.75, 1.25]]$.
- 5.C. The output shape is $E \times E \times L$, where $E = \lfloor \frac{N-K}{S} \rfloor + 1$.
- 5.D. $h_1 = Wh_0 + Ux_1 = [2, 2]$, $h_2 = Wh_1 + Ux_2 = [5, 3]$, $\hat{y}_2 = Vh_2 = [8, 5]$
- 5.E. Message passing tree for Node a .



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Solution:



Solution:

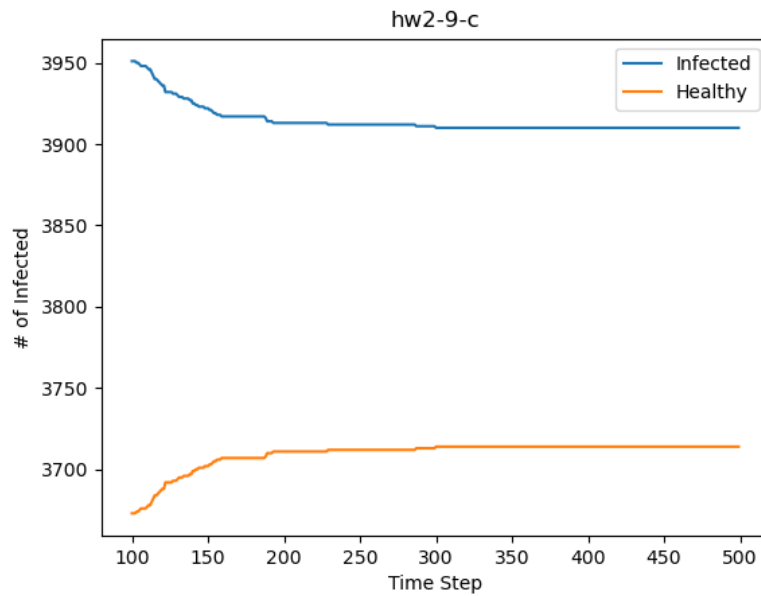
- 8.A. The first eigenvalue of the adjacent matrix of \mathbf{G} holds the following two properties at the same time:
 - 8.A.i. According to the SIS epidemic model, there exists a strong relationship between the "epidemic threshold τ " and the first eigenvalue of the adjacent matrix.
 - 8.A.ii. The first eigenvalue is also a good measurement for the property of the graph \mathbf{G} that how many loops and paths \mathbf{G} can hold, which also represents the connectivity of \mathbf{G} . Since the better connected a graph is then the more vulnerable the graph is, the first eigenvalue of the adjacent matrix of \mathbf{G} is also a good measurement of $V(\mathbf{G})$.
- 8.B. Cannot directly compare $V(\mathbf{G}_1)$ and $V(\mathbf{G}_2)$ when \mathbf{G}_1 and \mathbf{G}_2 do not share the same number of vertices.
- 8.C. It is an approximation instead of a real computation of the eigen-drop, and it is computational cheaper. In addition, as shown in the paper, the eigen-drop is directly related to the proposed '*Shield - value*'.
- 8.D. Suppose compute eigen vector cost $O(1)$ time. Step 1 costs $O(m)$, the first for-loop costs $O(n)$, the second nested for-loop costs $O(nk^2)$. Overall time complexity $O(nk^2 + m)$, where m is the number of edges and n is the number of vertices.

Solution:

9.A. $1 - (1 - \beta)^n$

9.B. 38.6013

9.C. Treating infected probability ≥ 0.6 as infected, getting an epidemic.



9.D. Treating infected probability ≥ 0.6 as infected, getting no epidemic.

