

Filtered Batch Normalization

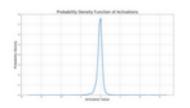
Peter Pazmany Catholic University Faculty of Information Technology and Bionics András Horváth, Jalal Al-afandi

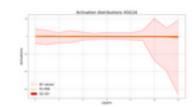
Do activations follow Gaussian dsitribution?

This is a common assumption in normalization techniques.

Most of the activations are Gaussian, but there are extreme outliers, which are oddly specific

Specificity is required from neurons, which goes against Gaussian distribution











Filtered batch normalization

Application of a batch norm and selection of samples in $T\sigma$ range

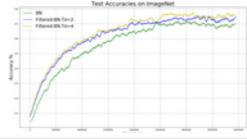
$$\hat{x'}_i = \frac{1}{\sigma_i} (x_i - \mu_i) \qquad f(x_k) = \begin{cases} 1 & \text{if } -T_\sigma \le \hat{x'}_k \le T_\sigma \\ 0 & \text{if } \hat{x'}_k < -T_\sigma \lor T_\sigma < \hat{x'}_k \end{cases}$$

Using the selected samples only for normalization:

$$\mu'_{i} = \frac{1}{\sum_{k \in S_{i}} f(x_{k})} \sum_{k \in S_{i}} f(x_{k}) x_{k} \qquad \sigma'_{i} = \sqrt{\frac{1}{\sum_{k \in S_{i}} f(x_{k})} \sum_{k \in S_{i}} f(x_{k}) (x_{k} - \mu'_{i})^{2} + \epsilon}$$

$$\sigma'_i = \sqrt{\frac{1}{\sum\limits_{k \in S_i} f(x_k)} \sum\limits_{k \in S_i} f(x_k)(x_k - \mu'_i)^2 + \epsilon}$$

Results



| | BNAP | BNAP ₅₀ | F-BNAP | F-BNAP ₅₀ |
|-----------|-------|--------------------|--------|----------------------|
| SEG(50K) | 23.87 | 44.56 | 25.41 | 45.42 |
| SEG(100K) | 26.86 | 45.55 | 27.34 | 52.40 |
| SEG(150K) | 28.66 | 51.80 | 34.15 | 55.43 |
| SEG(270K) | 36.47 | 58.07 | 37.06 | 58.92 |
| Box(50K) | 23.63 | 41.90 | 27.86 | 47.84 |
| Box(100K) | 28.16 | 48.43 | 28.74 | 49.65 |
| Box(150K) | 30.53 | 50.79 | 34.24 | 53.13 |
| Box(270K) | 40.01 | 61.32 | 41.12 | 61.71 |

Test results on MS-COCO

