## Disentangling Representations in Restricted Boltzmann Machines without Adversaries <br> J. Fernandez-de-Cossio-Diaz <br> PSL Junior Fellow AI <br> Ecole Normale Supérieure, Paris <br> In collaboration with: <br>  <br> S. Cocco \& R. Monasson <br> JFdCD, S.Cocco, R.Monasson, PRX 13, 021003 (2023)

## Representation learning

## Data

## Representation learning

Example: B/W
CelebA dataset of face images.
Grouped by facial
expression.
Data - "pixel" space

## Representation learning

Data - "pixel" space


## Representation space


representation variable 1

## Restricted Boltzmann machines

Simple generative model, implementing data / representation duality

Hidden units (h) - representation


Energy function:

$$
E(\mathbf{v}, \mathbf{h})=\sum_{\mu} \mathscr{V}_{i}\left(v_{i}\right)+\sum_{\mu} \mathscr{U}_{\mu}\left(h_{\mu}\right)-\sum_{i \mu} w_{i \mu} v_{i} h_{\mu}
$$

## Restricted Boltzmann machines

Simple generative model, implementing data / representation duality

Hidden units (h) - representation


Energy function:

$$
\begin{gathered}
E(\mathbf{v}, \mathbf{h})=\sum_{\mu} \mathscr{V}_{i}\left(v_{i}\right)+\sum_{\mu} \mathscr{U}_{\mu}\left(h_{\mu}\right)-\sum_{i \mu} w_{i \mu} v_{i} h_{\mu} \\
\text { Likelihood: } \mathscr{L}=\ln P(\mathbf{v})=\ln \sum_{\mathbf{h}} e^{-E(\mathbf{v}, \mathbf{h})}-\ln Z \\
-E_{\text {efff }}(\mathbf{v})
\end{gathered}
$$

Encodes for (higherorder) interactions

## Restricted Boltzmann machines

Simple generative model, implementing data / representation duality

Hidden units (h) - representation


Energy function:

$$
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$$



Model trained by max. likelihood of the data

$$
\frac{\partial \ln P(\text { data })}{\partial \omega}=\left\langle\frac{\partial\left(-E_{\mathrm{eff}}(\mathbf{v})\right)}{\partial \omega}\right\rangle_{\text {data }}-\left\langle\frac{\partial\left(-E_{\mathrm{eff}}(\mathbf{v})\right)}{\partial \omega}\right\rangle_{\text {model }}
$$ order) interactions

## RBM as generative models across diverse datasets

Some examples
(a)
CelebA


(b)


## Pfam



Bacteria
-HTISINPNKIGEIIGKG.
--VVNLPNDMKGRIIGRE.
Eukaryotic
----------YIGLLIGPR...
V-LTIPPEKIRDVVGTGG...
I-LTVPPSKAPRIVGKGG... LEIDVPNNDAGAIIGKGG... AKISIEAELAGGIIGKGG... LTINVPPKHHNSIIGAGG... TLTIPSDKIRDVIGKGGA... RILVSSNQIGCLLGKGGS...

Other recent applications (in biology) ...
Immunology: Bravi, et al. bioRxiv (2022): 2022-12; Cell systems 12.2 (2021): 195-202.
RNA: Di Gioacchino, et al. PLoS CB 18.9 (2022): e1010561, JFdCD, et al. bioRxiv (2023): 2023-05
Proteins: Tubiana Elife 8 (2019): e39397.

## RBM as generative models across diverse datasets

## Nature of the representations





Correlation between hidden units and label
Information about features is distributed across a large number of hidden units
Representations are generally entangled.

## Disentangled representations

Entangled
representation


Representation direction 1

> Representation



Representation direction 1 (correlated to label)


## Adversarial formulation

Setup: Dataset $\mathbf{v}^{1}, \ldots, \mathbf{v}^{B}$ with binary labels $u^{1}, \ldots, u^{B}$ e.g. faces smiling vs. or not


Mutual information (MI) is difficult to control ...

## Adversarial formulation

Setup: Dataset $\mathbf{v}^{1}, \ldots, \mathbf{v}^{B}$ with labels $u^{1}, \ldots, u^{B}$ e.g. faces smiling vs. or not

```
```

max \mathscr{L}\mathrm{ (data)}

```
```

max \mathscr{L}\mathrm{ (data)}
subject to
subject to
MI}(h,\mathrm{ label })=

```
```

MI}(h,\mathrm{ label })=

```
```

Adversarial classifier $\mathscr{L}_{\mathscr{A}}$

"Adversarial" training.
Similar to GAN

$$
\max \left(\mathscr{L}(\text { data })-\alpha \max _{\mathscr{A}} \mathscr{L}_{\mathscr{A}}(\text { labels } \mid \text { data })\right)
$$

## Adversarial formulation

Setup: Dataset $\mathbf{v}^{1}, \ldots, \mathbf{v}^{B}$ with labels $u^{1}, \ldots, u^{B}$ e.g. faces smiling vs. or not
Issues:

Adversarial classifier $\mathscr{L}_{\mathscr{A}}$
$\max \mathscr{L}$ (data)
subject to
$\operatorname{MI}(h$, label $)=0$

"Adversarial" training.
Similar to GAN
$\max \left(\mathscr{L}(\right.$ data $)-\alpha \max _{\mathscr{A}} \mathscr{L}_{\mathscr{A}}($ labels $\mid$ data $\left.)\right)$

If the best possible classifier $\mathscr{L}_{\mathscr{A}}$ is bad at predicting the label, then label information has been erased

## A hierarchy of explicit constraints

Setup: Dataset $\mathbf{v}^{1}, \ldots, \mathbf{v}^{B}$ with labels $u^{1}, \ldots, u^{B}$ e.g. faces smiling vs. or not

1) $\operatorname{MI}(h$, label $) \leq \operatorname{MI}\left(I=\mathbb{W}^{\top} \mathbf{v}\right.$, label $)$ - data processing inequality
2) $\operatorname{MI}\left(I=\mathbb{W}^{\top} \mathbf{v}\right.$, label $)=0$ implies that:


$$
\left\langle u I_{\mu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu} I_{\gamma}\right\rangle=0, \ldots
$$

(correlations between $I_{\mu}$ and label vanish at all orders)
Explicit conditions on the weights - No "adversary"

$$
\sum_{i} q_{i}^{(1)} w_{i \mu}=0, \sum_{i} q_{i j}^{(2)} w_{i \mu} w_{j \nu}=0, \text { etc. }, \ldots
$$

## A hierarchy of explicit constraints

1st-order: $\left\langle u I_{\mu}\right\rangle=0$
2nd-order: $\left\langle u I_{\mu} I_{\nu}\right\rangle=0$
Explicit conditions on the weights - No "adversary"

$$
\begin{array}{cc}
\sum_{i} q_{i}^{(1)} w_{i \mu}=0 & \sum_{i} q_{i j}^{(2)} w_{i \mu} w_{j \nu}=0 \\
q_{i}^{(1)}=\left\langle u v_{i}\right\rangle-\langle u\rangle\left\langle v_{i}\right\rangle & q_{i}^{(2)}=\left\langle u v_{i} v_{j}\right\rangle-\langle u\rangle\left\langle v_{i} v_{j}\right\rangle
\end{array}
$$

Learning algorithm

- Gradient ascent of likelihood
- Projection to satisfy constraints



## Trained RBM concentrates label information

Constraint imposed on ALL hidden units:
Partial Erasure of label information


Constraint imposed on a subset of hidden units: Concentrates label information


## Application to 2D-Ising model



2-Dimensional Ising model
$\mathrm{N}=32 \times 32$ and $64 \times 64$

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2-Dimensional Ising model
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RBM captures behaviour of observables

## Application to 2D-Ising model Label = sign(m)



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RBM captures behaviour of observables

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## Application to 2D-Ising model Label = sign(m)





Releasing one hidden unit recovers behavior of all observables

## Manipulating data through representation learning

Representation space


Not smiling -2 4 (4)

Model


No glasses ${ }^{-}$


Data space

## Likelihood cost in a Gaussian setting

$L L_{\text {Gauss }}=\frac{1}{2} \sum_{\mu}\left(\lambda_{\mu}-1-\ln \lambda_{\mu}\right)$
$\lambda_{\mu}$ eigenvalues of correlation matrix of data

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## Likelihood cost in a Gaussian setting

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$\lambda_{\mu}$ eigenvalues of correlation matrix of data Constraint: $\tilde{\mathbf{C}}^{\perp}=\mathbf{P} \tilde{\mathbf{C}} \mathbf{P}$

$$
\lambda_{1} \geq \lambda_{1}^{\perp} \geq \lambda_{2} \geq \lambda_{2}^{\perp} \geq \ldots \geq \lambda_{N} \geq \lambda_{N}^{\perp}=0\left(^{*}\right)
$$


(*) Poincaré separation theorem

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$$
\lambda_{1} \geq \lambda_{1}^{\perp} \geq \lambda_{2} \geq \lambda_{2}^{\perp} \geq \ldots \geq \lambda_{N} \geq \lambda_{N}^{\perp}=0 \text { (*) }
$$

Spectral gaps account for log-likelihood cost of erasure / disentanglement

$$
L L_{\text {constr. }}=L L_{\text {Gauss }}-\text { cost }
$$


(*) Poincaré separation theorem

## Likelihood cost in a Gaussian setting

MNISTO/1


Gaussian+Spin RBM

Ising Model



## Approximate "erasure" of information

$\mathrm{Ml}\left(I=\mathbb{W}^{\top} \mathbf{v}\right.$, label $)=0 \underset{?}{\longleftrightarrow}\left\langle u I_{\mu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu} I_{\gamma}\right\rangle=0, \ldots$

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\operatorname{MI}\left(I=\mathbb{W}^{\top} \mathbf{v}, \text { |abel }\right)=0 \underset{?}{\longleftrightarrow}\left\langle u I_{\mu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu}\right\rangle=0,\left\langle u I_{\mu} I_{\nu} I_{\gamma}\right\rangle=0, \ldots
$$



## Summary:

- Semi-supervised approach
- Concentrate information about attribute on small subset of latent variables
- Transfer attributes from one data-point to another



## Perspectives:

- Application to biological sequences. Transfer useful properties between natural sequences (specificity, stability, ...). Ex.: WW, HSP.
- ... other?

JFdCD, S.Cocco, R.Monasson, PRX 13, 021003 (2023)

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