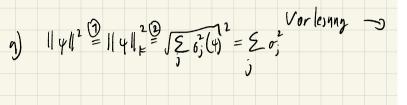
Let  $\psi \in \mathbb{C}^{m \cdot n}$  be a complex vector. We may interpret  $\psi$  as  $m \times n$  matrix and compute its SVD, for which we use the convention  $\psi = USV^T$  here, with isometries  $U \in \mathbb{C}^{m \times k}$ ,  $V \in \mathbb{C}^{n \times k}$  (such that  $U^{\dagger}U = I$  and  $V^{\dagger}V = I$ ),  $k = \min(m, n)$  and  $S = \operatorname{diag}(\sigma_1, \dots, \sigma_k)$ . (The V matrix appears without complex conjugation in the SVD.) As graphical diagram:

$$\psi = \begin{array}{c} U \\ V \end{array}$$

(a) Show that

$$\|\psi\|^2 = \sum_{j=1}^k \sigma_j^2.$$

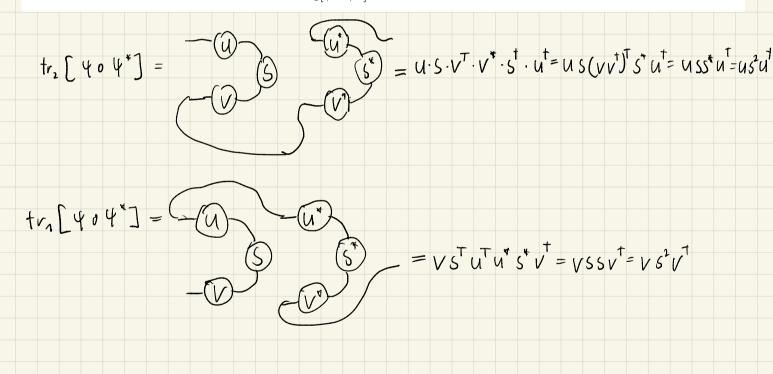
Hint: Revisit the definition and properties of the Frobenius norm, or use the diagrammatic representation.



• Frobenius norm:  
(2) 
$$\|A\|_{F} = \sqrt{\sum_{i,j} |\alpha_{i,j}|^{2}} = \|\operatorname{vec}(A)\|$$
  
Since  $\sum_{i,j} |a_{i,j}|^{2} = \operatorname{fr}[A^{+}A] = \sum_{j} \epsilon_{j}^{2}(A)$   
(2)  $\|A\|_{F} = \sqrt{\sum_{j} \epsilon_{j}^{2}(A)}$ 

(b) The partial trace has been introduced in Exercise 5.1. Here the two subsystems have dimension m and n, respectively. Verify that

$$\operatorname{tr}_2[\psi \circ \psi^*] = US^2U^{\dagger}$$
 and  $\operatorname{tr}_1[\psi \circ \psi^*] = VS^2V^{\dagger}$ .



In part (b) we have thus found the spectral decompositions of the "reduced density matrices" defined as  $\rho_1 = \operatorname{tr}_2[\psi \circ \psi^*]$  and  $\rho_2 = \operatorname{tr}_1[\psi \circ \psi^*]$  (potentially omitting zero eigenvalues). One observes that  $\rho_1$  and  $\rho_2$  have the same (non-zero) eigenvalues  $(\sigma_j^2)_{j=1,\dots,k}$ . In the following, we assume that  $\|\psi\|=1$ , such that  $\sum_{j=1}^k \sigma_j^2=1$  according to (a).

In general, a density matrix  $\rho$  is a Hermitian, positive semidefinite matrix with normalization  $tr[\rho] = 1$ . The von Neumann entropy of  $\rho$  is defined as

$$S(\rho) = -\operatorname{tr}[\rho \log(\rho)],$$

with the logarithm interpreted as matrix function, and the convention  $0\log(0) = \lim_{x\to 0} x\log(x) = 0$ .

In the present setting, the *entanglement entropy* between the two subsystems is defined as

$$\mathcal{S}_{\mathrm{ent}} = \mathcal{S}(\rho_1) = \mathcal{S}(\rho_2) = -\sum_{j=1}^k \sigma_j^2 \log(\sigma_j^2).$$

(You should convince yourself that  $S(\rho_1)$  and  $S(\rho_2)$  are indeed equal to the sum on the right.) Intuitively, the entanglement entropy measures how strongly the subsystems are intertwined.

(c) Which singular values  $(\sigma_j)_{j=1,\dots,k}$  minimize and maximize the entanglement entropy, respectively, under the normalization condition  $\sum_{j=1}^k \sigma_j^2 = 1$ ? (k should be regarded as given and fixed.)

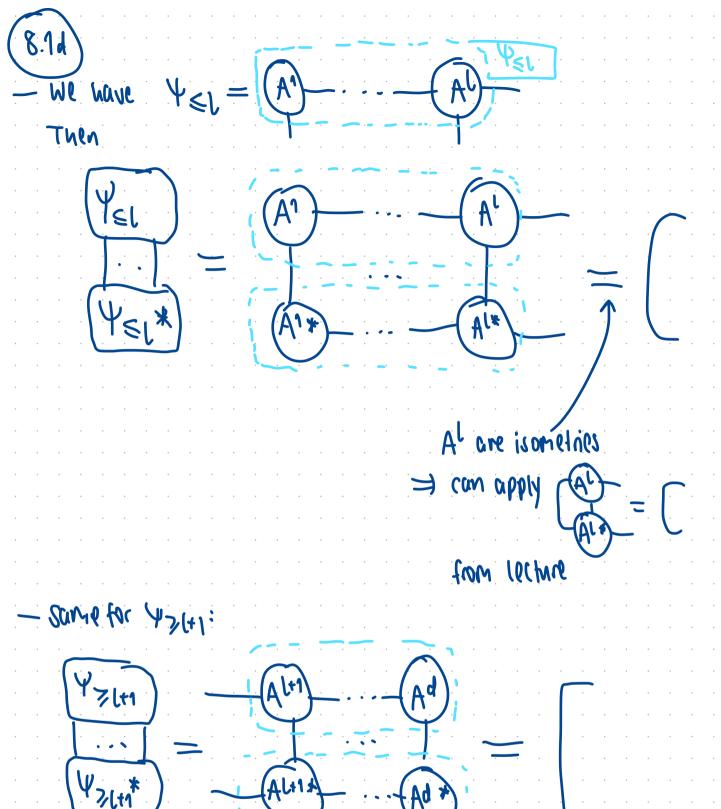
Hint: The smallest possible entanglement entropy is zero. Regarding maximization, first consider the case k=2.

minimal entropy: 
$$\sigma = (1, 0, ..., 0) \Rightarrow 1(0)(1) + (4-1) \cdot 0 \cdot (0) = 0$$

belie bijeer Index

maximal entropy: distribution as even as possible;

$$v = (\frac{1}{4}, \frac{1}{4}, \dots) = S = -k \cdot \frac{1}{k} \cdot (g(\frac{1}{k}) = (g(\frac{1}{k}))$$



# exercise8.2\_template

June 22, 2022

## 1 Canonical MPS forms

```
[1]: import numpy as np import matplotlib.pyplot as plt
```

### 1.1 Functions for conversion to canonical forms

```
[2]: def mps_orthonormalize_left(Alist, stop=-1):
          HHHH
         Left-orthonormalize a MPS using QR decompositions.
         The list of tensors in `Alist` are updated in-place.
         Returns the overall norm of the original MPS. (The updated MPS has norm 1.)
         dummy = np.array([[[1]]])
         d = len(Alist)
         if (stop > 0):
             d = stop
         for l in range(d):
             n, dlm, dl = Alist[1].shape
             A = Alist[1].reshape((n * dlm, dl))
             Q, R = np.linalg.qr(A)
             dl = Q.shape[1]
             Alist[1] = Q.reshape((n, dlm, dl))
             if (1 < len(Alist) - 1):</pre>
                  Alist[1 + 1] = np.moveaxis(np.tensordot(R, Alist[1 + 1], ([1], [1], [1]))
      \hookrightarrow [1])), 0, 1)
             else:
                  dummy = np.moveaxis(np.tensordot(R, dummy, ([1], [1])), 0, 1)
         dummy = dummy[0, 0, 0]
         if dummy < 0:</pre>
             dummy *= -1
             Alist[d - 1] = -1 * Alist[d - 1]
         return dummy
```

```
[3]: def mps_orthonormalize_right(Alist, stop=-1):
         11 11 11
         Right-orthonormalize a MPS using QR decompositions.
         The list of tensors in `Alist` are updated in-place.
         Returns the overall norm of the original MPS. (The updated MPS has norm 1.)
         MirList = []
         for l in range(len(Alist) - 1, -1, -1):
             MirList.append(np.moveaxis(Alist[1], 1, 2))
         nrm = mps_orthonormalize_left(MirList, stop)
         for l in range(len(Alist)):
             Alist[len(Alist) - 1 - 1] = np.moveaxis(MirList[1], 1, 2)
         return nrm
[4]: def mps_orthonormalize_center(Alist, j):
         Convert a MPS to site-canonical form with center at site `j`, such that
         all tensors to the left are left-orthonormal, and
         all tensors to the right are right-orthonormal.
         The list of tensors in `Alist` are updated in-place.
         mps_orthonormalize_right(Alist, stop=len(Alist) - j - 1)
         mps_orthonormalize_left(Alist, stop=j)
[5]: def mps_orthonormalize_bond(Alist, j):
         Convert a MPS to bond-canonical form, with a list of "singular values"
         between the 'j'-th and 'j+1'-th tensor.
         The list of tensors in `Alist` are updated in-place.
         Returns the singular value list.
         mps_orthonormalize_center(Alist, j)
         n, dlm, dl = Alist[j].shape
         A = Alist[j].reshape((n * dlm, dl))
         Q, R = np.linalg.qr(A)
         dl = Q.shape[1]
         Alist[j] = Q.reshape((n, dlm, dl))
         u, s, vh = np.linalg.svd(R)
         Alist[j] = np.tensordot(Alist[j], u, ([2], [0]))
         Alist[j+1] = np.moveaxis(np.tensordot(vh, Alist[j+1], ([1], [1])), 0, 1)
```

return s

return T

# 1.2 Utility functions

```
[6]: def is_left_orthonormal(A):
         Test whether a MPS tensor `A` is left-orthonormal.
         nnn
         s = A.shape
         assert len(s) == 3
         A = np.reshape(A, (s[0] * s[1], s[2]))
         return np.allclose(A.conj().T @ A, np.identity(s[2]))
[7]: def is_right_orthonormal(A):
         11 11 11
         Test whether a MPS tensor `A` is right-orthonormal.
         # call `is_left_orthonormal` with flipped left and right virtual bondu
      \hookrightarrow dimensions
         return is_left_orthonormal(np.transpose(A, (0, 2, 1)))
[8]: def mps_to_full_tensor(Alist):
         Construct the full tensor corresponding to the MPS tensors `Alist`.
         The i-th MPS tensor Alist[i] is expected to have dimensions (n[i], D[i], \Box
      \hookrightarrow D[i+1]),
         with `n` the list of logical dimensions and `D` the list of virtual bond \Box
      \rightarrow dimensions.
         Note: Should only be used for debugging and testing.
         # consistency check: dummy singleton dimension
         assert Alist[0].ndim == 3 and Alist[0].shape[1] == 1
         # formally remove dummy singleton dimension
         T = np.reshape(Alist[0], (Alist[0].shape[0], Alist[0].shape[2]))
         # contract virtual bonds
         for i in range(1, len(Alist)):
             T = np.tensordot(T, Alist[i], axes=(-1, 1))
         # consistency check: trailing dummy singleton dimension
         assert T.shape[-1] == 1
         # formally remove trailing singleton dimension
         T = np.reshape(T, T.shape[:-1])
```

```
[9]: def mps_bond_to_full_tensor(Alist, S, j):
          11 11 11
          Construct the full tensor corresponding to the bond-canonical MPS
          with tensors 'Alist' and "bond" singular values 'S' between
          the 'j'-th and 'j+1'-th tensor.
          # absorb bond singular values into j-th tensor
          Blist = [np.tensordot(Alist[i], np.diag(S), (2, 1)) if i == j else Alist[i]
       ⇔for i in range(len(Alist))]
          return mps_to_full_tensor(Blist)
[10]: def partial_trace(rho, dimA, dimB):
          Compute the partial traces of a density matrix 'rho' of a composite quantum
       ⇔system AB.
          Arqs:
              rho: density matrix of dimension dimA*dimB x dimA*dimB
              dimA: dimension of subsystem A
              dimB: dimension of subsystem B
          Returns:
              tuple: reduced density matrices for subsystems A and B
          # explicit subsystem dimensions
          rho = np.reshape(rho, (dimA, dimB, dimA, dimB))
          # trace out subsystem B
          rhoA = np.trace(rho, axis1=1, axis2=3)
          # trace out subsystem A
          rhoB = np.trace(rho, axis1=0, axis2=2)
          return rhoA, rhoB
[11]: def crandn(size):
          Draw random samples from the standard complex normal (Gaussian),
       \hookrightarrow distribution.
          11 11 11
          # 1/sqrt(2) is a normalization factor
          return (np.random.normal(size=size) + 1j * np.random.normal(size=size)) / __
       →np.sqrt(2)
[12]: def xlogx(x):
          11 11 11
          Compute x * log(x) (pointwise), such that the result is zero for x = 0.
          y = np.zeros_like(x)
          idx = x > 0
          y[idx] = x[idx] * np.log(x[idx])
```

## 1.3 Examples and tests

n = [2, 5, 3, 4, 6, 3]

```
D = [1, 3, 4, 7, 6, 5, 1]
[14]: # random MPS tensors (the scaling factor keeps the norm of the full tensor in a
      ⇔reasonable range)
      np.random.seed(142)
      Aref = [0.3 * crandn((n[i], D[i], D[i + 1])) for i in range(len(n))]
      # the tensors are randomly chosen, and in particular not of any normal form
      print([is_left_orthonormal(A) for A in Aref])
      print([is_right_orthonormal(A) for A in Aref])
      # construct the full (dense) tensor which this MPS represents, as reference
      ⇔(should only be constructed for testing and debugging)
      Tref = mps_to_full_tensor(Aref)
      # its shape must be equal to `n` from above:
      print("Tref.shape:", Tref.shape)
     [False, False, False, False, False]
     [False, False, False, False, False]
     Tref.shape: (2, 5, 3, 4, 6, 3)
     1.3.1 Left-orthonormalization
[15]: # first make a copy of the input tensors
      AL = [A.copy() for A in Aref]
      # function returns norm of input MPS
      nrmL = mps_orthonormalize_left(AL)
[16]: # these should all be True
      [is_left_orthonormal(A) for A in AL]
[16]: [True, True, True, True, True, True]
[17]: nrmL
[17]: (1.2965535991355326-0j)
[18]: # compare norm with reference
      abs(nrmL - np.linalg.norm(np.reshape(Tref, -1))) / abs(nrmL)
```

[13]: # logical and virtual bond dimensions (rather arbitrarily chosen)

```
[18]: 1.7125755932734126e-16
[19]: # compare full tensor with reference: difference should be zero (up to ...
       →numerical rounding errors)
      np.linalg.norm(nrmL * mps_to_full_tensor(AL) - Tref)
[19]: 1.1619396826252498e-15
     1.3.2 Right-orthonormalization
[20]: # first make a copy of the input tensors
      AR = [A.copy() for A in Aref]
      # function returns norm of input MPS
      nrmR = mps_orthonormalize_right(AR)
[21]: # these should all be True
      [is_right_orthonormal(A) for A in AR]
[21]: [True, True, True, True, True, True]
[22]: nrmR
[22]: (1.2965535991355326-0j)
[23]: # compare norm with reference
      abs(nrmR - np.linalg.norm(np.reshape(Tref, -1))) / abs(nrmR)
[23]: 1.7125755932734126e-16
[24]: # compare full tensor with reference: difference should be zero (up to
      →numerical rounding errors)
      np.linalg.norm(nrmR * mps_to_full_tensor(AR) - Tref)
[24]: 9.091941358304111e-16
     1.3.3 Site-canonical form
[25]: # again make a copy first
      AC = [A.copy() for A in Aref]
      # tensors are updated in-place, and overall norm is preserved (function has no_{\sqcup}
      ⇔formal return value)
```

jcenter = 2

mps\_orthonormalize\_center(AC, jcenter)

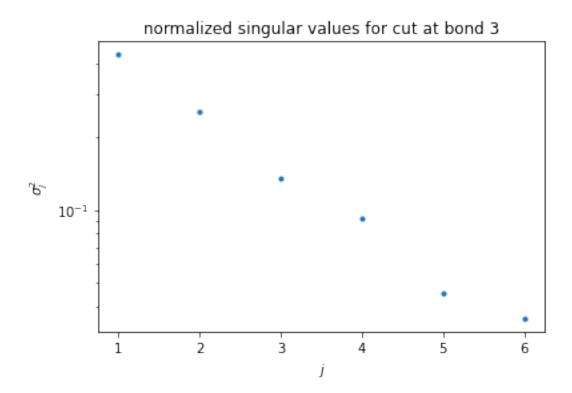
```
[26]: # these should all be True
      [is_left_orthonormal(A) for A in AC[:jcenter]]
[26]: [True, True]
[27]: # these should all be True
      [is right orthonormal(A) for A in AC[jcenter + 1:]]
[27]: [True, True, True]
[28]: # "center" tensor is not orthonormal in general
      is_left_orthonormal(AC[jcenter]) or is_right_orthonormal(AC[jcenter])
[28]: False
[29]: # compare full tensor with reference: difference should be zero (up to ...
       →numerical rounding errors)
      np.linalg.norm(mps_to_full_tensor(AC) - Tref)
[29]: 1.0487378834340819e-15
     1.3.4 Bond-canonical form
[30]: # again make a copy first
      AB = [A.copy() for A in Aref]
      jbond = 3
      S = mps_orthonormalize_bond(AB, jbond)
[31]: # list of singular values for "cut" at `jbond`
      S
[31]: array([0.85731111, 0.65318151, 0.47655434, 0.39473114, 0.27652958,
             0.24502551])
[32]: # these should all be True
      [is_left_orthonormal(AB[j]) if j <= jbond else is_right_orthonormal(AB[j]) foru
       →j in range(len(AB))]
[32]: [True, True, True, True, True, True]
[33]: \# compare full tensor with reference: difference should be zero (up to
      →numerical rounding errors)
      np.linalg.norm(mps_bond_to_full_tensor(AB, S, jbond) - Tref)
```

[33]: 1.7067211880195904e-15

### 1.3.5 Bond-singular values and entanglement entropy

```
[34]: # compute (reduced) density matrices, as reference
      ref = np.outer(Tref, Tref.conj())
      A, B = partial_trace(ref, np.prod(n[:jbond + 1]), np.prod(n[jbond + 1:]))
      print(" A.shape:", A.shape)
      print("B.shape:", B.shape)
     A.shape: (120, 120)
     B.shape: (18, 18)
[35]: # must be Hermitian
      np.linalg.norm(A - A.conj().T)
[35]: 0.0
[36]: # must be Hermitian
      np.linalg.norm(B - B.conj().T)
[36]: 0.0
[37]: A = np.linalg.eigvalsh(A)
      B = np.linalg.eigvalsh(B)
[38]: # most of them are actually zero
[38]: array([-1.04158612e-16, -5.04120978e-17, -4.50643064e-17, -3.09628817e-17,
             -2.92487789e-17, -2.39908171e-17, -2.17945332e-17, -1.98333707e-17,
            -1.89664610e-17, -1.81748522e-17, -1.74202110e-17, -1.62433203e-17,
            -1.57288746e-17, -1.43154575e-17, -1.31744569e-17, -1.26977622e-17,
            -1.22028703e-17, -1.15573641e-17, -1.02748257e-17, -9.90329461e-18,
            -9.32509903e-18, -9.11640131e-18, -8.80149185e-18, -8.23987295e-18,
            -7.97671527e-18, -7.68367130e-18, -6.95259961e-18, -6.71073554e-18,
             -5.75320734e-18, -5.72178755e-18, -5.40778056e-18, -5.29059690e-18,
            -5.02807036e-18, -4.98842715e-18, -4.42073308e-18, -4.03270891e-18,
            -3.93415140e-18, -3.55608057e-18, -3.31606560e-18, -3.18667250e-18,
            -2.89392410e-18, -2.68396704e-18, -2.42062683e-18, -2.39460665e-18,
            -2.06096854e-18, -1.85741554e-18, -1.56622145e-18, -1.37198632e-18,
            -1.12395548e-18, -1.03684293e-18, -8.92166230e-19, -7.53258851e-19,
             -5.07123027e-19, -2.83237633e-19, -8.94118762e-20, 3.69924403e-21,
             4.17532460e-20, 1.20141516e-19, 2.61110534e-19, 3.85164442e-19,
             5.68331019e-19, 8.42177785e-19, 9.82611577e-19, 1.06496995e-18,
             1.20556263e-18, 1.33102835e-18, 1.53859718e-18, 1.63588470e-18,
             1.87965451e-18, 2.09521344e-18, 2.26005779e-18, 2.32445198e-18,
             2.51498965e-18, 2.90614325e-18, 3.07378425e-18, 3.24704011e-18,
             3.54241293e-18, 3.84657522e-18, 4.22021222e-18, 4.46631477e-18,
             4.63791846e-18, 5.12476071e-18, 5.27075754e-18, 5.67435143e-18,
```

```
5.80687970e-18, 6.07796628e-18, 6.41923071e-18, 7.09885664e-18,
             7.31865144e-18, 8.01886322e-18, 8.41007922e-18, 8.81528485e-18,
             9.37137755e-18, 9.85957449e-18, 1.01493903e-17, 1.06423592e-17,
             1.17630356e-17, 1.19311664e-17, 1.27264057e-17, 1.33188034e-17,
             1.40625300e-17, 1.51276125e-17, 1.54795781e-17, 1.73981649e-17,
             1.83436600e-17, 2.02974773e-17, 2.20547510e-17, 2.32568787e-17,
             2.52686264e-17, 2.83287153e-17, 3.62885082e-17, 5.32190097e-17,
             6.48773579e-17, 9.00037809e-17, 6.00375012e-02, 7.64686066e-02,
             1.55812673e-01, 2.27104043e-01, 4.26646080e-01, 7.34982332e-01])
[39]: # filter out zero eigenvalues
      A = A[np.logical_not(np.isclose(A, 0, atol=1e-13))]
      B = B[np.logical not(np.isclose(B, 0, atol=1e-13))]
      # sort in descending order
      A = np.sort(A)[::-1]
      B = np.sort(B)[::-1]
[40]: A
[40]: array([0.73498233, 0.42664608, 0.22710404, 0.15581267, 0.07646861,
            0.0600375])
[41]: # compare: should agree
     np.linalg.norm(A - B)
[41]: 3.632164660233972e-16
[42]: # compare: should agree with bond-singular values from above
     np.linalg.norm(A - S ** 2)
[42]: 7.132224383467466e-16
[43]: # normalize singular values
     Snrm = S / np.linalg.norm(S)
     Snrm
[43]: array([0.66122303, 0.50378288, 0.36755468, 0.30444645, 0.21328048,
            0.18898217])
[44]: plt.semilogy(range(1, len(Snrm) + 1), Snrm ** 2, '.')
     plt.ylabel("$\\sigma_j^2$")
     plt.xlabel("$j$")
     plt.title("normalized singular values for cut at bond {}".format(jbond))
     plt.show()
```



```
[45]: # finally compute entanglement entropy
np.sum(-xlogx(Snrm ** 2))
```

[45]: 1.460203986361991