k-strip: A novel segmentation algorithm in k-space for the application of skull stripping

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Abstract—We present a novel deep learning-based skull stripping algorithm for magnetic resonance imaging (MRI) that works directly in the information rich complex valued k-space. Using three datasets from different institutions with a total of around 140000 MRI slices, we show that our network can perform skull-stripping on the raw data of MRIs while preserving the phase information which no other skull stripping algorithm is able to work with. For two of the datasets, skull stripping performed by HD-BET (Brain Extraction Tool) in the image domain is used as the ground truth, whereas the third dataset comes with per-hand annotated brain segmentations. All three datasets were very similar to the ground truth (DICE scores of 92%-99% and Hausdorff distances of under 5.5 pixel). Results on slices above the eye-region reach DICE scores of up to 99%, whereas the accuracy drops in regions around the eyes and below, with partially blurred output. The output of k-strip often has smoothed edges at the demarcation to the skull. Binary masks are created with an appropriate threshold. With this proof-of-concept study, we were able to show the feasibility of working in the k-space frequency domain, preserving phase information, with consistent results. Besides preserving valuable information for further diagnostics, this approach makes an immediate anonymization of patient data possible, already before being transformed into the image domain. Future research should be dedicated to discovering additional ways the k-space can be used for innovative image analysis and further workflows.

Index Terms—Complex convolutional networks, Deep learning, k-space, Magnetic resonance imaging (MRI), Skull stripping.

I. INTRODUCTION

MAGE scanners provide more data of patients, than can actually be manually reviewed and fully annotated in the current time-limited clinical routine. For example tumor size is often measured by maximum 2D tumor diameter, rather than a more complete tumor volume [1], [2]. Hence, there is a strong desire for automated or at least semi-automated methods, helping to process medical images, or medical information in general [3].

An important example is skull-stripping or brain extraction, the process by which the skull and non-brain tissues are removed from magnetic resonance images (MRI) [4]-[6]. Skull stripping is a fundamental step in neuroimage pre-processing because the accuracy of subsequent image processing, such as registration [7] or tumor segmentation [8], [9], relies on the accuracy of the skull-stripping. Not only is the process important for accuracy of further pipelines, but it is also an important step in anonymization [10]. Furthermore, the extracted skull information can be important for cranial implant design [11]. Unfortunately, manual removal of non-brain tissues is a complex laborious process [12], that often results in inter- and intra-rater incongruities affecting reproducibility in large scale studies [6]. However, in recent years due to theoretical advances in the field and a rise in availability of inexpensive computing power, many deep learning-based automatic skull stripping methods have been proposed [6], [12]-[14].

Medical images are much richer in information than what the human eye can discern [15], and a lot of this untapped data is in the k-space, or the matrix of raw MRI data [16]. Quantitative imaging features, also called “radiomic features,” can provide fuller information about intensity, shape, texture, size and volume [15], [17]. To our knowledge, the k-space has not yet been utilized for deep learning-based segmentation. In this proof-of-concept work, we show that skull stripping is already possible in the k-space, and reconstruction of the k-space results, leads to a stripped skull in the image space. By performing the skull strip directly in k-space and not using brain extraction masks in the complex image space, we want to use possibly hidden information of the frequency domain, which are not visible in the image domain. Skull stripping directly on the raw data also enables researcher to anonymize data even before being transformed into the image domain, greatly reducing the risks of violating privacy policies. Also,
this work is supposed to be a feasibility study which paves the way for future projects which can make better predictions with additional information from the k-space and advance deeper into the uncharted territory of using raw MRI data for segmentations and predictions.

II. RELATED WORK

The “gold standard” for brain extraction and tissue annotation is still a manual segmentation. But because of its high time effort and the problem of inter- and intra-individual variance, leading to non-reproducible results, there has been an urgent search for methods to automate this task [19]. The currently available techniques for brain extraction can be subdivided into five groups [19]:

- mathematical morphology-based methods,
- intensity-based methods,
- deformable surface-based methods,
- atlas-based methods,
- and hybrid methods.

Morphology-based methods, like by Brummer et al. [20], use thresholds and edge-detection algorithms to distinguish between brain and non-brain tissue. The output quality depends on morphological parameters, which have to be set beforehand. Intensity-based methods extract brain tissue by solely using intensity-thresholds, based on the different intensities of brain and non-brain tissues [21], [22]. Using curve evolution and energy functions, deformable surface-based methods perform a brain extraction by solving an optimization problem. A widely used tool applying deformable methods is BET (Brain Extraction Tool) by the FMRIB Software Library (FSL) [23]. Wang et al. [24] developed an algorithm that employs a predefined atlas to create a registration mask, followed by refinements.

Lately, with the advent of deep neural networks [25], [26], more and more algorithms have been published that use the benefits of machine learning, introducing another brain extraction method. Klessie et al. [27] introduced a 3D convolutional neural network (CNN), which is able to also work with pathological data, as most of the algorithms proposed before struggle when facing pathologies like tumorous tissue or abnormal anatomies. Another machine learning approach is HD-BET by Isensee et al. [28], which has the benefit of being trained on different sequences, like pre- and post-contrast T1, T2 and FLAIR. However, all these methods have one major property in common: They do the skull stripping in the image domain after a Fourier transformation has been performed.

Bassey et al. [29] published a survey about complex-valued neural networks (CVNN), giving an insight in different works that have been done with CVNNs. These networks can take complex valued data as input, which is of importance for this work. Another field of use for these kind of networks is Quantum Computing [30] by taking advantage of the representational capacity of complex valued numbers.

In the medical domain, deep learning approaches have mainly been used for interpolation and reconstruction on raw data. Recently, Han et al. [31] proposed an approach to interpolate missing k-space data for better reconstruction results by using a convolutional neural network and a low-rank Hankel matrix completion. Huang et al. [32] combine the task of reconstruction and segmentation, creating an end-to-end framework, which uses raw data information in the reconstruction process and attention modules, possibly preserving important image features.

By performing post processing in the image space, one does not only risk to work on data which has lost information after transformation by using undersampling reconstruction techniques, but also neglects half of the available data - the phase information. In this work, however, a novel network is proposed, which performs skull stripping in the frequency domain, the k-space. K-strip is a network, based on U-Net [33], extended by residual blocks and different complex valued layers, which can take complex data as input.

III. MATERIAL AND METHODS

A. Fourier Transformation

A Fourier transformation [34] converts a 2D-signal from the time-domain into the frequency-domain or from the spatial-domain into the spatial-frequency-domain by applying

$$S(k_x, k_y) = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} s(x, y) \exp(-i2\pi k_x x) \exp(-i2\pi k_y y) \, dx \, dy$$

(1)

The inverse form (inverse Fourier transformation) of this equation is used to transform the raw MRI data into image space. No information is lost during this process. There have been some implementations of neural networks using the Fourier domain to speed up training. Mathieu et al. [35] transform the input and the convolution kernel of a CNN into the Fourier domain. Convolutions in the spatial domain are equivalent to pointwise multiplications in the frequency domain. That way, by applying the FFT on the input data, the computational complexity and time can be reduced due to less operations. In this regard, Pratt et al. [36] were able to reduce computation time for large images in CNNs by applying Fourier pooling and convolution.

B. k-space

The k-space, or the frequency domain, is the raw data domain of MRI images. By applying a Fourier transformation, k-space data can be transformed into the image space [37].

The image, on which skull stripping in today’s algorithms is performed, consists of the transformed magnitude data. Raw data in MRI does not only consist of magnitude, but also phase information. This information can be used in differentiating tissue types, which do not differ in magnitude. Phase information can also be used for flow detection [38], [39]. A more detailed look into k-space and other aspects of magnetic resonance imaging can be found in [40].

Due to sparseness of available raw data, already transformed magnitudinal data from two of the three datasets, has been inverse Fourier transformed to create artificial k-space data. These two datasets will be used to compare our network with state-of-the-art algorithms and to show that it can hold up
with them even though our network is not intended to beat them, but to solve a whole different problem. One of the three datasets comes with magnitudinal and phase data, enabling us to show the feasibility of performing skull stripping on raw data consisting of magnitude and phase.

C. Datasets

Three datasets are used in this work, two of them provided from the University Hospital Essen\footnote{Approved by local ethics board: IRB 21-10487-BO}. The first of these two datasets consists of 30000 $T_1$ (1.5 T and 3.0 T) brain MRI 2D-slices from 207 patients in image space. Some of the scans contain pathologies like glioblastomas multiforme (GBM) \cite{42}, giving the possibility to prove the feasibility of working with pathological data in k-space. The second dataset also comes from the University Hospital Essen and consists of 83000 susceptibility weighted imaging (SWI) 2D-slices from 433 patients with a resolution of 2mm$^3$. This dataset also comes with the corresponding $T_2$ magnitude and phase images. To recreate real raw data, the magnitude and phase images are combined into complex valued images $z$ by scaling the phase data into the range $[0; 2\pi]$ and applying

$$z = r \cdot e^{i\phi},$$

with $r$ being the magnitude data and $\phi$ the scaled phase data. One difference of the SWI dataset to real raw data is the low-pass filtering of the phase information performed as a postprocessing step. Nevertheless we are able to show the feasibility of our algorithm on real world data with this dataset. The ground truth for both datasets is generated by applying the skull-stripping algorithm HD-BET \cite{28} on the $T_2$ images in the image domain. The last dataset is the publicly available Neurofeedback Skull-stripped (NFBS) repository (http://preprocessed-connectomes-project.org/NFB_skullstripped)\footnote{\url{http://preprocessed-connectomes-project.org/NFB_skullstripped}}, containing 24000 fully sampled brain $T_1$ MRI scans from 125 patients with a resolution of 1mm$^3$. The dataset is already anonymized and the ground truth is created by manual refinements of an initial brain segmentation by the BEaST algorithm \cite{43}. All slices are preprocessed by resizing them into the shape 256 × 256 pixel and transformed into k-space via the PyTorch Fast Fourier Transformation function torch.fft \cite{44}. Our network does not need further preprocessing and can work with unnormalized complex valued data. The data is augmented by randomly increasing the values by a factor in the range [0.7; 1.3] of the periphery-augmentation in all direction of the 2D-slice. This periphery-augmentation enables us to augment the data immediately in the complex valued k-space without the need to transform the data back into the image domain. All three datasets are split patient-wise into training, validation and test cases by 70%-20%-10%, respectively.

D. Network Architecture

K-strip is a complex valued convolutional neural network consisting, like U-Net, of a down-sampling (encoder) path and an up-sampling (decoder) path. The architecture of k-strip is shown in Fig.\ref{fig:architecture}. It takes as input the complex valued k-space data of the MRI scan, consisting of brain tissue and skull in the frequency domain, and outputs a complex valued k-space which only consists of the brain tissue in the frequency domain. In the down-sampling path (left side of Fig.\ref{fig:architecture}), the input is split into multiple feature channels and is downsampled via pooling. With increasing network depth, learned features are becoming more specific, while also increasing the computational complexity due to the increasing number of feature maps. By pooling after each convolution layer, this complexity is reduced to speed up the computation time and reduce the memory usage. The initial 2D-input size is $1 \times 256 \times 256$ pixel (number of channels × height × width) and is abstracted into feature maps via consecutive complex double convolutions inside the residual blocks to the size of $256 \times 32 \times 32$ pixel. The input is then up-sampled again, until it reaches its initial dimensionality.

The complex convolution blocks are wrapped inside residual blocks. Residual blocks have the benefit of allowing an easier gradient flow by using residual connections between in- and output of the convolution blocks, such that a bigger variety of information can be used by the network. In the k-strip network, in each encoder-layer the input is iterated through four residual blocks before being downsampled into the next deeper layer. The concept of complex convolution layers is the same as of normal convolution layers, with the difference, that instead of a simple convolution, we now work with a complex convolution matrix $W$, which acts as the kernel of size $3 \times 3$ and performs a complex convolution \cite{45}, as seen in \cite{46}:

Complex convolution matrix:
\[
W = X + iY
\]
Complex data:
\[
d = a + ib
\]
Complex convolution:
\[
W \ast d = (X \ast a - Y \ast b) + i(X \ast b - Y \ast a)
\]

Each cConv-block consists of two complex convolutions following a complex ReLU (cReLU) activation function and a complex Batch normalization. After each cConv-block, the number of features is doubled. cReLU applies a ReLU activation on the real and the imaginary part separately and combines the output back into a complex number:

\[
cReLU(\{d\}) = \text{ReLU}(Re\{d\}) + i\text{ReLU}(Im\{d\}).
\]

By applying a complex batch normalization \cite{46} after each activation function, the output is normalized per batch, preventing unbalanced gradients within the network.
Fig. 1. Network architecture of k-strip, with a down-sampling path (left branch) and an up-sampling path (right branch). The blue boxes correspond to the convolutions inside the residual blocks and their feature maps. The numbers beneath and at the side of the boxes depict the input numbers of channels, height and width. For a better gradient flow, residual connections between the double convolutions are implemented. In the downsampling branch and the bottleneck, each layer consists of four consecutive residual blocks. The upsampling branch uses nearest-neighbour-upsampling in combination with a complex valued convolution to increase the inputs dimensionality. Input and output are shown magnitudinal and logarithmically.

Fig. 2. Spectral pooling with a pooling kernel of size two. The k-space, pictured logarithmic and absolute valued, is halved with every pooling step, which leads to a decreasing resolution. Even after reducing the initial k-space by 95%, the object shape is still recognizable.

\[ \tilde{x} = (V)^{-\frac{1}{2}} (x - E[x]) \]

Covariance matrix:

\[
V = \begin{pmatrix}
V_{rr} & V_{ri} \\
V_{ir} & V_{ii}
\end{pmatrix}
= \begin{pmatrix}
\text{Cov}(Re\{x\}, Re\{x\}) & \text{Cov}(Re\{x\}, Im\{x\}) \\
\text{Cov}(Im\{x\}, Re\{x\}) & \text{Cov}(Im\{x\}, Im\{x\})
\end{pmatrix}
\]

Spectral pooling \[48\] reduces the image size, by cutting the periphery of the k-space by half its size in each layer. Even with cutting the high frequencies and thus reducing the input size by over 95%, the initial shape is still recognizable. By downsampling the input, the learned feature maps can focus on the most important structural elements, while reducing the computational complexity drastically. Spectral pooling on exemplary brain MRI images is shown in Fig. 2. In the upsampling (decoder) path, instead of the classical transposed convolution, we use a nearest neighbour upsampling approach combined with a complex valued convolution to increase the images dimensionality again. It showed in our experiments, that transposed convolutional layers led to vanishing gradients, hindering the ability of our network drastically. Skip connections provide an additional path for the gradient by skipping some layers and feeding the output directly into the next layers. That way, the problem of vanishing gradients can be avoided, as even when some gradients approach zero, they are complemented by gradients of previous layers \[49\].

IV. EXPERIMENTS

A. Training

For training, the Adam optimizer \[50\] with an initial learning rate of 1e-3, which is reduced by 50% each 50th epoch, a beta coefficient of 0.99 and an epsilon value of 1e-08 is used. After each encoder convolution a dropout of 5% is
chosen. The network output is compared with the ground truth using the complex L1-loss, also known as least absolute error (LAE). The ground truth consists of the skull-stripped brains transformed into k-space. Training stops with the 150th epoch, because the validation loss does not further decrease at around this point. With a batch size of 64, the overall training time takes three days on an NVIDIA A100 GPU with 86GB of graphics memory.

B. Evaluation Metrics

For evaluation we decided to use two metrics, one being the Dice coefficient (DSC) \[51\] as an overlap measure between the brain segmentation \(X\) and the reference mask \(Y\):

\[
\text{DSC} = \frac{2|X \cap Y|}{|X| + |Y|} = \frac{2TP}{2TP + 2FP + 2FN}. \quad (6)
\]

The Dice coefficient takes values in the range of \([0, 100\%]\), with 100\% being a perfect segmentation, identical to the ground truth. The directed Hausdorff distance (DHD) \[52\] is used for evaluating maximum deviations, with a value starting at zero pixel for no deviations, increasing with wider outliers in the segmentation mask:

\[
\text{DHD}(X,Y) = \max_{x \in X} \min_{y \in Y} ||x - y||. \quad (7)
\]

Accuracy, sensistivity and specificity are used as additional evaluation metrics. All results are compared to the BrainSuite algorithm (BSE) \[53\] from Shattuck and Leahy, whereas on the NFBS dataset we also compare to HD-BET and our own network with less training samples. Even though our approach is trying to solve a different problem than the compared methods (skull stripping in frequency domain and thus preserving phase information) we want to show, that it still can compete with state-of-the-art approaches in the brain regions in which phase information is desired to be preserved. All slices which consist of less than 5000 pixels of brain tissue are not considered for evaluation, which means that the lower part of the brain-stem and the top most brain slices are not evaluated. This can be justified by the fact that there are no more phase information of relevance for further workflows in these regions. To compare k-strip with methods working in the image domain, the output needs to be Fourier transformed, followed by creating a binary mask. Due to the nature of the Fourier transformation, the output contains some frequencies which result in shadows around the skull stripped image. That is the reason for creating the binary mask. A threshold is used to classify the two classes (brain and non-brain tissue). After quantitative evaluations, the threshold is set to 1.7 times the mean value of the predicted image domain data. All values below threshold are set to zero.

V. RESULTS

Fig. 3 and Fig. 4 show the predicted magnitude and phase from a sample of the SWI test set, respectively. For visualization the k-space is shown as the logarithmic magnitude (bottom row), but the networks input consists of the complex valued k-space. To understand the input and output data, the top row shows the Fourier transformed image domain, but it has to be kept in mind, that these images are not used in the whole workflow, except for visualization and evaluation. A binary mask of the output and ground truth in image domain is calculated via the threshold method to then calculate the difference (ground truth - prediction). The phase output consists of the segmented brain and the background noise, which makes it harder to appreciate the result. But still it is obvious that the phase data of the brain is successfully segmented when looking at the difference between the ground truth and the prediction on the right side. Unlike the other figure showing the magnitudinal output, the difference is not calculated on the binary masks, but on the output and the ground truth directly to show, that no phase information is lost in the process of segmenting the raw data. Fig. 5 shows an exemplary output for the NFBS test set of the region below the eyes. In this region of the brain, the network still reaches Dice scores from over 95\%. Below this region accuracy drops, below threshold are set to zero.
network output is smoothed around the edges in comparison to the ground truth. k-Strip achieves confident results also in the presence of large pathologies as seen in this example. The network predicts the center of the k-space more accurately than the periphery, with the largest deviations from the ground truth in the far periphery which is cut out earlier due to the spectral pooling. The calculated evaluation metrics for all test sets and in comparison with the BSE algorithm are listed in Table I. On the NFBS test set we also compared with the HD-BET algorithm. k-Strip reaches better scores on the SWI dataset, with an overall Dice score of over 96%. k-Strips results show that even without the phase information it can keep up with current state-of-the-art algorithms. k-Strips specificity is very high for every test set, ranging between 98.8% and 99.9%, whereas the sensitivity is lower with values between 94.4% and 97.1%, as the threshold method tends to cut out the blurry edge of the segmented brain. Brain extraction in the region above the eyes (as in Fig. 3) works very well with DSCs above 95%. The accuracy drops in regions around the eyes and below, with partially blurred output. Poor skull stripping may also occur because of threshold problems leading to erroneous binary masks. In Fig. 7 we show exemplary feature maps of two different convolution layer. For visualization the k-space shown in the figures is magnitudinal, whereas the networks actual feature maps are complex valued. The downsampling feature maps show a specialization into the k-space center, the low frequencies corresponding to texture features, and the k-space periphery, the high frequencies corresponding to image details, individually. The upsampling (decoder) path, in contrast, mainly focuses on the k-space center, while being stretched further into the periphery in each feature map.

When using skull stripping in the clinical routine or when processing large amounts of patient data, the inference time is one crucial factor for considering the proper algorithm. Our proposed method takes around 0.02s to segment one complex valued 2D slice, consisting of magnitude and phase information, with a shape of 256 × 256 pixels. For a volume consisting of 90 2D slices, this leads to a total inference time of around 2s. In our experiments, HD-BETs inference time for the same volume size with only the magnitude information in the image domain was 20s, whereas BSE took 18s. It has to be noted, that the inference times of HD-BET and BSE also included volume loading and saving, but this would only reduce the inference time by a few seconds, which still leads to inference times more than 10s longer than the one from our model.

VI. DISCUSSION

In this paper, we proposed a novel framework based on the U-Net architecture for brain extraction in k-space, in which the raw data of MRI is recorded. This proof-of-concept study shows the feasibility of working in the frequency domain and, thus, preserving phase information, while achieving consistent results. We performed training and testing on three different datasets consisting of T1, T2 and SWI scans, with one dataset containing real phase information.

In regions above the eyes, the predicted output almost matches the corresponding ground truth, whereas differing sometimes in regions of the eyes and below. It has to be noted, that with the provided training data in the GBM and SWI dataset, k-strip can not outperform HD-BET, as its skull strips act as the ground truth. The output of k-strip shows often smoothed edges at the demarcation to the skull, the reason being the nature of the k-space and the chosen approach. As we only change the values in k-space, k-strip is not able to...
TABLE I
Scores for all three test sets (SWI, GBM, NFBS) of our proposed k-Strip network and the BSE algorithm as comparison method. On the NFBS test set, HD-BET is used as an additional comparison method. The evaluation metrics are Dice score, directed Hausdorff distance, accuracy, sensitivity and specificity, listed in this order. On the SWI dataset, k-Strip is compared with itself when trained with a different amount of training data (25000 and 70000 slices).

| Test Set | BSE [53] | k-Strip (70000) | k-Strip (25000) |
|----------|---------|----------------|----------------|
| SWI      |         |                |                |
| Dice (%) | 93.4    | 97.4           | 96.9           |
| DHD (pixel) | 4.04 | 3.42           | 3.35           |
| Acc (%)  | 96.6    | 98.9           | 98.9           |
| Sens (%) | 95.5    | 97.5           | 97.2           |
| Spec (%) | 97.0    | 99.5           | 99.5           |
| GBM      |         |                |                |
| BSE [53] |         |                |                |
| k-Strip  | 94.6    | 93.9           |                |
| Dice (%) |          | 5.03           | 4.06           |
| DHD (pixel) |       |                |                |
| Acc (%)  | 97.0    | 97.4           |                |
| Sens (%) | 98.5    | 94.5           |                |
| Spec (%) | 94.2    | 98.8           |                |
| NFBS     |         |                |                |
| BSE [53] |         |                |                |
| HD-BET [28] |      |                |                |
| k-Strip  | 95.7    | 96.6           |                |
| Dice (%) |          | 3.94           | 3.21           |
| DHD (pixel) |       |                |                |
| Acc (%)  | 97.5    | 98.7           |                |
| Sens (%) | 97.1    | 98.4           |                |
| Spec (%) | 99.1    | 99.7           |                |

Fig. 7. Magnitudinal feature maps of the fourth downsampling convolution and the second upsampling convolution. The input size of the given convolution is written in brackets with the shape [channel, batch-size, height, width], whereas the feature maps in the downsampling path specialize on k-space center and periphery individually, the convolutions in the upsampling path seem to focus on the k-space center.

make exact cuts in the image domain. This may change further customization of the network.

In regions below the eyes, in the region of the brain stem, our threshold method for creating binary masks, does not perform very well and a different method for creating binary masks in this region needs to be found in future works.

With the center having values of magnitudes larger than the periphery, differences in the output are much more punished by the network (stronger weight-changes) than differences in the periphery. This leads to a higher deviation in the periphery of the k-space, leading to the smoothed edges of the segmentation. We might be able to resolve this in future works by implementing a logarithmic loss function which punishes deviations in the periphery stronger. We noticed, that HD-BET sometimes cuts out spots inside the brain, maybe due to unusual anomalies. K-strip does not seem to have problems with those cases, but does not produce as fine cuts as HD-BET or BSE does.

Reducing the size of the k-space input, using spectral pooling beforehand, would lead to faster training times, while preserving most of the details. A decision has to be made here whether the finest details provided by the k-space periphery are more important compared to faster training times, or vice versa.

Future work sees the training with real data directly from the scanner, implementing the network into more advanced workflows, for example enabling a immediate anonymization of the patient data even before being transformed into the
image domain. We also want to expand the presented concept to other segmentation tasks, like tumor segmentation, using valuable phase information for more precise results, as well as further optimization of the existing network.

VII. CONCLUSION

K-strip is a novel complex valued CNN, which enables brain extraction (segmentation) on raw data of MRI scans in the k-space. To the best of our knowledge, this is the first Deep Learning-based network doing skull stripping in the k-space of MRI data. Hence, this work acts as a proof-of-concept study, while achieving comparable results as HD-BET and BSE, state-of-the-art algorithms, working in the image space. Our network makes it possible to preserve the phase information of the raw data which are discarded otherwise in the further workflow. Our approach also allows an anonymization immediately after data comes out of the scanner, even before transformation into the image domain, hence reducing the risk of privacy violation of patient data. We hope that in future, more works will investigate the possibilities and benefits of working in k-space, for example, preserving the "additional" phase information for tumor classification and tissue differentiation.

VIII. REFERENCES

[1] Jan Egger et al. “A medical software system for volumetric analysis of cerebral pathologies in magnetic resonance imaging (MRI) data”. In: Journal of medical systems 36.4 (2012), pp. 2097–2109.
[2] Markus Zimmermann et al. “CT-based whole-body tumor volumetry versus RECIST 1.1: Feasibility and implications for inter-reader variability”. In: European Journal of Radiology 135 (2021), p. 109514.
[3] Lars Heiliger et al. “Beyond Medical Imaging-A Review of Multimodal Deep Learning in Radiology”. In: (2022).
[4] P Kalavathi and VB Prasath. “Methods on skull stripping of MRI head scan images—a review”. In: Journal of digital imaging 29.3 (2016), pp. 365–379.
[5] Snehashis Roy et al. “Robust skull stripping using multiple MR image contrasts insensitive to pathology”. In: Neuroimage 146 (2017), pp. 132–147.
[6] Siddhesh P Thakur et al. “Skull-stripping of glioblastoma MRI scans using 3D deep learning”. In: International MICCAI Brainlesion Workshop. Springer. 2019, pp. 57–68.
[7] Arno Klein et al. “Evaluation of 14 nonlinear deformation algorithms applied to human brain MRI registration”. In: Neuroimage 46.3 (2009), pp. 786–802.
[8] Bjoern H Menze et al. “The multimodal brain tumor image segmentation benchmark (BRATS)”. In: IEEE transactions on medical imaging 34.10 (2014), pp. 1993–2024.
[9] Zeynettin Akkus et al. “Deep learning for brain MRI segmentation: state of the art and future directions”. In: Journal of digital imaging 30.4 (2017), pp. 449–459.
[10] Hendrik Mattern et al. “Chemical shift–based prospective k-space anonymization”. In: Magnetic resonance in medicine 85.2 (2021), pp. 962–969.
[11] Ana Morais, Jan Egger, and Victor Alves. “Automated computer-aided design of cranial implants using a deep volumetric convolutional denoising autoencoder”. In: World Conference on Information Systems and Technologies. Springer. 2019, pp. 151–160.
[12] Roberto Souza et al. “An open, multi-vendor, multi-field-strength brain MR dataset and analysis of publicly available skull stripping methods agreement”. In: Neuroimage 170 (2018), pp. 482–494.
[13] Li-Ming Hsu et al. “Automatic Skull stripping of rat and mouse brain MRI data using U-net”. In: Frontiers in neuroscience 14 (2020), p. 935.
[14] Riccardo De Feo et al. “Automated joint skull-stripping and segmentation with Multi-Task U-Net in large mouse brain MRI databases”. In: NeuroImage 229 (2021), p. 117734.
[15] Michele Avanzo et al. “Machine and deep learning methods for radiomics”. In: Medical physics 47.5 (2020), e185–e202.
[16] Cynthia B Paschal and H Douglas Morris. “K-space in the clinic”. In: Journal of Magnetic Resonance Imaging: An Official Journal of the International Society for Magnetic Resonance in Medicine 19.2 (2004), pp. 145–159.
[17] Philippe Lambin et al. “Radiomics: extracting more information from medical images using advanced feature analysis”. In: European journal of cancer 48.4 (2012), pp. 441–446.
[18] Katriin Tingelhoff et al. “Analysis of manual segmentation in paranasal CT images”. In: European archives of oto-rhino-laryngology 265.9 (2008), pp. 1061–1070.
[19] P Kalavathi and VB Prasath. “Methods on skull stripping of MRI head scan images—a review”. In: Journal of digital imaging 29.3 (2016), pp. 365–379.
[20] Marijn E Brunner et al. “Automatic detection of brain contours in MRI data sets”. In: IEEE Transactions on medical imaging 12.2 (1993), pp. 153–166.
[21] Benoit M Dawant et al. “Automatic 3-D segmentation of internal structures of the head in MR images using a combination of similarity and free-form transformations. I. Methodology and validation on normal subjects”. In: IEEE transactions on medical imaging 18.10 (1999), pp. 909–916.
[22] Zu Y Shan, Guang H Yue, and Jing Z Liu. “Automated histogram-based brain segmentation in T1-weighted three-dimensional magnetic resonance head images”. In: NeuroImage 17.3 (2002), pp. 1587–1598.
[23] Stephen M Smith. “Fast robust automated brain extraction”. In: Human brain mapping 17.3 (2002), pp. 143–155.
[24] Yaping Wang et al. “Robust deformable-surface-based skull-stripping for large-scale studies”. In: International Conference on Medical Image Computing
[25] Jan Egger et al. “Deep learning—a first meta-survey of selected reviews across scientific disciplines, their commonalities, challenges and research impact”. In: PeerJ Computer Science 7 (2021), e773.

[26] Jan Egger et al. “Medical deep learning—A systematic meta-review”. In: Computer Methods and Programs in Biomedicine 221 (2022), p. 106874. ISBN: 0169-2607. DOI: https://doi.org/10.1016/j.cmpb.2022.106874 URL: https://www.sciencedirect.com/science/article/pii/S0169260722002565

[27] Jens Kleesiek et al. “Deep MRI brain extraction: A 3D convolutional neural network for skull stripping”. In: NeuroImage 129 (2016), pp. 460–469.

[28] Fabian Isensee et al. “Automated brain extraction of multisequence MRI using artificial neural networks”. In: Human brain mapping 40.17 (2019), pp. 4952–4964.

[29] Joshua Bassey, Lijun Qian, and Xianfang Li. “A survey of complex-valued neural networks”. In: arXiv preprint arXiv:2101.12249 (2021).

[30] Shangshang Shi et al. “Quantum-inspired complex convolutional neural networks”. In: Applied Intelligence (2022), pp. 1–10.

[31] Yoseo Han, Leonard Sunwoo, and Jong Chul Ye. “{(k)}-space deep learning for accelerated MRI”. In: IEEE transactions on medical imaging 39.2 (2019), pp. 377–386.

[32] Qiaoying Huang et al. “Brain segmentation from k-space with end-to-end recurrent attention network”. In: International Conference on Medical Image Computing and Computer-Assisted Intervention. Springer. 2019, pp. 275–283.

[33] Olaf Ronneberger, Philipp Fischer, and Thomas Brox. “U-net: Convolutional networks for biomedical image segmentation”. In: International Conference on Medical image computing and computer-assisted intervention. Springer. 2015, pp. 234–241.

[34] Ronald Newbold Bracewell and Ronald N Bracewell. The Fourier transform and its applications. Vol. 31999. McGraw-hill New York, 1986.

[35] Michael Mathieu, Mikael Henaff, and Yann LeCun. “Fast training of convolutional networks through ffts”. In: arXiv preprint arXiv:1312.5851 (2013).

[36] Harry Pratt et al. “Fccn: Fourier convolutional neural networks”. In: Joint European Conference on Machine Learning and Knowledge Discovery in Databases. Springer. 2017, pp. 786–798.

[37] Ronald Newbold Bracewell and Ronald N Bracewell. The Fourier transform and its applications. Vol. 31999. McGraw-hill New York, 1986.

[38] David T Wymer et al. “Phase-contrast MRI: physics, techniques, and clinical applications”. In: Radiographics 40.1 (2020), pp. 122–140.

[39] Sofia Chavez, Qing-San Xiang, and Li An. “Understanding phase maps in MRI: a new cutline phase unwrapping method”. In: IEEE transactions on medical imaging 21.8 (2002), pp. 966–977.

[40] Donald W McRobbie et al. MRI from Picture to Proton. Cambridge university press, 2017.

[41] Jan Egger et al. “GBM volumetry using the 3D Slicer medical image computing platform”. In: Scientific reports 3.1 (2013), pp. 1–7.

[42] Benjamin Puccio et al. “The preprocessed connectomes project repository of manually corrected skull-stripped T1-weighted anatomical MRI data”. In: Gigascience 5.1 (2016), s13742–016.

[43] Simon F Eskildsen et al. “BEaST: brain extraction based on nonlocal segmentation technique”. In: NeuroImage 59.3 (2012), pp. 2362–2373.

[44] Adam Paszke et al. “PyTorch: An Imperative Style, High-Performance Deep Learning Library”. In: Advances in Neural Information Processing Systems 32. Ed. by H. Wallach et al. Curran Associates, Inc., 2019, pp. 8024–8035. URL: http://papers.neurips.cc/paper/9015-pytorch-an-imperative-style-high-performance-deep-learning-library.pdf

[45] Elizabeth K Cole et al. “Analysis of deep complex-valued convolutional neural networks for MRI reconstruction”. In: arXiv preprint arXiv:2004.01738 (2020).

[46] Mohamed Trabelsi, Panagiotis Kakosimos, and Hasan Komurcugil. “Mitigation of grid voltage disturbances using quasi-Z-source based dynamic voltage restorer”. In: 2018 IEEE 12th International Conference on Compatibility, Power Electronics and Power Engineering (CPE-POWERENG 2018). IEEE. 2018, pp. 1–6.

[47] Sergey Lioffe and Christian Szegedy. “Batch normalization: Accelerating deep network training by reducing internal covariate shift”. In: International conference on machine learning. PMLR. 2015, pp. 448–456.

[48] Oren Rippel, Jasper Snoek, and Ryan P Adams. “Spectral representations for convolutional neural networks”. In: Advances in neural information processing systems 28 (2015).

[49] Michal Drozdal et al. “The importance of skip connections in biomedical image segmentation”. In: Deep learning and data labeling for medical applications. Springer. 2016, pp. 179–187.

[50] Diederik P Kingma and Jimmy Ba. “Adam: A method for stochastic optimization”. In: arXiv preprint arXiv:1412.6980 (2014).

[51] Lee R Dice. “Measures of the amount of ecologic distances in biological communities”. In: Ecology 26.3 (1945), pp. 297–302.

[52] Abdel Aziz Taha and Allan Hanbury. “An efficient algorithm for calculating the exact Hausdorff distance”. In: IEEE transactions on pattern analysis and machine intelligence 37.11 (2015), pp. 2153–2163.

[53] David W Shattuck and Richard M Leahy. “BrainSuite: an automated cortical surface identification tool”. In: Medical image analysis 6.2 (2002), pp. 129–142.