Multiplicative Intrinsic Component Optimization Software Manual

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1 Introduction

This manual describes the usage of the Multiplicative Intrinsic Component Optimization (MICO) software. The MICO software is an implementation of an algorithm for simultaneous bias field estimation and segmentation of three-dimensional (3D) MR brain images [2, 3]. It can be used for:

- Bias correction.
- Segmentation of independent patient scans.
- Segmentation of longitudinal series of brain images.

The segmentations contain different labels for cerebrospinal fluid (CSF), gray matter (GM), white matter (WM), and the value zero for background (BG). The bias field is estimated by a linear combination of a number of smooth basis functions, which are constructed as 20 polynomials up to the third degree.

MICO can be used on the command-line using the `mico` command or in C++ code by linking to the `mico` library. Note that only the most important options of the `mico` command are documented in the following. For more details on the available options, run the command with the option `--help`. This will output a brief description together with a list of required and optional arguments. For a list of available options only, use `--helpshort` instead. If you want to use MICO directly in your C++ code, please refer to the API documentation.

2 Preparation

Any input patient data has to be skull stripped first. This can be done using `bet` [4], for example. In case of longitudinal studies, all time points must further be co-registered across time using a rigid registration with six degrees of freedom. Therefore, FSL's `flirt` [1] command is commonly applied. Please refer to the documentation of the named third-party tools for further information on how they are applied.

Note that the input images must be three-dimensional images with scalar voxel type of either DT_UNSIGNED_CHAR, DT_SIGNED_SHORT, DT_SIGNED_INT, or DT_FLOAT, and stored in the ANALYZE 7.5 or the NIfTI-1 file format.

For your convenience, we included 11 scans of a single subject referred to as `BC` which were acquired at different time points. The directory where these files are installed is referred to in the following as `example` shell variable. Further, we assume that the path to the `mico` command is in your `PATH` environment variable.

```
$ prefix=/top/directory/of/MICO/installation
$ setenv PATH "${prefix}/bin:${PATH}"
$ example=${prefix}/share/sbia/mico/example
```

Or in case of BASH:

```
$ prefix=/top/directory/of/MICO/installation
$ export PATH="${prefix}/bin:${PATH}"
$ example=${prefix}/share/sbia/mico/example
```

3 Segmentation of MR Brain Images

In order to segment a given MR brain image into CSF, GM, WM, and BG, simply run the MICO command with the file path of the input image as argument, i.e.,

```
$ mico ${example}/BC01-T1-byte_cbq
```

The resulting segmentation (label image) will in this case be written to the file `BC01-T1-byte_cbq_segments.nii.gz` located in the current working directory. Use the `--outputdir` option to specify a different output directory and `--suffix` to change the file name suffix of the segmentation image, optionally including a different NIfTI-1 file format extension. Moreover, you can specify more than one input image to segment. Note, however, that each input image is segmented independently.

```
$ mico --outputdir segmentations --suffix .hdr
        ${example}/BC01-T1-byte_cbq
        ${example}/BC02-T1-byte_cbq_flirtedToY16dof
        ${example}/BC03-T1-byte_cbq_flirtedToY16dof
        ${example}/BC04-T1-byte_cbq_flirtedToY16dof
        ${example}/BC05-T1-byte_cbq_flirtedToY16dof
        ${example}/BC06-T1-byte_cbq_flirtedToY16dof
        ${example}/BC07-T1-byte_cbq_flirtedToY16dof
        ${example}/BC08-T1-byte_cbq_flirtedToY16dof
        ${example}/BC09-T1-byte_cbq_flirtedToY16dof
        ${example}/BC10-T1-byte_cbq_flirtedToY16dof
        ${example}/BC11-T1-byte_cbq_flirtedToY16dof
```

Alternatively, you can list the image file paths in a text file, one file path per line, and use the `--inputlist` option instead, i.e.,

```
$ mico --inputlist ${example}/BC.lst --outputdir segmentations --suffix .hdr
```

Either command stores the segmentations in the two file NIfTI-1 image file format under the same file name as the corresponding input image, but in the subdirectory `segmentations` of the current working directory.

4 Segmentation of Longitudinal Study

In Section 3 we have demonstrated how the `mico` command can be used to segment 3D brain images into the three major tissue classes. This, however, is done independently, i.e., no longitudinal information given across time is used to maintain consistency among the segmentations of the different time points. In order to take the longitudinal information into consideration, use the option `--4d`. To segment the longitudinal example study, run the command:

```
$ mico --4d --outputdir segmentations --suffix _labels
        ${example}/BC01-T1-byte_cbq
        ${example}/BC02-T1-byte_cbq_flirtedToY16dof
        ${example}/BC03-T1-byte_cbq_flirtedToY16dof
        ${example}/BC04-T1-byte_cbq_flirtedToY16dof
        ${example}/BC05-T1-byte_cbq_flirtedToY16dof
        ${example}/BC06-T1-byte_cbq_flirtedToY16dof
        ${example}/BC07-T1-byte_cbq_flirtedToY16dof
        ${example}/BC08-T1-byte_cbq_flirtedToY16dof
        ${example}/BC09-T1-byte_cbq_flirtedToY16dof
        ${example}/BC10-T1-byte_cbq_flirtedToY16dof
        ${example}/BC11-T1-byte_cbq_flirtedToY16dof
```

Alternatively, you can list the image file paths in a text file, one file path per line, and use the `--inputlist` option instead, i.e.,

```
$ mico --4d --inputlist ${example}/BC.lst --outputdir segmentations
        --suffix _labels
```

5 Bias Correction of MRI Brain Images

The MICO algorithm performs a bias field estimation simultaneously with the segmentation. Hence, the bias correction is always applied even if only the final segmentations are saved to disk. In order to save also the bias corrected image(s), use the `--bias-correct` option. If only the bias correction should be performed, use the option `--bias-correct-only` instead.

For example, to perform a bias correction of the baseline image of the given longitudinal example study, run the command:

```
$ mico --bias-correct-only ${example}/BC01-T1-byte_cbq
```

This will output the bias corrected image and save it in the current working directory as the file `BC01-T1-byte_cbq_biascorrected.nii.gz`. If you want to use a different file name suffix or file format, use the `--bias-correct-suffix` option to specify a different suffix for the file names of the bias corrected images.

6 Notes

- Recognized file format extensions are `.hdr` or `.img` for header and data NIfTI-1 or ANALYZE 7.5 image file pairs, `.hdr.gz` and `.img.gz` for compressed header and data NIfTI-1 image file pairs, `.nii` for uncompressed NIfTI-1 images, and `.nii.gz` for compressed NIfTI-1 images. Only if an input image was stored in the ANALYZE 7.5 format and no particular format has been specified for the output images, these output images are stored in the ANALYZE 7.5 format as well.

- Increase the weight for a certain tissue class if it is over segmented, and decrease the weight if it is under segmented. The default weights used by `mico` are reported in the help output of this command, i.e., `mico --help`.

- If there is almost no intensity inhomogeneity in the input image, a large weight (e.g. 10) can be used for the fuzzy C-means (FCM) term, the parameter `--lambda` of `mico`. In this case, the performance of the MICO algorithm is close to the performance of the FCM algorithm. If the intensity inhomogeneity is significant, however, set the weight of the FCM term to zero or a very small positive number (e.g. 0.00001). Typically, for 3T MR images, this parameter can be set to zero. For 1.5T MR images, this parameter can be set to 1 if the intensity inhomogeneity is not strong, and to 10 if there is almost no inhomogeneity.

- By default, only the label map with the labels of the segmented structures is output. The output of the membership images, one for each segmented structure, can be requested using the `--fuzzy` option. These images are commonly also referred to as fuzzy segmentation(s).

References

[1] Jenkinson, M., Bannister, P.R., Brady, J., Smith, S.: Improved optimization for the robust and accurate linear registration and motion correction of brain images. Neuroimage 17, 825–841 (2002)

[2] Li, C., Gatenby, C., Wang, L., Gore, J.C.: A robust parametric method for bias field estimation and segmentation of MR images. CVPR pp. 218–223 (2009)

[3] Li, C., Li, F., Davatzikos, C., Gore, J.C.: Multiplicative intrinsic component optimization for bias field estimation and tissue segmengation for MRI (2011)

[4] Smith, S.: Fast robust automated brain extraction. Hum Brain Mapp pp. 143–55 (2002)