VOP_overestimation_postprocessing_GPU_hybrid_tri

Algorithm for post processing the overestimation of an existing set of VOPs

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Syntax

```
[VOP,Sglobal_new]=VOP_overestimation_postprocessing_GPU_hybrid_tri(filename_in,
VOP_start, Sglobal, options)
```

Description

This function takes a VOP set from a previous compression and calculates the necessary overestimation as proposed by Orzada et al.(1). Each of the VOPs gets an individual overestimation matrix.This is a new version with much enhanced speed. This enhancement is achieved by exchanging the CC criterion presented by Lee et al.(2) with the CO criterion presented by Gras et al.(3) in parts of the algorithm. A paper for this algorithm is under review at Magnetic Resonance in Medicine.

Input arguments

`filename_in` – Character array containing filename and path pointing to a full set of SAR matrices.

The file must contain an array with the name "matrices", either in the form N_{ch} by N_{ch} by number of SAR matrices, or in triangular form (use function `format_sq2tri(matrices)` to get the right form). If you want to use a GPU, it is recommended to use `single` format.

`VOP_start` – N_{ch} by N_{ch} by N_{VOPs} array, containing the VOPs as produced by our compression algorithm (including overestimation).

`Sglobal` – N_{ch} by N_{ch} overestimation matrix as provided in the files from our compression algorithm.

`options` – Struct with options for post-processing

There are many options to influence the behavior of the algorithm. For standard usage, it is not necessary to use the options. The following table shows the available options. Example: `options.name_save = 'Test_8ch'`. There are default values for all options if you do not explicitly specify them.

`name_save`	Character array with the name in which the post processed VOPs are saved. Will be saved under the name `['PP_' name_save]`. Default is `filename_in`.
`use_GPU`	Default is `FALSE`. If set to `TRUE` the algorithm will use the GPU only at the beginning for a short time. If your GPU is not supported, the algorithm will revert to performing the specific calculation on CPU. There is hardly a difference in total time for the algorithm whether you use GPU or CPU.
`numMat4GPU`	Number of matrices that are transferred to GPU in a batch. Default is 1e5.
`numMat4Pageeig`	Number of matrices that are transferred to pageeig function in a batch. Default is 10,000. Like the GPU calculation, this is

	only done once at the beginning of the algorithm and only takes a very small fraction of the total calculation time.
N_block	Size of the block of matrices send to rQstar in a batch. Default is 400. For computers with extreme numbers of CPU cores, you might experience a speed gain by increasing this number.
sort_order	The order in which the SAR matrices are sorted before starting the post processing. Default 'ascend'. Ascending order has shown better results than 'descend'.
overestimationReduction	Experimental option! The default value of 1 means, that all of the original overestimation is taken away from the VOPs before post processing. If you use a number below 1, you leave some of the original overestimation on the VOPs.
exponent_cwv	Experimental option! The default value is 1. By changing the value, you change the weighting of the coefficients for adding overestimation.
use_global_opt	Default is FALSE. If set to TRUE, the CC criterion is calculated with a global optimization. This is much slower and might not even improve the results, as the optimization problem is convex anyway.
use_parallel	Default is FALSE. If set to TRUE, the CC criterion is calculated with Matlab's fmincon's parallel option. This might be faster on some systems. This still needs to be checked.

Outputs

VOP – The VOPs with individual overestimation matrices added (N_{ch} by N_{ch} by N_{VOPs}). This is a complete set of VOPs that can be used for pulse design or power supervision. (Please note that checking for validity is the users responsibility.)

Sglobal_new – Individual overestimation matrices for all VOPs, in the same format as the VOPs.

Furthmerore, the algorithm saves a .mat file by the name specified in the options (see above), which contains the following information:

VOP – The VOPs (N_{ch} by N_{ch} by N_{VOPs}) with their individual overestimation matrices already added.

Sglobal_new – The individual overestimation matrices (N_{ch} by N_{ch} by N_{VOPs}).

Sglobal – The original overestimation matrix.

elapsed_time – The total calculation time in second.

eps_G – the original overestimation factor.

max_Value_S – The maximum eigenvalue over all individual overestimation matrices. Note that this is not identical to the actual maximum overestimation!

1. Orzada S, Fiedler TM, Quick HH, Ladd ME. Post-processing algorithms for specific absorption rate compression. Magn Reson Med 2021;86(5):2853-2861.

2. Lee J, Gebhardt M, Wald LL, Adalsteinsson E. Local SAR in parallel transmission pulse design. Magn Reson Med 2012;67(6):1566-1578.
3. Gras V, Boulant N, Luong M, Morel L, Le Touz N, Adam JP, Joly JC. A mathematical analysis of clustering-free local SAR compression algorithms for MRI safety in parallel transmission. IEEE Trans Med Imaging 2023;PP.