# musclesyneRgies: factorization of electromyographic data in R with sensible defaults

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Summary

Coordinated movements such as walking or playing a musical instrument are the result of accurately timed muscle activations produced by the central nervous system. Mathematical tools can help scientists to visualize which muscle is active during a specific phase of the considered movement and how important is the contribution of each muscle to the overall task. musclesyneRgies is an R package (R Core Team, 2022) that implements one of the existing mathematical models of motor coordination. From the raw data and until the final factorization of electromyographic activities, the package offers a complete analysis framework with sensible defaults that can be flexibly modified at need. musclesyneRgies is addressed to scientists of any programming skill level working in fields such as neuroscience, biomechanics, biomedical engineering, robotics or sport science.

Statement of need

The great amount of muscles and joints in the body of vertebrate animals makes the problem of motor control a high-dimensional one: while producing and controlling movement, the central nervous system is constantly dealing with an over-abundant number of degrees of freedom. Amongst the existing theories that attempt to describe the modular coordination of movements, one proposed by Nikolai Bernstein (Bernstein, 1967) assumes that the central nervous system can simplify the production of movements by implementing orchestrated activations of functionally related muscle groups (i.e. muscle synergies) rather than by sending commands to each muscle individually. While the theory did not receive direct proof as of yet (Cheung & Seki, 2021; Tresch & Jarc, 2009), its neural basis has been indirectly shown in several animal models (Bizzi & Cheung, 2013). With the end of the twentieth century and the advent of modern computational tools, the first rigorous mathematical models of muscle synergies based on linear decomposition of electromyographic (EMG) data came to life (Lee & Seung, 1999; Tresch et al., 1999). In the past two decades, several approaches have been used to model muscle synergies as low-dimensional sets of muscle activations and weightings (Bruton & O'Dwyer, 2018). Non-negative matrix factorization (NMF) has often proved to be one of the most reliable and widely employed (Ebied et al., 2018; Rabbi et al., 2020). Yet, poor consensus exists on the best practices to preprocess EMG data, the most suitable NMF algorithms and convergence criteria and so on (Devarajan & Cheung, 2014; Ebied et al., 2018; Oliveira et al., 2014; Santuz et al., 2017; Taborri et al., 2018). Researchers with little to none coding experience will find in the R package musclesyneRgies a complete framework for the preprocessing, factorization and visualization of EMG data, with sensible defaults deriving from peer-reviewed studies on the topic. More advanced users will find musclesyneRgies to be fully customizable, depending on the specifics of the study design (e.g. the considered biological system, the motor task, the measurement devices used, etc.). musclesyneRgies aims at filling

the existing gap of tools available to researchers of all levels in fields that deal with the analysis of vertebrate movement control such as neuroscience, biomechanics, biomedical engineering, robotics or sport science.
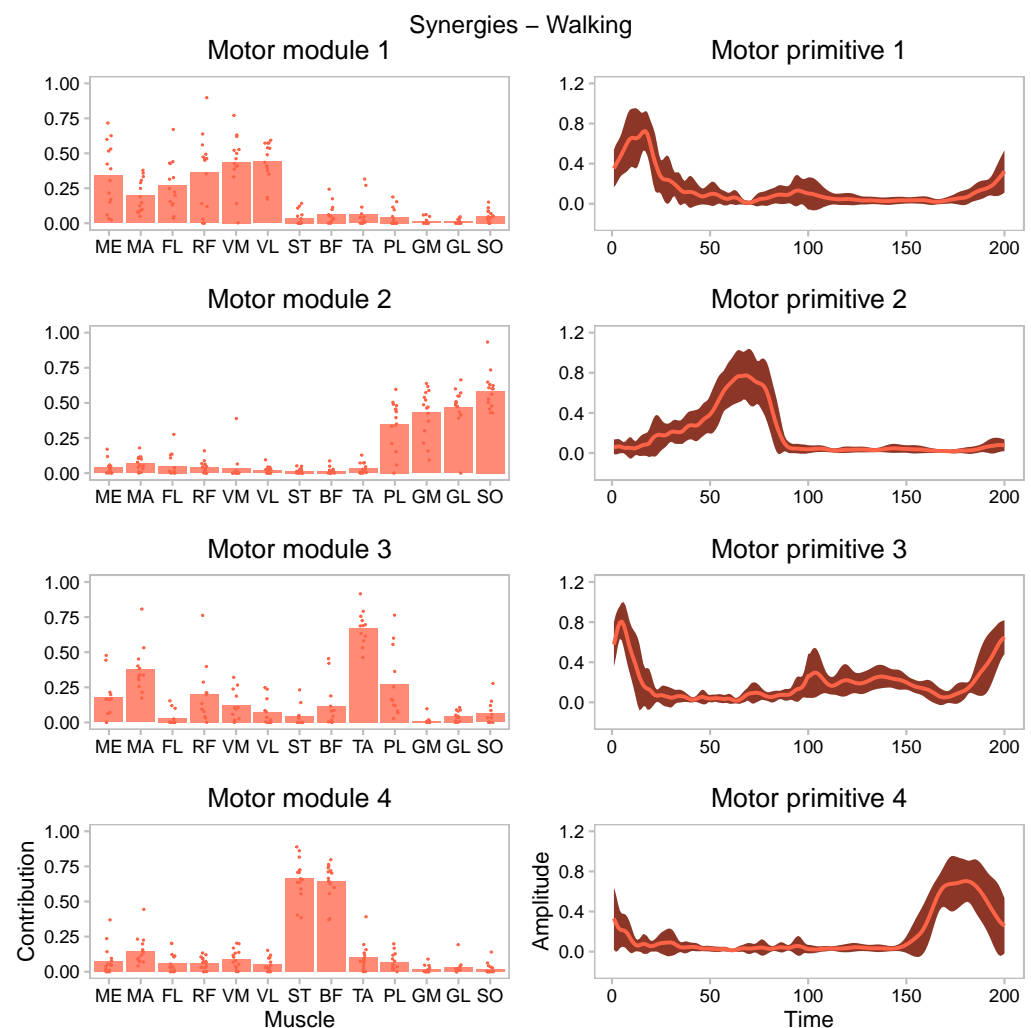
Typical workflow

The typical workflow when using `musclesyneRgies` consists of six main steps:

1. Data preparation (to read raw data sets and covert them into the needed format)
2. Raw data processing (e.g. rectification, filtering, time-normalization, etc.)
3. Synergy extraction (via NMF)
4. Synergy classification (via k-means)
5. Synergy analysis
   i. Linear methods: full width at half maximum and center of activity (Martino et al., 2014)
   ii. Non-linear methods: local complexity or Higuchi's fractal dimension (Higuchi, 1988; Santuz & Akay, 2020), global complexity or Hurst exponent (Hurst, 1951; Santuz & Akay, 2020), short-term maximum Lyapunov exponents (Kang & Dingwell, 2006; Rosenstein et al., 1993; Santuz et al., 2020)
6. Plots (available at each of the previous steps, see Figure 1 for an example).

Using the native pipe operator (R $>=$ `4.1.0` is required), a typical analysis pipeline can be synthetically written as follows:

```r
SYNS_classified <- lapply(RAW_DATA, filtEMG) |>        # Filter raw data
  lapply(function(x) normEMG(x, cycle_div = 100)) |>   # Time-normalization
  lapply(synsNMF) |>                                   # Synergy extraction
  classify_kmeans()                                    # Synergy classification
```

Defaults are specifically targeted at the analysis of human and mouse locomotion, but they can be flexibly overridden by specifying the arguments of the relevant functions. Extensive documentation is available on GitHub and the Comprehensive R Archive Network.

Figure 1: Four muscle synergies for human walking extracted from 13 leg-muscles after functional classification. Muscle abbreviations: ME = gluteus medius, MA = gluteus maximus, FL = tensor fasciæ latæ, RF = rectus femoris, VM = vastus medialis, VL = vastus lateralis, ST = semitendinosus, BF = biceps femoris, TA = tibialis anterior, PL = peroneus longus, GM = gastrocnemius medialis, GL = gastrocnemius lateralis, SO = soleus. The image was generated using `musclesyneRgies` v1.1.3.

Availability

The latest development version of `musclesyneRgies` is freely available on GitHub. A stable release is freely available via the Comprehensive R Archive Network. Documentation and examples are contained in each version's manual pages, vignettes and readme file. To install the latest development version, `devtools` needs to be installed beforehand and then `musclesyneRgies` can be installed directly from GitHub with the following:

```
install.packages("remotes")
remotes::install_github("alesantuz/musclesyneRgies")
```

The latest stable release appearing on CRAN can be installed with:

```
install.packages("musclesyneRgies")
```

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Acknowledgments

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