

# MG7: Configurable and scalable 16S data analysis

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## ABSTRACT

As part of the Cambrian explosion of omics data, metagenomics brings to the table a specific, defining trait: its social essence. The *meta* prefix exerts its influence, with multitudes manifesting themselves everywhere; from samples to data analysis, from actors involved to (present and future) applications. Of these dimensions, data analysis is where needs lay further from what current tools provide. Key features are, among others, scalability, reproducibility, data provenance and distribution, process identity and versioning. These are the goals guiding our work in MG7, a 16S metagenomics data analysis system. The basic principle is a new approach to data analysis, where configuration, processes, or data locations are static, type-checked and subject to the standard evolution of a well-maintained software project. Cloud computing, in its Amazon Web Services incarnation, when coupled with these ideas, produces a robust, safely configurable, scalable tool. Processes, data, machine behaviors and their dependencies are expressed using a set of libraries which bring as much as possible checking and validation to the type level, without sacrificing expressiveness. Together they form a toolkit for defining scalable cloud-based workflows composed of stateless computations, with a static reproducible specification of dependencies, behavior and wiring of all steps. The modeling of taxonomy data is done using Bio4j, where the new paradigm of graph databases allows for both a simple expression of taxonomic assignment tasks and the calculation of taxa abundance values considering the hierarchic structure of the taxonomy tree. MG7 includes a new 16S reference database, *16S-DB7*, built with a flexible and sustainable update system, and the possibility of project-driven personalization.

Keywords: Metagenomics, 16S, taxonomic profiling, Bio4j, Graph databases, Cloud computing, NGS, Genomics, big data, Microbiome, Environmental, 16S Database

## INTRODUCTION

During the past decade, metagenomics data analysis is growing exponentially. Some of the reasons behind this are the increasing throughput of massively parallel sequencing technologies (with the derived decrease in sequencing costs), and the wide impact of metagenomics studies (Oulas et al., 2015), especially in human health (diagnostics, treatments, drug response or prevention) (Bikel et al., 2015). We should also mention what could be called the microbiome explosion: all kind of microbiomes (gut, mouth, skin, urinary tract, airway, milk, bladder) are now routinely sequenced in different conditions of health and disease, or after different treatments. The impact of microbiome analysis is also being felt in environmental sciences (Ufarté et al., 2015), crop sciences, the agrifood sector (Coughlan et al., 2015), bioenergy (Yang et al., 2016), and biotechnology in general (Cowan et al., 2015) (Kodzius and Gojbori, 2015). These new possibilities for exploring the diversity of micro-organisms in the most varied environments are opening new research areas, and drastically changing the existing ones.

As a consequence, the challenge is thus moving (as in other fields) from data acquisition to data analysis: the amount of data is expected to be overwhelming in a very short time (Stephens et al., 2015).

Genome researchers have raised the alarm over big data in the past (Hayden, 2015), but even a more serious challenge might be faced with the metagenomics boom. If we compare metagenomics data with other genomics data used in clinical genotyping we find a differential feature: the key role of time. Thus, for example, in some longitudinal studies, serial sampling from the same patient (Faust et al., 2015) along several weeks (or years) is being used for the follow up of some intestinal pathologies,

for studying the evolution of the gut microbiome after antibiotic treatment, or for colon cancer early detection (Zeller et al., 2014) (Garrett, 2015). This need of sampling across time adds more complexity to metagenomics data storage and demands adapted algorithms to detect state variations across time as well as idiosyncratic commonalities of the microbiome of each individual (Franzosa et al., 2015). In addition to the intra-individual sampling-time dependence, metagenomic clinical test results vary depending on the specific region of extraction of the clinical specimen. This local variability adds complexity to the analysis since different localizations (different tissues, different anatomical regions, healthy or tumor tissues) are required to have a sufficiently complete landscape of the human microbiome. Moreover, re-analysis of old samples using new tools and better reference databases might be also demanded from time to time.

Other disciplines such as astronomy or particle physics have faced the big data challenge before. A key difference is the existence of standards for data processing (Stephens et al., 2015); in metagenomics global standards for converting raw sequence data into processed data are not yet well defined, and there are shortcomings derived from the fact that most bioinformatics methodologies used for metagenomics data analysis were designed for scenarios very different from the current one. These are some of the aspects that have suffered crucial changes and advances with a direct impact in metagenomics data analysis:

1. **Sequence data:** the reads are larger, the sequencing depth and the number of samples of each project are considerably bigger. The first metagenomics studies were very local projects, while nowadays the most fruitful studies are done at a global level (international, continental, national). This kind of global studies has yielded the discovery of clinical biomarkers for diseases of the importance of cancer, obesity or inflammatory bowel diseases and has allowed exploring the biodiversity of varied earth environments.
2. **The genomics explosion:** its effect being felt in this case in the reference sequences. The immense amount of sequences available in public repositories demands new strategies for curation, update and storage of metagenomics reference databases: current models will (already) have problems to face the future avalanche of metagenomic sequence data.
3. **Cloud computing:** the appearance of new models for massive computation and storage such as the cloud-based platforms, or the widespread adoption of programming methodologies like functional programming, or, more speculatively, dependently typed programming. The new possibilities that these advances offer must have a direct impact in metagenomics data analysis.
4. **Open science:** the new social manner to do science, particularly so in genomics, brings its own set of requirements. Metagenomics evolves in a social and global scenario following a science democratization trend in which many small research groups from distant countries share a common big metagenomics project; this global cooperation demands systems allowing for reproducible data analysis, data interoperability, and tools and practices for asynchronous collaboration between different groups.

## RESULTS

### Overview

Considering the current new metagenomics scenario and to tackle the challenges posed by metagenomics big data analysis outlined in the Introduction we have designed a new open source methodology for analyzing metagenomics data. It exploits the new possibilities that cloud computing offers to get a system robust, programmatically configurable, modular, distributed, flexible, scalable and traceable in which the biological databases of reference sequences can be easily updated and/or frequently substituted by new ones or by databases specifically designed for focused projects.

These are some of the more innovative MG7 features:

- Static reproducible specification of dependencies and behavior of the different components using *Statika* and *Datasets*
- Parallelization and distributed analysis based on AWS, with on-demand infrastructure as the basic paradigm
- Definition of complex workflows using *Loquat*, a composable system for scaling/parallelizing stateless computations especially designed for AWS

- A new approach to data analysis specification, management and specification based on working with it in exactly the same way as for a software project, together with the extensive use of compile-time structures and checks
- Modeling of the taxonomy tree using the new paradigm of graph databases (Bio4j, (Pareja-Tobes et al., 2015)). It facilitates the taxonomic assignment tasks and the calculation of the taxa abundance values considering the hierarchic structure of taxonomy tree
- Exhaustive per-read taxonomic assignment using two complementary assignment algorithms Lowest Common Ancestor and Best BLAST Hit
- Using a new 16S database of reference sequences (16S-DB7) with a flexible and sustainable system of updating and project-driven customization

## Libraries and resources

In this section we describe the resources and libraries developed by the authors on top of which MG7 is built. All MG7 code is written in [Scala](#), a hybrid object-functional programming language. Scala was chosen based on the possibility of using certain advanced programming styles, and Java interoperability, which let us build on the vast number of existing Java libraries; we take advantage of this when using Bio4j as an API for the NCBI taxonomy. It has support for type-level programming, type-dependent types (through type members) and singleton types, which permits a restricted form of dependent types where types can depend essentially on values determined at compile time (through their corresponding singleton types). Conversely, through implicits one can retrieve the value corresponding to a singleton type.

### Statika: machine configuration and behavior

[Statika](#) is a Scala library developed by AA and EPT which serves as a way of defining and composing machine behaviors statically. The main component are **bundles**. Each bundle declares a sequence of computations (its behavior) which will be executed in an **environment**. A bundle can *depend* on other bundles, and when being executed by an environment, its DAG (Directed Acyclic Graph) of dependencies is linearized and run in sequence. In our use, bundles correspond to what an EC2 instance should do and an environment to an AMI (Amazon Machine Image) which prepares the basic configuration, downloads the Scala code and runs it.

### Datasets: a mini-language for data

[Datasets](#) is a Scala library developed by AA and EPT with the goal of being a Scala-embedded mini-language for datasets and their locations. **Data** is represented as type-indexed fields: keys are modeled as singleton types, and values correspond to what could be called a denotation of the key: a value of type `Location` tagged with the key type. Then a **Dataset** is essentially a collection of data, which are guaranteed statically to be different through type-level predicates, making use of the value–type correspondence which can be established through singleton types and implicits. A dataset location is then just a list of locations formed by locations of each dataset key. All this is based on what could be described as an embedding in Scala of an extensible record system with concatenation on disjoint labels, in the spirit of (Harper and Pierce, 1990) (Harper and Pierce, 1991). For that *Datasets* uses the [ohnosequences/cosas](#) library.

Data keys can further have a reference to a **data type**, which, as the name hints at, can help in providing information about the type of data we are working with. For example, when declaring Illumina reads as a data, a data type containing information about the read length, insert size or end type (single or paired) is used.

A **location** can be, for example, an S3 object or a local file; by leaving the location type used to denote particular data free we can work with different “physical” representations, while keeping track of to which logical data they are a representation of. Thus, a process can generate locally a `.fastq` file representing the merged reads, while another can put it in S3 with the fact that they all correspond to the “same” merged reads is always present, as the data that those “physical” representations denote.

### Loquat: Parallel data processing with AWS

[Loquat](#) is a library developed by AA, EK and EPT designed for the execution of embarrassingly parallel tasks using S3, SQS and EC2 Amazon services.

A *loquat* executes a process with explicit input and output datasets (declared using the *Datasets* library described above). Workers (EC2 instances) read from an SQS queue the S3 locations for both input and

149 output data; then they download the input to local files, and pass these file locations to the process to be  
150 executed. The output is then put in the corresponding S3 locations.

151 A manager instance is used to monitor workers, provide initial data to be put in the SQS queue and  
152 optionally release resources depending on a set of configurable conditions.

153 Both worker and manager instances are *Statika* bundles. The worker can declare any dependencies  
154 needed to perform its task: other tools, libraries, or data.

155 All configuration such as the number of workers or the instance types is declared statically, the  
156 specification of a loquat being ultimately a Scala object. Deploy and resource management methods make  
157 easy to use an existing loquat either as a library or from (for example) a Scala REPL.

158 The input and output (and their locations) being defined statically has several critical advantages.  
159 First, composing different loquats is easy and safe; just use the output types and locations of the first one  
160 as input for the second one. Second, data and their types help in not mixing different resources when  
161 implementing a process, while serving as a safe and convenient mechanism for writing generic processing  
162 tasks. For example, merging paired-end Illumina reads generically is easy as the data type includes the  
163 relevant information (insert size, read length, etc) to pass to a tool such as FLASH.

### 164 **Type-safe eDSLs for BLAST and FLASH**

165 We developed our own Scala-based type-safe eDSLs (embedded Domain Specific Languages) for **FLASH**  
166 ([Magoč and Salzberg, 2011](#)) and **BLAST** ([Camacho et al., 2009](#)) expressions and their execution.

167 In the case of BLAST we use a model where we can guarantee for each BLAST command expression  
168 at compile time that

- 169 • all required arguments are provided
- 170 • only valid options are provided
- 171 • correct types for each option value
- 172 • valid output record specification

173 Generic type-safe parsers returning a heterogeneous record of BLAST output fields are also available,  
174 together with output data defined using *Datasets* which have a reference to the exact BLAST command  
175 options which yielded that output. This lets us provide generic parsers for BLAST output which are  
176 guaranteed to be correct.

177 In the same spirit as for BLAST, we implemented a type-safe eDSL for FLASH expressions and their  
178 execution, supporting features equivalent to those outlined for the BLAST eDSL.

### 179 **Bio4j and Graph Databases**

180 Bio4j ([Pareja-Tobes et al., 2015](#)) is a data platform integrating data from different resources such as  
181 UniProt, the NCBI taxonomy, or GO, in a graph data paradigm. In the assignment phase we use a  
182 subgraph containing the NCBI Taxonomy, wrapping in Scala its Java API in a tree algebraic data type.

### 183 **16S-DB7 Reference Database Construction**

184 The starting point for our 16S reference database is RNA Central ([Consortium et al., 2014](#)), [version 5](#).  
185 RNACentral was chosen being the most up to date, comprehensive RNA sequence repository, including  
186 among others all RNA data from Silva, GreenGenes, RDP, ENA, and RefSeq. First we take those  
187 sequences which

- 188 1. are annotated as being of rRNA type<sup>1</sup>
- 189 2. their length is at least 1300<sup>2</sup>
- 190 3. have at least one taxonomic assignment to a descendant of *Bacteria* or *Archaea*
- 191 4. their lineage does not contain a set of taxa deemed uninformative<sup>3</sup>

192 After this first step, we drop redundant assignments: if sequences  $S_1 \subseteq S_2$  share an assignment  $T$ , it  
193 gets dropped from  $S_1$ ; sequences which as a result end up having no assignments are removed.

<sup>1</sup>We are aware of the existence of a gene annotation corresponding to 16S in RNACentra, that we are **not using** due to a significant amount of 16S sequences lacking it

<sup>2</sup>Note that 16S sequences are sometimes part of an entry corresponding to whole small subunits; that's why we do not set a maximum length threshold

<sup>3</sup>for example: "unclassified Bacteria (miscellaneous)" or "unclassified". Assigning a read to an "unclassified" taxon defeats the first and foremost goal of taxonomic profiling: *classification*.

194 Once we have non-redundant set of RNA sequences containing all those corresponding to 16S, we  
195 can apply our procedure for checking internal consistency of taxonomic assignments.

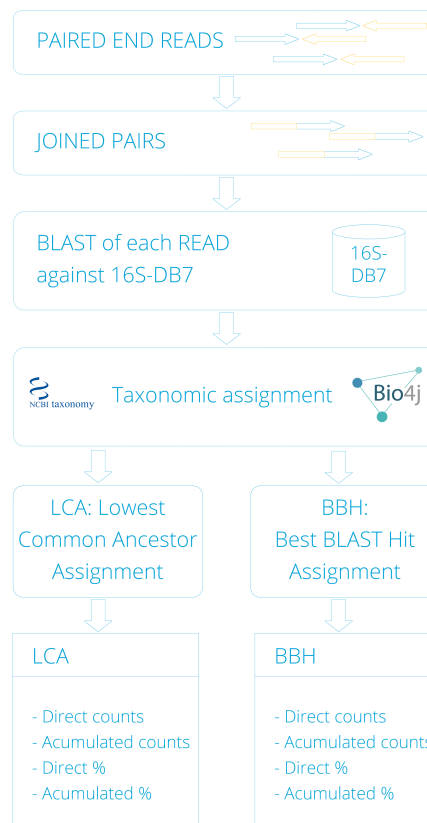
196 We run MG7 using this set of sequences as query, and with reference all but the one we are trying to  
197 assign. Explain

- 198 1. which kind of misassignments can be detected
- 199 2. how
- 200 3. why it is OK for sequences assigned to strange taxa, with no close 16S seq (they will get no hits)
- 201 4. we analyze every assignment independently

202 All these steps are automated, and integrated with every release of our reference database. The whole  
203 process can be repeated and adapted to other subsets of RNACentral; we do this for a 18S reference  
204 database.

### 205 Workflow Description

206 The MG7 analysis workflow is summarized in Figure 1. The input files for MG7 are the FASTQ files  
207 resulting from a paired-end NGS sequencing experiment.



**Figure 1. MG7 analysis workflow.** The paired reads in fastq format are merged resulting in only one sequence per read pair. The next step is a parallelized BLASTN of every merged sequence against the 16S reference database 16S-DB7. Then, the mapping of the detected similar sequences in the database to the taxonomy node to which they belong is carried out. This is done using Bio4j that includes a module with all the NCBI taxonomy in a graph connected with the Gene Ontology, Uniprot, and RefSeq graphs. Then the taxonomic assignment is done for each sequence following two different approaches: LCA and BBH, and finally the abundances corresponding to direct and cumulative assignments for each node in percentage and absolute counts are provided for each assignment mode.

### Joining reads of each pair using FLASH

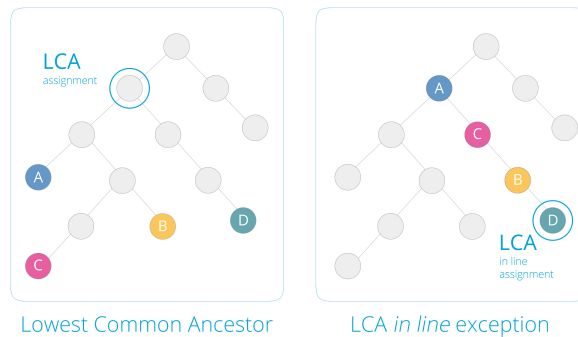
In the first step the paired-end reads, designed with an insert size that yields pairs of reads with an overlapping region between them, are assembled using FLASH (Magoč and Salzberg, 2011). FLASH is designed to merge pairs of reads when the original DNA fragments are shorter than twice the length of reads. Thus, the sequence obtained after joining the 2 reads of each pair is larger and has better quality since the sequence at the ends of the reads is refined merging both ends in the assembly. To have a larger and improved sequence is crucial to do more precise the inference of the bacterial origin based on similarity with reference sequences.

### Parallelized BLASTN of each read against the 16S-DB7

The second step is to search for similar 16S sequences in our 16S-DB7 database. The taxonomic assignment for each read is based on BLASTN of each read against the 16S database. Assignment based on direct similarity of each read one by one compared against a sufficiently wide database is considered in different reviews of metagenomics analysis methodologies (Segata et al., 2013) (Morgan and Huttenhower, 2012) as a very exhaustive method for assignment. Some methods of assignment compare the sequences only against the 16S genes from available complete bacterial genomes or avoid computational cost clustering or binning the sequences first, and then doing the assignments only for the representative sequence of each cluster. MG7 carries out an exhaustive comparison of all the reads under analysis and it does not apply any binning strategy. Every read is specifically compared with all the sequences of the 16S database. We select the best BLAST hits (10 hits by default) obtained for each read to do the taxonomic assignment.

### Taxonomic Assignment Algorithms

All the reads are assigned under two different algorithms of assignment: i. Lowest Common Ancestor based taxonomic assignment (LCA) and ii. Best BLAST Hit based taxonomic assignment (BBH). Figure 2 displays schematically the LCA algorithm applied *sensu stricto* (left panel) and the called ‘in line’ exception (right panel) designed in order to gain specificity in the assignments in the cases in which the topology of the taxonomical nodes corresponding to the BLAST hits support sufficiently the assignment to the most specific taxon.



**Figure 2. Lowest Common Ancestor algorithm for taxonomic assignment.** The Left panel displays an example of the application of LCA algorithm in a *sensu stricto* mode. A, B, C and D represent taxonomy tree nodes with assigned reads. Right panel displays the *in line* mode of assignment which is an exception for the *sensu stricto* mode of application of LCA algorithm. The *in line* mode is used when all the nodes are located in a line without bifurcations. In that case the taxon assigned is the most specific (the most distant from the root).

**Lowest Common Ancestor based Taxonomic Assignment** For each read, first, we select the BEST BLAST HITS (by default 10 Hits) over a threshold of similarity. To evaluate similarity for this first filtering of hits we use the Expect value (by default  $value \leq e^{-15}$ ) that describes the number of hits one can “expect” to see by chance when searching a database of a particular size. In a second filtering step we filter those hits that are not sufficiently good comparing them with the best one. We select the best HSP (High Similarity Pair) per reference sequence and then choose the best HSP (that with lowest E-value)



241 between all the selected ones. The bitscore of this best HSP (called  $S$ ) is used as reference to filter the rest  
242 of HSPs. All the HSPs with bitscore below the product  $pS$  are filtered.  $p$  is a coefficient fixed by the user  
243 to define the bitscore required, e.g. if  $p = 0.9$  and  $S = 700$  the required bitscore threshold would be 630.  
244 Once we have the definitive HSPs selected, we obtain their corresponding taxonomic nodes using the  
245 taxonomic assignments that NCBI provides for all the nt database sequences. Now we have to analyze  
246 the topological distribution of these nodes in the taxonomy tree: i. If all the nodes forms a line in the  
247 taxonomy tree (are located in a not branched lineage to the tree root) we should choose the most specific  
248 taxID as the final assignment for that read. We call to this kind of assignment the ‘in line’ exception (see  
249 Figure 2 right panel). ii. If not, we should search for the *sensu stricto* Lowest Common Ancestor (LCA) of  
250 all the selected taxonomic nodes (See Figure 2 left panel). In this approach we decided to use the bitscore  
251 for evaluating the similarity because it is a value that increases when similarity is higher and depends a lot  
252 on the length of the HSP. Some reads could not find sequences with enough similarity in the database and  
253 then they would be classified as reads with no hits. Advanced metagenomics analysis approaches (Huson  
254 and Weber, 2012) have adopted LCA-based assignment algorithms because it provides fine and trusted  
255 taxonomical assignment.

256 **Best BLAST hit taxonomic assignment** We decided to maintain the simpler method of Best BLAST  
257 Hit (BBH) for taxonomic assignment because, in some cases, it can provide information about the  
258 sequences that adds information to that obtained using the LCA algorithm. With the LCA algorithm, when  
259 some reference sequences with BLAST alignments over the required thresholds map to a not sufficiently  
260 specific taxID, the read can be assigned to an unspecific taxon near to the root of the taxonomy tree. If the  
261 BBH reference sequence maps to more specific taxa, this method, in that case, gives us useful information.

#### 262 **Output for LCA and BBH assignments**

263 MG7 provides independent results for the 2 different approaches, LCA and BBH. The output files  
264 include, for each taxonomy node (with some read assigned), abundance values for direct assignment  
265 and cumulative assignment. The abundances are provided in counts (absolute values) and in percentage  
266 normalized to the number of reads of each sample. Direct assignments are calculated counting reads  
267 specifically assigned to a taxonomic node, not including the reads assigned to the descendant nodes in  
268 the taxonomy tree. Cumulative assignments are calculated including the direct assignments and also the  
269 assignments of the descendant nodes. For each sample MG7 provides 8 kinds of abundance values: LCA  
270 direct counts, LCA cumu. counts, LCA direct %, LCA cumu. %, BBH direct counts, BBH cumu. counts,  
271 BBH direct % and BBH cumu. %.

#### 272 **Data analysis as a software project**

273 The MG7 16S data analysis workflow is indeed a set of tasks, all of them based in *Loquat*. For each task,  
274 a set of inputs and outputs as well as configuration parameters must be statically defined. The user is  
275 also free to leave the reasonable defaults for configuration, needing only to define the input and output of  
276 the whole workflow. The definition of this configuration is Scala code and the way of starting an MG7  
277 analysis is compiling the project code and launching it from the Scala interactive console.

278 Code compilation prior to launching any analysis assures that no AWS resources are launched if the  
279 analysis is not well-defined, avoiding expenses not leading to any analysis. Besides compile-time checks,  
280 runtime checks are made before launch to ensure existence of input data and availability of resources.

281 An MG7 analysis is then a Scala project where the user only needs to set certain variables at the code  
282 level (input, output and parameters), compile the code and run it. To facilitate the process of setting up  
283 the Scala project, a template with sensible defaults is provided.

284 In order to be able to exploit AWS infrastructure for the MG7 analysis, the user needs to set up an  
285 AWS account with certain IAM (Identity and Access Management) permission policies that will grant  
286 access to the resources used in the workflow.

#### 287 **Availability**

288 MG7 is open source, available at <https://github.com/ohnosequences/mg7> under an [AGPLv3](#) license.

#### 289 **DISCUSSION**

290 We could summarize the most innovative ideas and developments in MG7:

1. Treating data analysis as a software project. This makes for radical improvements in *reproducibility*, *reuse*, *versioning*, *safety*, *automation* and *expressiveness*
2. Checking at compile-time: input and output data, their locations and type are expressible and checked at compile-time using *Datasets*
3. Management of dependencies and machine configurations using *Statika*
4. Automation of AWS cloud resources and processes, including distribution and parallelization through the use of *Loquat*
5. Taxonomic data and related operations are treated natively as what they are: graphs, through the use of *Bio4j*
6. MG7 provides a sustainable model for taxonomic assignment, appropriate to face the challenging amount of data that high throughput sequencing technologies generate

We will expand on each item in the following sections.

## A new approach to data analysis: data analysis as a software project and checking at compile-time

MG7 proposes to define and work with a particular data analysis task as a software project, using Scala. The idea is that *everything*: data description, their location, configuration parameters and the infrastructure used should be expressed as Scala code, and treated in the same way as any (well-managed) software project. This includes, among other things, using version control systems (*git* in our case), writing tests, making stable releases following *semantic versioning* or publishing artifacts to a repository.

What we see as key advantages of this approach (when coupled with compile-time specification and checking), are

- **Reproducibility** the same analysis can be run again with exactly the same configuration in a trivial way.
- **Versioning** as in any software project, there can be different versions, stable releases, etc.
- **Reuse** we can build standard configurations on top of this and reuse them for subsequent data analysis. A particular data analysis *task* can be used as a *library* in further analysis.
- **Decoupling** We can start working on the analysis specification, without any need for available data in a much easier way.
- **Documentation** We can take advantage of all the effort put into software documentation tools and practices, such as in our case Scaladoc or literate programming. As documentation, analysis processes and data specification live together in the files, it is much easier to keep coherence between them.
- **Expresiveness and safety** For example in our case we can choose only from valid illumina read types, and then build a default FLASH command based on that. The output locations, being declared statically, are also available for use in further analysis.

## Input and output data declaration

An important aspect of the MG7 workflow is the way it deals with data resources. All the data that is going to be used in the analysis or produced as an output is described as Scala code using rich types from the *Datasets* language. This allows the user to specify information about types of data, information that can then be utilized by tools analyzing this data. For example, we can specify that, for the first part of the MG7 workflow, running FLASH in parallel requires illumina paired end reads and produces joined reads.

On one hand, specification of the input data allows us to restrict its type and force users to be conscious about what they pass as an input. On the other hand, specification of the output data helps to build a workflow as a *composition* of several parts: we can ensure on the Scala code type level that the output of one component fits as an input for the next component. This is crucial as, obviously, the way a data analysis task works depends a lot on the particular structure of the data. For instance, in the MG7 workflow, using BLAST eDSL, we can precisely describe which format will have the output of the BLAST step, which information it will include, and then in the next step we can reuse this description to parse BLAST output and retrieve the part of the information needed for the taxonomy assignment analysis. Having the data structure described statically as Scala code allows us to be sure that we will not have parsing problems or other issues with incompatible data passed between workflow components.

All this does not compromise flexibility in how the user works with data in MG7: having static data declarations as a part of the configuration allows the user to reuse analysis components, or modify them



344 according to particular needs. Besides that, an important advantage of the type-level control is the added  
345 protection from the execution (and deployment) of a wrongly configured analysis task, which may lead to  
346 significant costs in both time and money.

### 347 **Tools, data, dependencies and automated deployment**

348 Bioinformatics software often has a complicated installation process and requires various dependencies  
349 with unclear versions. This makes the deployment of the bioinformatics tools an involved task and  
350 resolving it manually is not a solution in the context of cloud computations. To face this problem,  
351 one needs an automated system of managing tools and resources, which will allow an expressive way  
352 for describing dependencies between parts of a pipeline and provide a reproducible procedure of its  
353 deployment. We have developed *Statika* for this purpose and successfully used it in MG7.

354 Every external tool involved in the workflow is represented as a *Statika* bundle, which is essentially a  
355 Scala project describing the installation process of this tool and declaring dependencies on other bundles  
356 which will be installed prior to the considered tool itself. Describing relationships between bundles on  
357 the code level allows us to track the directed acyclic graph of their dependencies and linearize them to  
358 automatically install them sequentially in the right order. Meanwhile, describing the installation process  
359 on the code level allows the user to utilize the wide range of available Scala and Java APIs and tools,  
360 making installation a well-defined sequence of steps rather than an unreliable script, dependent on a  
361 certain environment. *Statika* offers an easy path towards making deployment an automated, reproducible  
362 process.

363 Besides bioinformatics tools like BLAST and FLASH, *Statika* bundles are used for wrapping data  
364 dependencies and all inner components of the system that require cloud deployment. In particular, all  
365 components of *Loquat* are bundles; the user can then define which components are needed for the parallel  
366 processing on each computation unit in an expressive way, declaring them as bundle dependencies of the  
367 loquat “worker” bundle. This modularization is also important for the matter of making components of  
368 the system reusable for different projects and liberating the user from most of the tasks related to their  
369 deployment.

### 370 **Parallel computations in the cloud**

371 The MG7 workflow consists of certain steps, each of which performs some work in parallel, using  
372 the cloud infrastructure managed by *Loquat*. It is important to notice the horizontal scalability of this  
373 approach. Irrespectively of how much data needs to be processed, MG7 will handle it, by splitting data into  
374 chunks and performing the analysis on multiple computation units. The Amazon Elastic Compute Cloud  
375 (EC2) service provides a transparent way of managing computation infrastructure, called autoscaling  
376 groups. The User can set MG7 configuration parameters, adjusting for each task the amount and hardware  
377 characteristics of the EC2 instances they want to use for it. But it is important to note that, as each  
378 workflow step is not very resource demanding, it is not needed to hire EC2 instances with some advanced  
379 hardware. Instead, an average type will work and you can reduce execution time by simply scaling out the  
380 number of instances.

### 381 **Taxonomy and Bio4j**

382 The hierarchic structure of the taxonomy of the living organisms is a tree, and, hence, is also a graph in  
383 which each node, with the exception of the root node, has a unique parent node. It led us to model the  
384 taxonomy tree as a graph using the graph database paradigm. Previously we developed Bio4j (Pareja-  
385 Tobes et al., 2015), a platform for the integration of semantically rich biological data using typed graph  
386 models. It integrates most publicly available data linked with sequences into a set of interdependent  
387 graphs to be used for bioinformatics analysis and especially for biological data. MG7 works based on the  
388 Bio4j taxonomy module, which contains all the NCBI taxonomy data. It opens the possibility to connect  
389 the taxonomic profiling data obtained with MG7 to all the biological knowledge associated to each taxon.  
390 Using the information available in Bio4j for all the proteins assigned to each taxon we are connected to  
391 all the functional data available in Uniprot related with it.

### 392 **Future developments**

#### 393 **Shotgun metagenomics**

394 It is certainly possible to adapt MG7 to work with shotgun metagenomics data. Simply changing the  
395 reference database to include whole genome sequence data could yield interesting results. This could also

396 be refined by restricting reference sequences according to all sort of criteria, like biological function or  
397 taxonomy. Bio4j would be an invaluable tool here, thanks to its ability to express complex predicates on  
398 sequences using all the information linked with them (GO annotations, UniProt data, NCBI taxonomy,  
399 etc).

#### 400 **Comparing groups of samples**

401 The comparison of the taxonomic profiles between different groups of samples is a need for many  
402 metagenomics studies. Tasks related with this group-based analysis, such as the extraction of the minimal  
403 tree with all the taxa with some direct or accumulated assignment, will be part of a new MG7 module,  
404 already in development.

#### 405 **Interactive visualizations based on Biographika**

406 New visualization tools for metagenomics results are undoubtedly needed. Interactivity is a especially  
407 interesting feature for metagenomics data visualization, since the expert needs to explore the results in a  
408 knowledge-driven way. The majority of the available metagenomics data visualizations are static. We are  
409 working in the *Biographika* project (Tobes et al., 2015), to provide interactive rich visualizations on the  
410 web for Bio4j data. The development of visualizations specific for MG7 is one of Biographika current  
411 goals. Biographika is based on D3.js, the de-facto standard JavaScript data visualization library, and is  
412 open source.

## 413 **MATERIALS AND METHODS**

### 414 **Amazon Web Services**

415 MG7 uses the following Amazon Web Services:

- 416 • [EC2](#) (Elastic Compute Cloud) autoscaling groups for launching and managing computation units
- 417 • [S3](#) (Simple Storage Service) for storing input and output data
- 418 • [SQS](#) (Simple Queue Service) for communication between different components of the system
- 419 • [SNS](#) (Simple Notification Service) for e-mail notifications

420 These services are used through a Scala wrapper of the official [AWS Java SDK v1.9.25](#): [ohnosequences/aws-](#)  
421 [scala-tools v0.13.2](#).

### 422 **Scala**

423 MG7 itself and all the libraries used are written in Scala v2.11.

### 424 **Statika**

425 MG7 uses [ohnosequences/statika v2.0.0](#) for specifying the configuration and behavior of EC2 instances.

### 426 **Datasets**

427 MG7 uses [ohnosequences/datasets v0.2.0](#) for specifying input and output data, their type and their location.

### 428 **Loquat**

429 MG7 uses [ohnosequences/loquat v2.0.0](#) for the specification of data processing tasks and their execution  
430 using AWS resources.

### 431 **BLAST eDSL**

432 MG7 uses [ohnosequences/blast v0.2.0](#). The BLAST version used is v2.2.31+.

### 433 **FLASH eDSL**

434 MG7 uses [ohnosequences/flash v0.1.0](#). The FLASH version used is v1.2.11.

### 435 **Bio4j**

436 MG7 uses [bio4j/bio4j v0.12.0-RC3](#) and [bio4j/bio4j-titan v0.4.0-RC2](#) as an API for the NCBI taxonomy.

## 437 DISCLOSURE/CONFLICT-OF-INTEREST STATEMENT

438 All authors work at the *Oh no sequences!* research group, part of Era7 Bioinformatics. Era7 offers  
439 metagenomics data analysis services based on MG7. MG7 is open source, available under the OSI-  
440 approved AGPLv3 license.

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## 442 AUTHOR CONTRIBUTIONS

- 443 • **AA** developed *MG7*, *Loquat*, *Statika*, *Datasets*, and *aws-scala-tools*; wrote the paper;
- 444 • **EK** developed *nispero* (a prototype for *Loquat* (Kovach et al., 2014)) and *aws-scala-tools*.
- 445 • **MM** *MG7* workflow design; curation and design of the *16S-DB7* reference database; wrote the  
446 paper.
- 447 • **PPT** design and development of the first *MG7* prototype
- 448 • **EP** *MG7* workflow design; wrote the paper.
- 449 • **RT** *MG7* workflow design, assignment strategy; curation and design of the *16S-DB7* reference  
450 database; wrote the paper.
- 451 • **EPT** developed *MG7*, *Statika*, *Datasets*, *FLASH/BLAST eDSLs*; data analysis approach and design;  
452 reference database automated curation and filtering; wrote the paper.

453 All authors have read and approved the final manuscript.

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