EvoSpace-Interactive: A framework for Interactive Evolutionary Algorithms

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ABSTRACT

Evolutionary art (EvoArt) encompasses a variety of research devoted to the development of evolutionary systems than can help produce artistic artifacts in an automated or semi-automated process. Given the difficulty of evaluating subjective artistic preferences, one of the main approaches used by EvoArt researchers is to use interactive evolution where user input guides de search. However, despite the growth of EvoArt over recent years the research area still lacks a comprehensive software tool that can help in the development of EvoArt applications. Therefore, this work presents EvoSpace-Interactive, an open source framework for the development of collaborative-interactive evolutionary algorithms for art and design. The main components of the framework are: (i) *Evospace*, a population store for the development of cloud-based evolutionary algorithms, implemented using Redis key-value server; and a (ii) *Web Application* where end-users collaborate in a social network sharing, collecting, rating and ultimately evolving individuals. Individuals are presented as multimedia elements or artistic artifacts (images, animations, sound) using the Processing programming language, a development language specifically aimed at artists. EvoSpace-Interactive is designed to be easy to use and setup, allowing researchers, and more importantly artists, to quickly develop distributed and collaborative EvoArt applications. This paper presents the main details of EvoSpace-Interactive and two example applications to illustrate the potential of the tool.

Categories and Subject Descriptors

H.4 [**Information Systems Applications**]: Miscellaneous; D.2.8 [**Software Engineering**]: Metrics—*complexity measures, performance measures*

Keywords

Interactive evolutionary computation, Interactive Systems, Cloud-based platforms

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1. INTRODUCTION

Currently, evolutionary computation (EC) techniques are applied in a wide variety of different applications and problem domains. Among them, definitely one of the most intriguing application areas corresponds to what is broadly referred to as evolutionary art or EvoArt for short [1, 16]. EvoArt encompasses many works that seek to enhance the design abilities of researchers and even artists by exploiting the powerful search, optimization and learning capabilities of EC algorithms. In other words, EvoArt is an attempt by the EC community to enhance the creative process of artists and designers, or in a more ambitious scenario, reproduce a similar creative process in an autonomous system.

This goal is not trivial, particularly given the difficulty of modeling and expressing human artistic preferences in a computational system. Therefore, one important approach in EvoArt systems is to use interactive evolutionary algorithms (IEA), where humans interact with the evolving population in a specific way, particularly to evaluate the quality of the evolving population [16, 15]. Through the use of IEAs many EvoArt applications have been successfully developed and deployed, as local applications or distributed over the web. Indeed, the promise in EvoArt and the quality of the research developed thus far is clear, given the large number of workshops and tutorials that are currently part of all of the major EC conferences.

However, there is much work and research questions that still lie in the horizon, issues that are in some instances theoretic while in others they are pragmatic. In this work we are concerned with the latter, in particular the current lack of a complete and integrate software tool for rapid development of EvoArt applications. The proposed platform is called EvoSpace-Interactive, it is aimed at computer scientists who are interested in studying art, or at artists that what to exploit tools from computer science to enhance their abilities. Furthermore, EvoSpace-Interactive provides a research and development tool that addresses the following specific issues within EvoArt.

Firstly, a common problem IEAs is what is referred to as user fatigue, when an individual gets tired or simply bored with evaluating a large number of individuals, many of which will not be interesting at all. EvoSpace-Interactive takes a collaborative approach, where preferences of multiple users are considered and integrated into the evolutionary process, thus EvoSpace-Interactive is a collaborative IEA or C-IEA. This is done by exploiting the use of social networking and using a distributed computing model. A noteworthy feature of the approach taken in EvoSpace-Interactive, is that it at-

tempts to integrate the way creative elements are shared between users, and how different preferences are integrated into a single search process. Thus, the term memetic evolution, as originally defined by Richard Dawkins [3], relying on both minds and computers could be finally a main component in the development of automatic artistic designs. Secondly, the distributed approach proposed in EvoSpace-Interactive follows current trends in software and system development, where computational resources are shared across the web and applications are available on heterogenous computational devices. This is known as the Cloud computing model, where infrastructure, platforms and applications are shared across the internet. EvoSpace-Interactive provides a platform that easily integrates into the the Cloud model, and can be used to develop EvoArt services that reside on the cloud. Thirdly, an important aspect of EvoArt is the overlap between artists and computer science researchers, individuals that usually have very different academic backgrounds. Therefore, EvoSpace-Interactive attempts to integrate design tools that can be used by both In particular, EvoSpace-Interactive exploits the Processing programming language to generate artistic designs, since Processing allows for easy representation of images, animations, audio, and data processing procedures that are intuitive to the non-programmer.

This paper provides a comprehensive presentation of the EvoSpace-Interactive tool, describing the overall goals of the system, design principles and implementation details. Moreover, to example applications are reviewed, to illustrate how EvoSpace-Interactive could be used for the deployment of distributed collaborative EvoArt systems. The remainder of the paper, proceeds as follows.

2. RELATED WORK

The most common use of evolutionary algorithms, is to search for solutions that are optimal with respect to a specific objective or fitness function that can be computed automatically. Conversely, as stated above, in EvoArt the goal is to evolve artistic designs where quality evaluation, almost by definition, will have a large subjective component. Therefore, over the years interactive algorithms have been developed and matured [16, 15]. However, are not new, indeed some of the earliest EAs were open-ended interactive systems, such as the well-known Biomorphs program [4]. In what follows, relevant examples of interactive systems used in EvoArt are reviled. In particular, examples of collaborative systems where many users interact and evaluate an evolving population, guiding the search based on an aggregate of subjective preferences and considerations; what are here referred to as C-IEAs.

Langdon [11] developed one of the first C-IEAs, which evolves fractal representations of virtual creatures within a simulated environment. The proposed system is a distributed EA where the evolving population resides on a central web server and individuals are distributed to remote web-clients using Javascript. Users evaluate individuals locally and preferred individuals are returned to the server, at which point they can be distributed to other clients.

More recent examples can be found in the work of Secretan et al. [14] and Clune and Lipson [2], both of whom use a web-based IEA to evolve artistic artifacts using a generative encoding. In [14], the system is used to evolve static images and in [2] evolved objects are 3-D sculptures. Users of the systems can concentrate their search on specific artifacts, and collaboration is encouraged by allowing users to continue an evolutionary lineage created by others in a sequential manner. Both works offer webpages (see Picbreeder.org and EndlessForms.com), where users can select or create random individuals and evolve lineages of artifacts. Therefore, evolved artifacts can be the product of a collaborative search process. Another feature is that evolved artifacts can be rated by users, and since users can create individual accounts, the ratings provide a way to rank users, or to select previously evolved artifacts based on the particular style of each user. Furthermore, the collaborative process is captured by the system, since it is possible to visualize how, and when, different users influenced a genetic lineage.

Another example is the work of Kowaliw et al. [10], where ecosystemic models are evolved also using a generative encoding based on multi-agent systems that generate high quality artistic drawings. Users interact with the system through a website and a Java applet, where they can evolve their own images and have the option to add evolved images to a central collection such that other users can see the resulting images.

The present work builds on previous proposals and extends the C-IEA approach. First, it promotes collaborative evaluations of artistic artifacts in a dynamic and parallel manner, instead of the sequential approach followed in [14, 2]. Second, it incorporates explicit user interactions by encouraging the use of social networking. Third, by exploiting the Processing programming language for graphics programming, it facilitates rapid development for artists with a limited computer science background. Fourth, it focuses on the evolution of artistic animations, not static pictures or paintings; another feature facilitated by the use of Processing. Fifth, it facilitates the ability to save and share promising artifacts. Finally, it emphasizes the use of a distributed model, to exploit current trends in software and hardware technology.

3. ARCHITECTURE

The goal of this work is to develop an open source framework for Web and Cloud-based C-IEA systems, using current web standards and libraries for mobile devices. Developers of C-IEA applications are liberated from the need to design and program a platform for distributed user collaboration. Only three components of the framework must to be defined for each application (marked with double lines in Figure 1), namely: an *individual* representation; a *processing script* that renders each individual; and a *worker* script that encodes the evolutionary operators will need to be defined according to the representation and problem domain. However, in future versions of the framework much of this work could be predefined, but also left open for advanced users to change as they require. What the framework offers for free is: a central repository for the population implemented as an EvoSpace service; a Web Application script implemented using Django, a mature full stack Web Framework with a BSD license developed in Python.

The main components of the EvoSpace-Interactive are shown in Figure 1. The Interactive part is a Django [] web-based application, together with a client-side component implemented using JQuery and processingjs Javascript libraries. This application shows users a number of multimedia objects rendered in HTML5 Canvas elements. These

multimedia objects are the phenotypes of individuals drawn from the Evospace population store. Evospace is responsible for storing and retrieving the data of each individual. An Evolution Worker is responsible for generating new individuals from a sample taken from EvoSpace. The evolution process is decoupled from the interactive application; thous giving IEC designers the opportunity to define their own variations of the algorithm. In the following sections each component is described in detail, staring with the population store Evospace, and then the Interactive and Collaborative components.

4. EVOSPACE

The EvoSpace model is presented in detail in [6], only brief description of the functionality related to this work is given next. EvoSpace is inspired on the Linda language by Gelernter and Carriero [7]; Linda is a model of coordination and communication among several parallel processes operating upon objects stored in and retrieved from a shared, virtual, associative memory called *tuplespace*. In a tuplespace, tuples are read and removed by processes; once a tuple is taken, no other process can read it until it is written back. EvoSpace consists of two main components (see figure 2):

- the EvoSpace container that stores the evolving population and
- remote clients called EvoWorkers, which execute the actual evolutionary process, while EvoSpace acts only as a population repository.

In a basic configuration, EvoWorkers take a random sample of the population, and use it as the initial population for a local EA executed on the client machine. When taken by an EvoWorker, individuals remain in a phantom state until their sample is returned. If an EvoWorker does not returns a sample in a certain amount of time, for instance because of a lost connection; individuals are re-spawned (re-inserted) by the ReInsertionManager. Similar to video games in which characters once killed are re-spawned after a certain time. This can also happen when the EvoSpace container starves or the population size is below some threshold. Figure 2 illustrates the main components and dataflow within EvoSpace.

For this version of EvoSpace-Interactive, a new type of Worker is needed: Human users. Users are responsible for subjectively evaluating individuals, the process is depicted in Figure 3: (i) first a random sample of six individuals are taken from EvoSpace, (ii) the chromosome of each individual parameterizes a Processing script, that renders to the user, (iii) users select those individuals they like, this is stored in each individual's data, (iv) finally the sample is returned to EvoSpace. The fitness assigned to each individual can depend on the ratings given by a certain number of users. In this case the EvoWorker process is replaced by an `Evolve` method, that is executed after a certain number of samples have been returned. Unlike the normal operation of EvoSpace, when a User takes a sample of users, these are returned with their identity unchanged, other than the rating added by the current user. The internal representation of individuals is presented next.

Individuals..

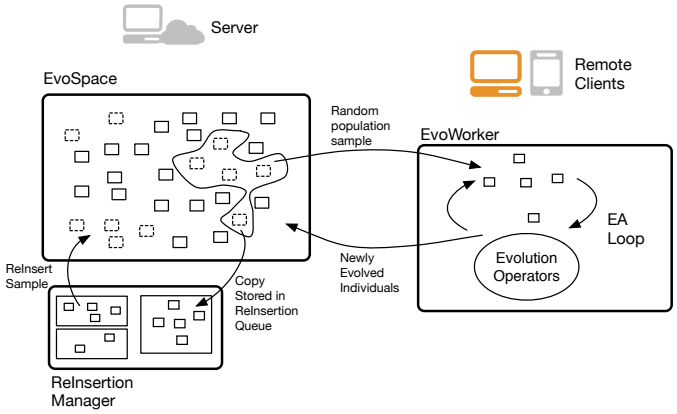

Figure 2: Main components and dataflow within EvoSpace.

As stated above, the objects stored in EvoSpace are individuals in an EA. Explicitly, individuals are stored as *dictionaries*, an abstract data type that represents a collection of unique keys and values with a one to one association. In this case, keys represent specific properties of each object and the values can be of different types, such as numbers, strings, lists, tuples or other dictionaries. In the current implementation, individuals are described by the following basic fields. An **id** string that represents a unique identifier for each object. A **chromosome** string, which depends on the EA and the representation used. The **fitness** dictionary for each individual; In EvoSpace-Interactive it stores pairs of user's ids and timestamp values, which represent that a user has rated the individual with a like. Currently a user can rate more than one time each individual. The **views** The number of times the individual has been presented to a user. If a user has seen an individual and did not assigned it a like, this can be used as a probable not-like rating. A **parents** dictionary with identifiers of the individual(s) from which it was produced. Finally, a **GeneticOperator** string that specifies the operator that produced it.

Individuals are stored in-memory, using the Redis key-value database. Redis was chosen over a SQL-based management system, or other non-SQL alternatives, because it provides a hash based implementation of sets and queues which are natural data structures for the EvoSpace model. For example, selecting a random key from a set has a complexity of O(1). The logic of EvoSpace is implemented as a python module exposed by the same Django framework used by the web-based application. The EvoSpace web service interacts is called directly by a JQuery script running in the client-side. This is done by a JQuery ajax request, and using the JSON-RPC protocol. The EvoSpace module is available with a Simplified BSD License from `https://github.com/evoWeb/EvoSpace`. The components required for the interaction between individuals and users are presented next.

5. INTERACTIVE EVOLUTION

In this section, the components needed to enable the interaction between users and individuals are presented. The first subsection the rendering and representation of individuals is discussed and next how fitness is assigned.

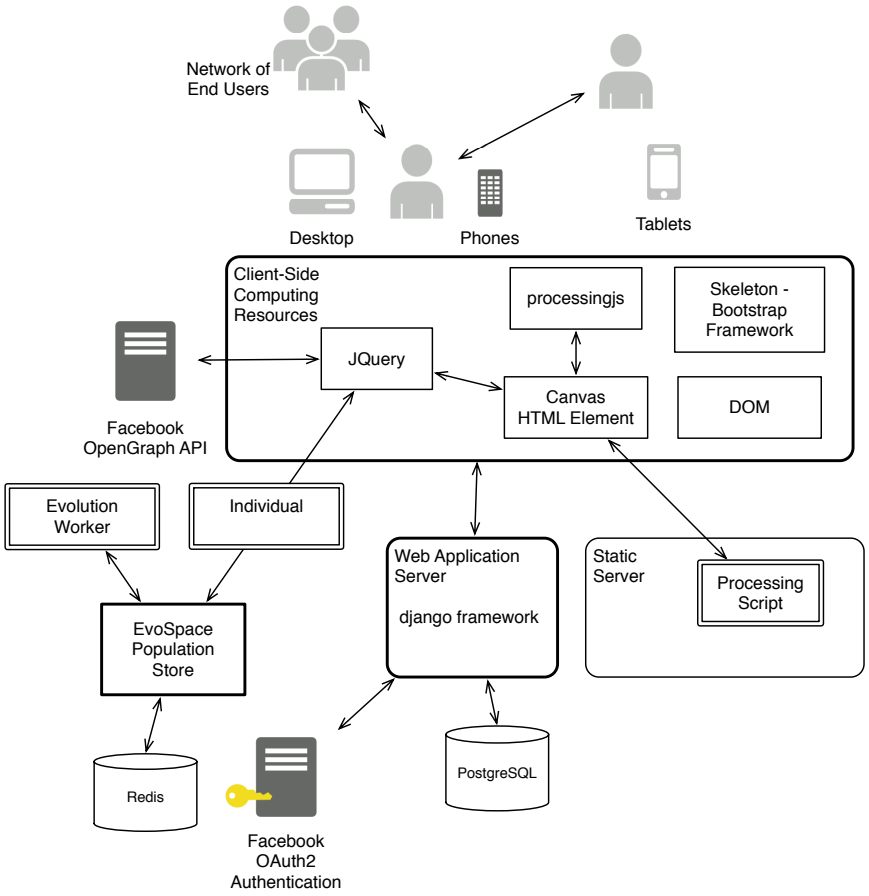

Figure 1: Main components of EvoSpace-Interactive.

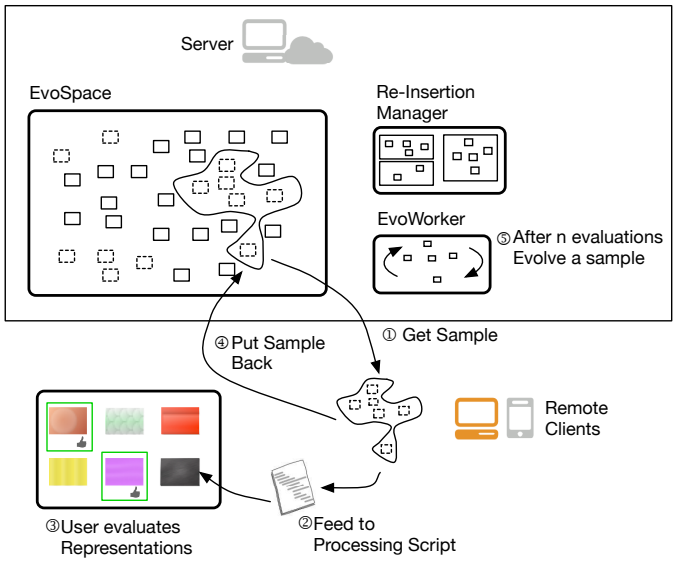

Figure 3:

5.1 Processing Scripts

Processing is a programming language and development environment initially created to serve as a software sketchbook and as a tool to teach fundamentals of computer programming within a visual context. Currently is used by artists, designers, architects, and researchers for visualization applications, games and interactive animations projects [13]. Processing is a subset of Java directed to novice programmers and generative artists [12], which are the intended users of the EvoSpace-Interactive framework. As a complement there is a javascript library *processingjs* that allows Processing scripts to be run by any HTML5 compatible browser. Processing scripts are responsible of rendering individuals which can involve animations, sound or even interactive artifacts. Before calling the `draw()` method of the processing script a local array of parameters are replaced with those of each individual's chromosome. Each individual's script has its own Canvas entity; defined by the HTML5 standard, as an element that provides scripts with a resolution-dependent bitmap canvas which can be used for rendering graphics on the fly. Although the combination of an HTML5 Canvas element and a Processing script is supported by default, other combinations could be used. For instance, images, embedded audio, or other libraries capable of drawing in the Canvas. Also, a fallback implementation must be considered for applications intended for non-HTML5 capable browsers.

To create a new C-IEC application, the rendering script

must be defined, and its parameters encoded as a chromosome.

5.2 Fitness

As stated before, the assignment of the fitness for each individual takes into account the evaluation given by several users. Initially in EvoSpace-Interactive users can only give positive evaluations explicitly when they select an individual, giving it a rating of *Like*. When a user evaluates a sample of individuals, some (or all) of them will not receive a like, in each case the `views` property will be incremented by 1. For instance, if an individual has a high number of views with with only two likes, he considered to be worse than an individual with two views and two likes. The ratio $Likes/Views$ is more informative, but it does not distinguish between an individual with many views and another with only one view if they both have zero likes; also views must be >=1 to avoid dividing by zero. Fitness, therefore, it is proposed to be given by $(Likes+1)/(Views+1)$. As a future work more options can be defined, for instance taking into account the number of "shares" or the times an individual has been stored in a collection.

5.3 Breeding Process

Once individuals have been evaluated by a minimum number of users, these can participate in the breeding process. As the genetic operators of the evolution process, will depend of the particular application; this algorithm must be implemented in python. Python libraries as DEAP or PyEvolve can be used for this purpose. Both examples presented in this work were implemented using only the NumPy library for array operations. As this process is executed in the server, the communication with EvoSpace-Redis is directly through a library. Only clients connect to the Web Service. There are a few additional parameters that are used for the `Evolve()` method: `EVOLUTION-INTERVAL` indicates the number of that must returned to trigger an `Evolve()` call; the `SAMPLE-SIZE` parameter indicates how many individuals are taken from EvoSpace to participate in the Evolution, `MINIMUM-VIEWS` is the minimum views needed for each individual to participate in the breeding process.

6. COLLABORATION

Using their Facebook account, users can collaborate with their Facebook friends, sharing those individuals they like, or taking individual from the collections of friends, as an introduction to this section de general user experience is described next.

6.1 User Interface.

Users interact with the web interface depicted in Figure 4, which is composed of five elements. First, at the top left corner user login and authentication. Users can login with their Facebook account or participate as anonymous users. Second, if a user chooses to login a list of Facebook friends that have also linked their account with the C-IEA application is presented on the left, to encourage users to interact with the system. The third element is a central *Wall* area, where a population sample of n individuals is shown to the user. These are n random individuals taken from the EvoSpace server. Here, the user can interact with the system in two ways. He can click on the individuals he prefers, a clicked image is highlighted and this counts as a "like" for the individual. Additionally, a user can choose to add an image to one of their *Collections*. A collection is a special directory to store individuals a user prefers and wishes to save. After the user finishes interacting with the current crop of individuals on the Wall, he can choose to retrieve a new sample from EvoSpace. This is done with the fourth element of the interface, located at the top of the screen, the *GetMore* button. The button returns the current group of individuals to EvoSpace, and brings back a new one. Each time a user performs a *GetMore* click, it increments the number of samples returned, and this could trigger a server-side *Evolve()* method. The fifth element of the interface is shown at the bottom left corner, the *Collections* section. The user can create several collections, to group and organize his favorite artifacts. Moreover, a user can browse the content of each collection and from there share images through the social network. When a user browses over an individual a detail pane shows how many users have liked the individual. The pane also includes a link to the individual's details, the parents, genetic operators that created it, and genealogy information.

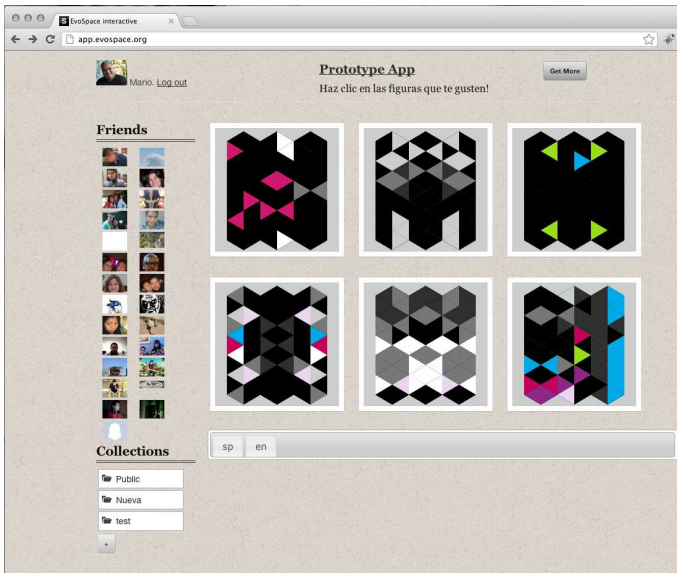

Figure 4:

6.2 Facebook API and OAuth2.0

Applications developed with the EvoSpace-Interactive framework must be defined as Facebook Web Applications. Other social networks are going to be enabled in further versions of the framework; but initially Facebook was selected as a Social Network platform for the following reasons:

- Popularity. Facebook is currently the social network with more active users, with more than 1 billion.
- Applications. Facebook applications are also common, popular applications like Youtube, Pinterest, Netflix, XBOX Live and Spotify allow users to share their activities.

In order to enable the application's collaborative functionality, end-users must be authenticated with their Facebook account. This is done using the OAuth2.0 protocol [8]. The

OAuth 2.0 login flow generates an access token, which you can use to make API calls on behalf of a user. As part of this flow, users also give certain permissions to the application, so it can access their private data. Currently the framework uses the most basic permission, having access only to their public profile and list of friends. The public profile includes their profile picture, username, gender and locale. An important information is the list of friends, that includes which friends also have the application installed.

6.3 Django Framework Application

The Django web development framework [9], is a set of Python libraries, that provide high-level abstractions of common Web development patterns. In Django a web application consists of different python scripts following a Model-View-Controller (MVC) design pattern. Using a separation of concerns design principle, the application logic is separated in mainly in four scripts:

- The `models.py` script contains a class based description of the database schema. These classes are Object-Relational mappers with methods to create, retrieve, update, and delete records in your database using Python code instead of SQL.
- The `views.py` file contains the business logic for each web page defined as special "View" functions. These functions receive as parameters and http request data, do operations on the model (database) , and return the data to feed HTML generator templates.
- The `urls.py` file specifies which view is called for a given URL pattern.
- Various HTML template files that describes the design of the page.
- `settings.py` file where the configuration of the project is stored.

In Django, a project can be an aggregation of multiple reusable applications, each incorporating a particular functionality. Each application has its own model, and views. For EvoSpace-Interactive the database model is presented in Figure 5. There is a many to one relationship between facebook sessions and users, this is because sessions and access tokens can expire. The database is stored in a PostgreSQL database system. Individuals are not stored in this database, they are stored in a Redis server as JSON text. The model for individual is presented in Figure 6

The main view functions for the application are:

`evospace()` This function receives JSON-RPC requests from JQuery code in the client. Main methods are `getSample()` and `putSample()`.

`home()` This view is for the main page, if the user is authenticated the list of friends and profile data is retrieved.

`individual_view()` This view function returns the details of Individuals.

`facebook_login()` Initializes the OAuth 2.0 flow. The facebook_get_login is also related.

`dashboard()` Returns a JQuery dashboard page, for administration of EvoSpace.

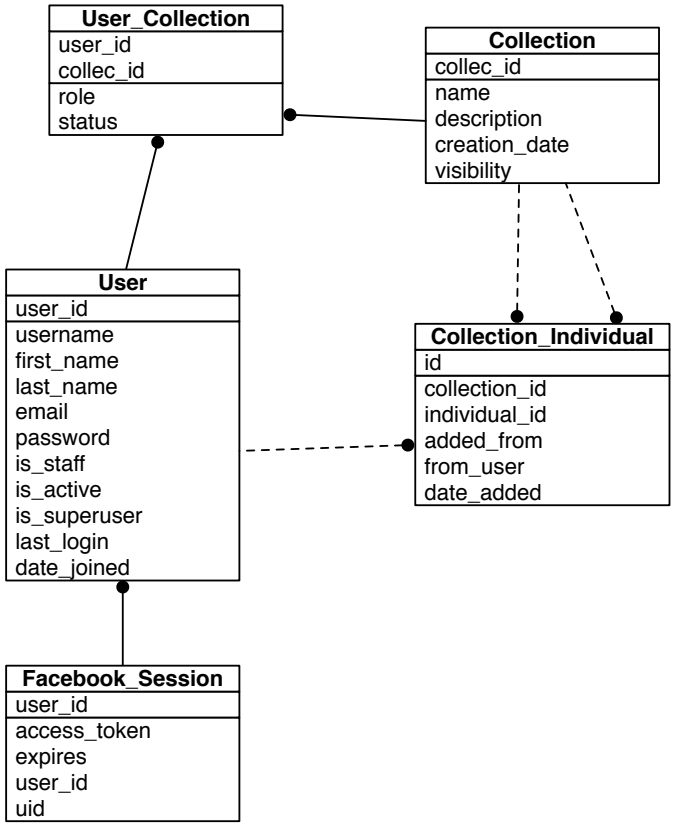

Figure 5: Django data model for the Interactive application

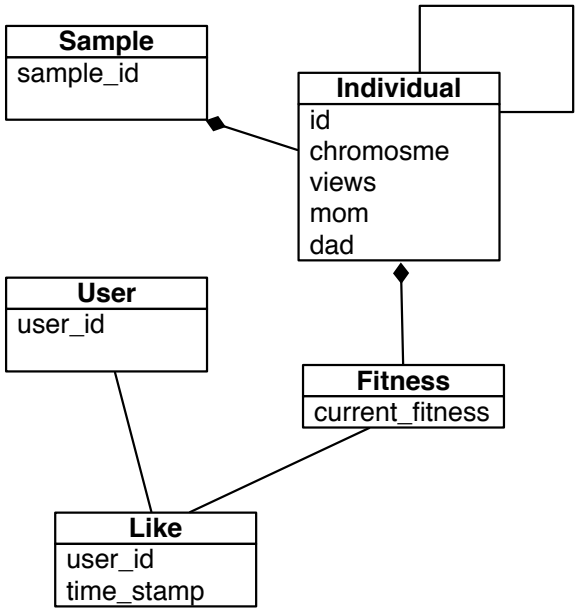

Figure 6: Individual's JSON representation

6.4 Client-Side

Client-side scripting is used extensibly by the framework. As mentioned earlier, JQuery is used to implement the eval-

uation of individuals as shown earlier in Figure 3, sending `getSample()` and `putSample()` requests. Also the Javascript library processingjs is used to render each individual in its corresponding HTML5 Canvas element. Other controls such as Modal Windows, Lists, Buttons are also implemented using JQuery-UI library.

6.5 Collections

TO-DO

7. EXAMPLE APPLICATION

As a proof of concept a C-EIA application was implemented with the EvoSpace-Interactive framework, this application is detailed in [5]. The application is called *Shapes*, and implements each EvoSpace-Interactive component as follows.

In *Shapes*, individuals represent a two dimensional 11 by 6 array of equilateral triangles, these arrays are sometimes used in Op-Art style paintings. Each triangle has a color drawn from a twelve color palette. The array is represented by a 66 element chromosome vector $\mathbf{v} = (v_1, ..v_{66})$, with $v_i \in \{1, 2, ..11\}$. The background of the painting is Light Gray, this can give the effect of a missing triangle when it has the same color. A processing script is used to render a static version of the image. The breeding process uses tournament selection of size 6 to select two individuals from EvoSpace, and generates two offspring. The offspring replace the worst individuals from both tournament groups. Crossover operators are used with crossover rate of 1, these are vertical and horizontal one-point crossovers. Several mutations are used with a mutation rate of 0.3, these are: (1) single *point mutation*; (2) vertical and horizontal *mirrors* at a random point; (3) *shuffle* that gives a new permutation of the chromosome.

8. EVALUATION

TO-DO

9. CONCLUSIONS

TO-DO

10. ACKNOWLEDGMENTS

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