CODE OCEAN

Code Ocean is a centralized platform for the creation, sharing, publication, preservation and reuse of executable code and data. Now, you can deliver a platform to your researchers, faculty and students to work better and smarter; you can support the re-

use and reproducibility of research as needed; and you gain better insight to the totality of research that is done at your institution.



EBSCO

A Single Environment

Give your researchers, faculty and students an umbrella of tools to save time and do their work in one place. Using Code Ocean, they can create, collaborate on, share, execute, and publish computational code and data from anywhere, with anyone. All work is contained in a compute capsule, which includes the computational code, data, results and metadata. Using container technologies, code execution is agnostic to programming languages, versions or operating systems. The compute capsule ensures that your researchers, faculty and students can then run their algorithms and (re-)produce results any time — today, tomorrow and in the years ahead.

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Commands		Overview of this repo This 'capsule' houses all of the code and analyses for the manuscript entitled "Variable gene	Sep 17, 2019 Published Version 1.0
Tabs	¥ README.md 4.13 IP run 25 SupplementaryCodeFile.rmd 86.73	expression and parasite load predict treatment outcome in cutaneous leishmaniasis". A link to the raw fastq file data hosted on GEO is provided here. The abstract for the manuscript is copied below: Abstract	Author ran Sep 17, 2019 © 00:03:19 V Published Result Output 16.84 K8 SupplementaryCodeFile 1.96 M8
	Christensen_plosNTD_2016 1.81 0.4 66091 creadMapping 1.63 flowdataframe.tot 25 UCENSE StudyDesign_Christensen_pl 1.58 StudyDesign_tt 12 gitignore Results Tesults	determine whether genes whose expression is highly variable in lisions might influence disease outcome, we obtained biopsies of lesions from patients prior to drug treatment, performed transcriptomic profiling, and identified highly variable genes whose expression correlated with treatment outcome. Amongst the most variable in genes were components of the cyclolytic pathway, the expression of which appeared to be driven by parasite load in the skin. We demonstrated that treatment failure can be directly linked to the cyclolytic pathway activated during infection. Using this host-pathogen biomarker profile, we show that treatment outcome can be predicted before the start of treatment. These findings on clock calles the possibility of direct of care distance is (detail).	O Sep 17, 2019
		The locations of the core components of this repo are outlined in the file system map below. In short, there are the following main directories:	0



Teaching and Learning

Use Code Ocean in teaching and learning. Faculty can set up a capsule on behalf of students, who can then duplicate the capsule and start working individually or as part of a group. As a result, students save significant time as they will not spend time downloading languages, configuring files and dependencies. Faculty will also have insight into the student's work and can see, for example, how much time a student spends in the capsule, runs and reproduces the work.

Reproducibility and Re-use

With Code Ocean, the research community can readily reproduce and re-use computational code and data in support of open science mandates. Once researchers are up and running, Code Ocean also speeds the time in which research is produced and disseminated, so they can collaborate and iterate in near real-time.

Increased Citations

Code Oceans supports the minting of a DOI for each published compute capsule, which can be associated with the published paper. As a result, researchers can be cited for more than just their article.

Institutional Stewardship

When you provide a centralized platform to your researchers, you gain much-needed stewardship over the totality of the institution's research output. This means you can readily collect computational code and data for inclusion in the (institutional) repository, preserve it, and understand its impact through in-depth analytics.



Enterprise Benefits

An institutional subscription offers the following benefits:

- Premium benefits for researchers in your organization including private groups and priority support .
- Administrative dashboard where an administrator can manage users and groups .
- Institutional- and capsule-level metrics .
- Transfer of individual files of any published compute capsule to the institutional repository .
- Preservation of individual files of any published compute capsule to CLOCKSS (Controlled LOCKSS) archive .
- Single sign-on to the platform (SSO) .
- Onsite workshops and online training sessions

Publisher Integrations

Through Code Ocean's many publisher partnerships, compute capsules may be automatically included with the author's manuscript submission. Examples of publisher partnerships include:

- Cambridge University Press
- Nature
- IEEE
- F1000
- T&F
- SPIE
- De Gruyter .
- Cell Press
- Elsevier .
- Gigascience (OUP)
- AACR
- BMJ

Cell Systems

Efficient Parameter Estimation Enables the Prediction of Drug.

Highlights Summary Graphical Abstrac Keywords Introduction Results Discussion STAR Methods



Comments



Introduction

High-throughput experimental techniques are key for the comprehensive understanding of biological processes (Garnett et al., 2012, Marcotte et al., 2016, Seashore-Ludiow et al., 2015, The Cancer Genome Atlas Network, 2012). The analysis integration, and interpretation of high-throughput data require computational methods. At the heart of this endeavor are usually mathematical models (Aldridge et al., 2006, Eduati et al., 2017). As widespread statistical models do not provide mechanistic insights, mechanistic models become increasingly important (Sanghvi et al., 2013). Mechanistic models featuring ordinary differential equations (ODEs) aim at a quantitative description of biological processes by systematic integration of prior knowledge and experimental data. These models have been used for the analysis of signal processing mechanisms (Bachmann et al., 2011), for the identification of drug targets (Schoeberl et al., 2009), as well as the development of prognostic signatures (Eduati et al., 2017, Fey et al., 2015). In the field of cancer research, mechanistic modeling has facilitated the study of oncogene addiction (Weinstein and Joe, 2006), synthetic-lethal phenotypes (Kaelin, 2005), and many other relevant phenomena (Zhang et al., 2009).

