Paper ID 9804 - Hierarchically-Organized Latent Modules for Exploratory Search in Morphogenetic Systems

We thank reviewers (named R2-R3-R4) for their valuable feedback. We are glad they shared a great interest in the research problem and in the experimental framework, highlighting the relevance of the targeted complex dynamical systems (R3) as well as the importance for novel methods for automating discovery in those (R2,R3,R4). We are pleased that our evaluation and interactive visualisations successfully conveyed the limitations of existing approaches and the relevance of the proposed meta-diversity objective (R4). We are also encouraged that our modular approach for incremental learning of diverse organized representations was considered novel, more efficient than monolithic architectures and more suitable for integrating human-guided interventions (R2,R3,R4) which was recognized as necessary to fully specify the exploratory task (R4), and with broader interesting implications for continual learning scenarios (R3). We answer reviewers comments below and will incorporate all feedback in the the final paper version.

Paper organization & Clarity One primary concern of reviewers was the difficulty of grasping how the different components of our method fit together. Especially, it was suggested to improve section 3 (R3,R4) and to redo the main figure with a more high-level overview (R2,R3). We agree and propose to update the paper as follows:
1) Replace Figure 1 (see on the right) to integrate both the representation learning part (hierarchical clustering, section 3.1) and the exploration part (goal-based intrinsic motivation, section 3.2). Please zoom in for full-size view.

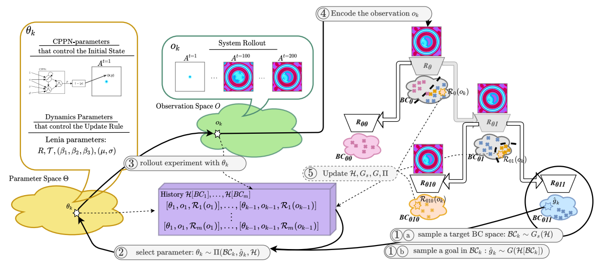

Figure 1: IMGEP-HOLMES overview

2) Simplify section 3.2 with intuitive explanations of the different steps (now-illustrated from 1 to 5 in the figure), as suggested by R3. Moreover, shortening 3.2 will free up some space for the following proposed updates.
3) Emphasize the clustering of the different patterns in section 3.1, which we agree is central (R4). There are two main choices: the training strategy that determines the latent distribution of patterns (we use VAEs) and the clustering algorithm itself (K-means). We recall that *"the genericity of HOLMES architecture [...] allows many other design choices to be considered in future work"* (last sentence of 3.1) and that our choices are discussed in appendix A.1.
4) Add a paragraph in section 5 with prior work on interactive exploration of patterns (R2) such as:
Langdon (2005) "Pfeiffer – A distributed open-ended evolutionary system", AISB ;
Secretan et al. (2011) "Picbreeder: A case study in collaborative evolutionary exploration of design space", Evolutionary Computation.

Comparison of the different methods in Lenia R3 expressed his interest to *"better understand what kind of diversity other approaches have produced in the Lenia system"*. First, evaluating the *kind* of diversity that is produced in a complex system like Lenia raises important questions, and we hope to have contributed in 3 ways with (i) several quantitative diversity metrics (relevant from the point of view of their novelty criteria); (ii) empirical evaluations with several visualisations and interactive web-interfaces and (iii) hybrid evaluations that rely on a human evaluator to select meaningful quantitative metrics (as proposed in section 4.3 and detailed in appendix B.3). Secondly, as we are ultimately evaluating diversity, our baselines are diversity-driven algorithms (population-based IMGEPs as in [50] that are similar to Novelty Search) that mainly differ in the BC space definition and for which we compared several hand-defined and unsupervisedly learned variants in section 4.1 and appendix D.2. In addition we also compare with a random exploration approach, and while we can hardly compare quantitatively with manual approaches from [6,7] that only keeps few "interesting" discoveries, our project website provides several videos and links to visualise those manually-identified discoveries - together with the full database of the automatically-identified discoveries of all the considered baselines. Additional clarifications asked by R3 are hopefully addressed below:
- Our claims on the novelty of the identified *pattern-emitting* behaviors are based on [7] which states the *"open questions raised in the original Lenia paper (Chan, 2019): Do self-replicating and pattern-emitting lifeforms exist in Lenia?"*
- The chosen analytic BC spaces (including PatchBetaVAE) are fully motivated and described in appendix B.1.1 but not focused in the main paper as many others could be envisaged. Similarly, our intuitions on why monolithic VAEs are better suited for exploring one type of diversity but not the other can be found in appendix D.2.
- The original flat-topology PNN architecture assumes a predefined sequence of tasks and cannot, as-it-is, be applied to our problem: it will need to autonomously handle the clustering of the incoming data distribution and dynamically expand accordingly over its lifetime. However, we refer to section E in Appendix for a comparison with other recently-proposed architectures that also share conceptual similarities with the original PNN architecture.

Generalisation to other domains As stated by R3, Lenia can produce combinatorial outcomes with appearances and dynamics comparable to real-world biology making it a very interesting and intuitive test-bed. Yet, we agree with R2 and R4 and are currently working on applying the proposed meta-diversity search framework to explore other complex systems: (i) the morphological affordances of bio-inspired robot designs and (ii) the behavior-space of real "wet" systems for which bio-chemists still lack of an intuitive understanding, such as the oil-droplet system studied in [19].