Visualizing Coevolution with CIAO Plots

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Abstract In a previous article, we introduced a number of visualization techniques that we had developed for monitoring the dynamics of artificial competitive coevolutionary systems. One of these techniques involves evaluating the performance of an individual from the current population in a series of trials against opponents from all previous generations, and visualizing the results as a 2D grid of shaded cells or pixels: qualitative patterns in the shading can indicate different classes of coevolutionary dynamics. As this technique involves pitting a *current individual* against *ancestral opponents*, we referred to the visualizations as *CIAO* plots. Since then, a number of other authors studying the dynamics of competitive coevolutionary systems have used CIAO plots or close derivatives to help illuminate the dynamics of their systems, and it has become something of a de facto standard visualization technique. In this very brief article we summarize the rationale for CIAO plots, explain the method of constructing a CIAO plot, and review important recent results that identify significant limitations of this technique.

Keywords
Coevolution, visualization, CIAO plot

1 Introduction

Attempting to define and monitor "progress" in the context of coevolutionary systems can be a somewhat nightmarish experience. In a *coevolutionary* system, by definition, evaluating the fitness of any one individual genotype requires that the effects of other genotypes be taken into account. For instance, consider the case where two separate populations are maintained, such that the fitness of individual genotypes in population A is dependent in some way on the genomes in population B, and vice versa. Then the fitness landscape for each population is partially determined at any one time by the distribution of genotypes in the other population at that time. As the distribution of genotypes changes in each population (as a result of directed selection or of genetic drift), the other population's fitness landscape may change, sometimes dramatically; and these changes in the landscape can occur even when the function used to evaluate fitness is constant throughout the evolutionary process.

This reciprocity in the fitness evaluation process can make monitoring progress much more difficult than in the non-coevolutionary case. Simple graphs of best/average fitness measures over time in coevolutionary systems can be totally misleading. For example, genuine progress may be occurring in the sense that there is continual evolutionary innovation in both populations, yet if any evolutionary innovation in one population is rapidly met with a counter-innovation in the other, then the graph of the population best/average fitness over time can be essentially flat, which would conventionally be interpreted as a sign of *no* progress. For further discussion of the range of problems that can occur, see [2, 1].

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In a previous article [2], we discussed a number of visualization techniques that we had developed and found useful for monitoring progress in artificial competitive coevolutionary systems. Use of all of these was demonstrated on real data from our experiments exploring the coevolution of sensory morphologies and continuous-time recurrent neural-network *controllers* for autonomous agents that engaged in pursuit and evasion. In those experiments we maintained a population of *predators,* selected for their pursuit behavior, and a separate population of *prey,* selected for evasion behaviors. A single run of one experiment, simulating a few hundred generations of coevolution, could take many days (or even weeks) of real time. These long running times were due to a variety of reasons that were particular to our experiments, but we argued that such long experiment times would become the norm rather than the exception as coevolutionary GAs were increasingly applied to non-toy autonomous-agent design problems. Our view was that if progress in coevolutionary systems was not monitored accurately (or, at least, if lack of progress was not readily detectable), then very large amounts of computer time could be wasted. Hence we thought that the development of appropriate new visualization techniques for monitoring progress in artificial coevolutionary systems would meet a significant and growing need. The techniques we developed allowed us to better describe the coevolutionary dynamics of our system, and to demonstrate the presence or absence both of desirable and of pathological coevolutionary phenomena.

Of the three new visualization techniques we introduced in [2], one particular technique that we named *CIAO plots* has since become something of a de facto standard in the artificial life, evolutionary computation, and adaptive behavior literature on artificial coevolutionary systems. For example, Cartlidge and Bullock's critical survey [1] points to usage of CIAO plots in recent articles on evolutionary robotics [3, 4, 7], on coevolution of game-playing strategies [8], and on coevolution of simple linguistic interactions [5]. Most recently, Izuka and Ikegami used CIAO plots in their analysis of the coevolutionary dynamics of turn-taking behaviors in autonomous agents [6]. In this very brief article, we only give details of the method for constructing a CIAO plot; but we urge the reader to consult Cartlidge and Bullock's [1] recent elegant studies of how qualitatively different coevolutionary dynamics manifest themselves (or fail to manifest themselves) in CIAO plots, which reveals some significant weaknesses—discussed briefly later in this article.

2 How to CIAO

The process of constructing a CIAO plot is very simple in practice. Let $e(p,g)$ denote the genome of the elite (best-scoring) individual from population p in generation g, and consider two competitively coevolving populations A and B. To construct a CIAO plot for population A at generation G, take $e(A,G)$ and record its fitness scores in a sequences of competitions where each competition involves scoring $e(A,G)$ against $e(B,g)$ for all generations $g \in \{0,1,\ldots,G\}$. This gives a vector of G scalar scores. Repeat this process for $e(A,G-1)$, $e(A,G-2)$, $\ldots$, $e(A,0)$, thereby generating a sequence of score vectors of diminishing length. To visualize the values in this sequence of vectors, fill the square cells in a triangular grid such as that shown in Figure 1 with grayscales or colors that vary in accordance with the scalar values. For example, normalize over all scores, and then shade the highest-scoring cell black, shade the lowest-scoring cell white, and assign appropriate shades of gray to cells with intermediate scores. Coevolutionary dynamics, such as limited evolutionary memory or intransitive dominance cycling, will then be revealed as certain qualitative visual patterns, idealizations of which are shown in Figure 2. These could in principle be detected by performing simple image processing on the CIAO plots. CIAO plots of real data, such as that shown in Figure 3, tend to be more noisy and harder to interpret than the idealizations of Figure 2.

Defined this way, CIAO plots are manifestly useful in generational coevolutionary systems where individuals compete one-on-one and are rated using an extrinsic fitness evaluation function, but the visualization technique would need to be modified if it were to be applied to less explicitly sequenced systems, such as steady-state systems; or to systems where the fitness function is implicit or intrinsic. Note also that the computational cost of calculating the data for a CIAO plot rises as $O(\frac{1}{2}G^2)$ and so

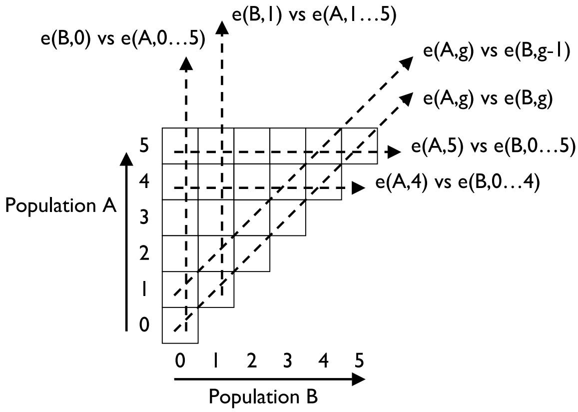

Figure 1. Schematic for constructing a CIAO plot for population *A*. The square cells would be shaded or colored to represent scores in competitions, the dashed lines indicate different vectors of scores that could be visualized as conventional two-dimensional *x*-*y* graphs, and e(*P*,*g*) denotes the elite individual from population *p* at generation *g*.

can easily become greater than the actual computational cost of the coevolutionary experiment that the plot is generated to visualize.

3 Goodbye to All That?

We are of course pleased that other authors whose work we respect have approvingly used the CIAO plot technique that we introduced, as it demonstrates that our intuition regarding the need for such visualization tools was correct. Nevertheless, we are even more pleased that Cartlidge and Bullock [1] have conducted a careful dissection of the limitations of our method. Although CIAO plots have been used by several authors over the years, the article by Cartlidge and Bullock is the first detailed exploration of the strengths and weaknesses of this visualization technique. The central motivation for Cartlidge and Bullock's article is the observation that no CIAO plots of real experimental data have ever been published that resemble the idealized plots of Figure 2. Instead, they note, almost all CIAO plots of real data are much more reminiscent of banded tartan patterns familiar from plaid textiles, and they explore why these tartan patterns occur, and what these patterns might reveal about

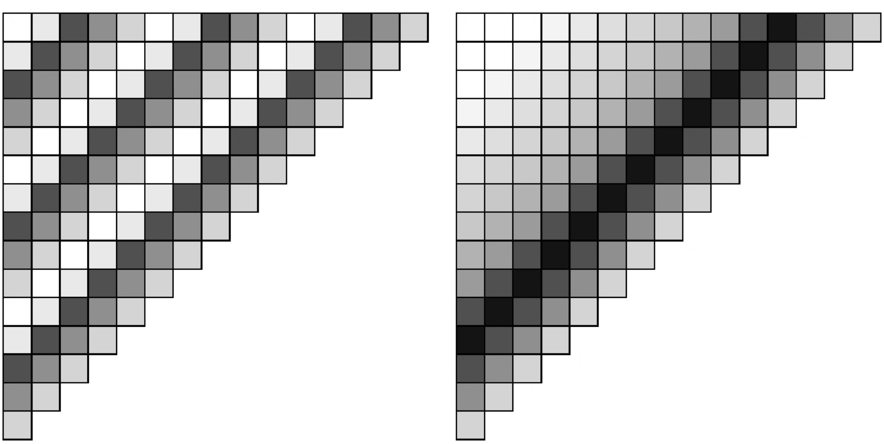

Figure 2. Idealized CIAO plot patterns, with darker shading indicating higher scores. Left: intransitive dominance cycling, where current elites score highly against opponents from 3, 8, and 13 generations ago but not so well against generations in between. Right: limited evolutionary memory where the current elites do well against opponents from three, four, and five generations ago, but much less well against more distant ancestral opponents.

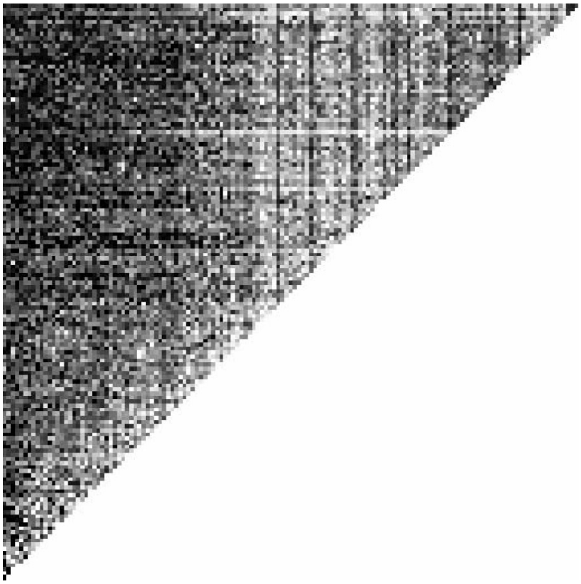

Figure 3. A CIAO plot showing 700 generations of real data, from [2].

the underlying coevolutionary dynamics. In doing so, they expose some significant weaknesses of CIAO plots. The main point of their article is that prominent bands appear in the CIAO plot only when there is periodic cycling through set of strategies, whereas aperiodic trajectories through strategy space may not be readily identified from a CIAO plot.

Progress in any field is rarely if ever monotonic: The clear challenge now is to develop visualization techniques better able to reveal qualitative, or even quantitative, differences in coevolutionary dynamics.

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