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Product family formation for reconfigurable assembly systems

Mohamed Kashkoush, Hoda ElMaraghy*

Intelligent Manufacturing Systems (IMS) Centre, University of Windsor, 401 Sunset Avenue, Windsor N9B 3P4, ON, Canada

* Corresponding author. Tel.: +1-519-253-3000 (Ex. 5034) .E-mail address: hae@uwindsor.ca.

Abstract

Appropriate formation of product families for Reconfigurable Manufacturing Systems (RMS) is of a great importance for a cost-effective and productive manufacturing. One key aspect that differentiates assembly systems from other manufacturing systems is that they often require parallel operations, which is not common for other types of manufacturing systems such as dedicated manufacturing systems. This paper introduces the first product family formation method that particularly addresses Reconfigurable Assembly Systems (RAS). Product assembly sequences are used, along with product demand and commonality, as similarity coefficients. Product assembly sequences are represented in the form of binary rooted trees and, based on well-established tree matching techniques used in Biology and Phylogenetics, a new sequence-based similarity coefficient is introduced to measure the distance between any given pair of assembly sequence trees. Hierarchical clustering is then applied to generate various groups of product families that may be formed based on each similarity coefficient. A novel consensus tree-based method is applied to find the best aggregation for the three different hierarchical clustering trees. The proposed method is applied to an example of eight products. Applying the proposed method to a Reconfigurable Assembly System should significantly improve system efficiency and productivity and hence supporting cost effective production.

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1. Introduction

Reconfigurable Manufacturing Systems (RMS) is a modern manufacturing system paradigm [1, 2] that was designed to increase responsiveness, sustainability and cost-effectiveness. Reconfigurable Manufacturing Systems (RMS) [3] are designed at the outset for rapid change in structure, as well as in hardware and software components, in order to quickly adjust production capacity and functionality within a part family in response to sudden changes in market or regulatory requirements. In RMS, similar products are grouped together into groups or families of products in which a customized system configuration is designed for each product family. Similarity in terms of common components is one example for a similarity criterion that is used to form families of products. The foundation for the success for RMS lies in recognizing appropriate sets of product families [4]. The effectiveness of

RMS is best realized by formation of product families that maximizes system utilization and productivity. Methods have been recently developed for grouping products into families for RMS [5-8] considering commonality, modularity, operations sequence and other similarity coefficients as grouping criteria.

Existing product family formation methods would not be suitable to Reconfigurable Assembly Systems (RAS), particularly when operation-sequence (assembly sequence) is to be considered as a similarity coefficient. Assembly sequence is often non-linear which means that parallel operation could take place at the same time (non-linear assembly). Hence, using existing operation-based similarity coefficient that considers the operation sequence of a given product as a strict order of serial operations is no longer valid.

The assembly sequence tree, also known as partial assembly tree is proposed as a representation of products

assembly sequence as illustrated in Figure 1 for a product consisting of five components. Components 1 and 3 may be assembled before, after, or at the same time as components 2 and 4. Component 5 is then added to sub-assembly (1, 3, 2, 4) to obtain the final product (1, 3, 2, 4, 5).

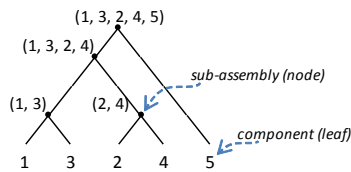


Fig. 1. An assembly sequence tree for a product of five components [9].

A new product family formation method is proposed for Reconfigurable Assembly Systems (RAS) in which a novel assembly-sequence based similarity coefficient is introduced based on Robinson-Foulds distance [10], a commonly used tree matching measure in Biology and Phylogenetics. Average linkage hierarchical clustering [11] is used to construct three different hierarchical clustering product trees based on the proposed assembly sequence similarity coefficient as well as product commonality and demand. A consensus tree is then constructed for the three trees using a consensus tree construction method recently developed by the authors for master assembly sequencing [9]. This method is also inspired by Phylogenetics where a consensus classification tree for a group of species is derived from a set of conflicting trees.

2. Literature Review

Group Technology (GT) is a manufacturing philosophy in which similar parts are identified and grouped together into groups or families to take advantage of their similarities in design and production. GT is the conceptual foundation for Cellular Manufacturing. Methods particularly addressing product family formation for RMS have arisen from part family formation methods used in Cellular Manufacturing (e.g. Classification and Coding Systems [12] and Production Flow Analysis (PFA) [13]).

Abdi and Labib [14] proposed an algorithm for grouping products for RMS based on their operational similarities using Jaccard similarity coefficient [15], a commonly used similarity coefficient for part-cell formation in Cellular Manufacturing. Galan et al. [5] based their method on five similarity coefficients; modularity, commonality, compatibility, reusability and demand. Analytic Hierarchy Process (AHP) is used as a weighing method to aggregate the five similarity coefficients in one single coefficient. Average linkage hierarchical clustering [11] is then used to cluster the products into a binary rooted tree, known as dendrogram. Goyal et al. [6] proposed a similarity coefficient based on operations sequence and employed it, solely, to cluster products using average linkage hierarchical clustering. Considering alternative process plans, Rakesh et al. [4] proposed a modified average linkage clustering algorithm based on Jaccard similarity coefficient.

A Reconfigurable Assembly System (RAS) is basically a Reconfigurable Manufacturing System (RMS) for assembly

processes [16]. For Reconfigurable Assembly Systems (RAS), only Eguia et al. [8] proposed a product family formation method for Reconfigurable Disassembly Systems (RDS), which resembles RAS. Eguia et al. applied average linkage clustering using a similarity coefficient which requires the following information: a) types and quantities of the products to disassemble within a certain time horizon, b) existing RMT and available modules library, c) operations and processing times required to disassemble each product type, and d) machines and modules required for each disassembly task.

Thus, among the mentioned product family formation methods for RMS or RDS, only Goyal et al. [6] has considered operation sequence as a clustering criterion. However, this similarity coefficient, as well as other operation sequence-based similarity coefficients used in Cellular Manufacturing [17-19], are not suitable for RAS as they all deal with serial order of operations not non-linear assembly sequences.

3. Proposed Product Family Formation Method for RAS

This section describes the proposed method for product family formation for Reconfigurable Assembly Systems (RAS). Figure 2 shows an IDEF0 model of the proposed method illustrating the main activities as well as their inputs, outputs, controls and mechanisms. IDEF0 is a compound acronym for a function modeling methodology [20].

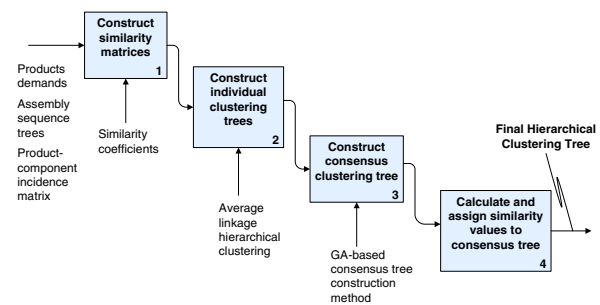


Fig. 2. IDEF0 model for the proposed product family formation method.

3.1. Proposed similarity coefficient based on assembly sequence

The assembly sequence of a given product could be represented in a binary rooted tree form as shown in Figure 1. The Robinson-Foulds (RF) distance [10] is the most widely used metric for comparing phylogenetic trees [21], hence, it is used to assess the similarity/dissimilarity between any given pair of assembly trees.

Given two trees $T1$ and $T2$, having $m1$ and $m2$ number of leaves, $C1$ is a set that includes $m1-1$ subsets each representing one of the $m1-1$ nodes of $T1$ and the elements inside each subset are the elements belonging to the node representing the subset. Similarly, $C2$ contains $m2-1$ subsets representing the $m2-1$ nodes of $T2$. Robinson-Foulds distance (RF) is then given by Equation 1, where “ Δ ” refers to symmetric difference (a set theory operation). Equation 1 could be further detailed as in Equation 2, where “ \setminus ” refers to set difference operation. Hence, RF is simply a normalized

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