Gene expression

xHeinz: an algorithm for mining cross-species network modules under a flexible conservation model

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Abstract

Motivation: Integrative network analysis methods provide robust interpretations of differential high-throughput molecular profile measurements. They are often used in a biomedical context—to generate novel hypotheses about the underlying cellular processes or to derive biomarkers for classification and subtyping. The underlying molecular profiles are frequently measured and validated on animal or cellular models. Therefore, the results are not immediately transferable to human. In particular, this is also the case in a study of the recently discovered interleukin-17 producing helper T cells (Th17), which are fundamental for anti-microbial immunity but also known to contribute to autoimmune diseases.

Results: We propose a mathematical model for finding active subnetwork modules that are conserved between two species. These are sets of genes, one for each species, which (i) induce a connected subnetwork in a species-specific interaction network, (ii) show overall differential behavior and (iii) contain a large number of orthologous genes. We propose a flexible notion of conservation, which turns out to be crucial for the quality of the resulting modules in terms of biological interpretability. We propose an algorithm that finds provably optimal or near-optimal conserved active modules in our model. We apply our algorithm to understand the mechanisms underlying Th17 T cell differentiation in both mouse and human. As a main biological result, we find that the key regulation of Th17 differentiation is conserved between human and mouse.

Availability and implementation: xHeinz, an implementation of our algorithm, as well as all input data and results, are available at http://software.cwi.nl/xheinz and as a Galaxy service at http://services.cbib.u-bordeaux2.fr/galaxy in CBIB Tools.
1 Introduction

Many computational methods have been proposed for the analysis of molecular profiles under different conditions. Studies employing these methods aim to better understand the molecular changes in the underlying cellular processes or to discover biomarkers as to classify between different conditions. Traditionally, analysis methods have been gene-centric, that is, they consider genes in isolation to establish differential patterns by simple statistical methods based on univariate statistical tests. For example, one of the first studies used gene expression measurements to differentiate between two leukemia classes (Golub et al., 1999). With the availability of increasingly reliable biological network data for human and model organisms, gene-centric approaches have been increasingly complemented by integrative network analysis methods (Dittrich et al., 2008; Ideker et al., 2002; Mitra et al., 2013). These methods yield active modules, that is, sets of genes that are connected in the network and show overall differential behavior. By taking the network topology into account, integrative analysis methods allow for a more robust interpretation of the measurements and result in more meaningful mechanistic insights.

Frequently, for ethical or practical reasons, molecular profiles are measured and validated on animal or cellular models and the results are therefore not immediately transferable to human (Okyere et al., 2014). In fact, the low phase-I survival rate of 25% of potential drug compounds is largely attributed to the lack of transferability between model systems and human (Csérmely et al., 2013). This is also an issue in the recently discovered interleukin-17 producing helper T cells (Th17). These cells form a separate subset of helper T cells with a differentiation pathway distinct from those of the established Th1 and Th2 cells (Park et al., 2005). Th17 cells are known to contribute to pathogenesis of inflammatory and autoimmune diseases such as asthma, rheumatoid arthritis, psoriasis and multiple sclerosis and play also a role in cancer immunology (Wilke et al., 2011). Understanding the pathways and regulatory mechanisms that mediate the decision making processes resulting in the formation of Th17 is a critical step in the development of novel therapeutics. Unfortunately, the vast majority of data collected so far originates from studies performed on mice (Tuomela et al., 2012) and, most importantly, a comprehensive comparison of the Th17 differentiation process in model organisms and in human is missing. Several studies indicate that the differentiation and phenotype of human and mouse Th17 cells are similar (Annunziato and Romagnani, 2009). Both subsets serve similar pro-inflammatory functions and produce the same hallmark cytokines and similar receptors. Furthermore, most of the already identified regulator genes show high sequence conservation. Other studies, however, show stimulus requirements for effective differentiation of human cells that differ from those required for mice (Annunziato et al., 2009; McGechey and Cua, 2008; O’Garra et al., 2008). A characterization of the similarities and differences will not only increase our understanding of this fundamental process, but is also essential for sound translational research.

To do so, we suggest finding conserved active modules whose comprising genes show overall differential behavior, induce a connected subnetwork and are largely conserved across the species. Well-conserved modules make it possible to perform the experimental work and data analysis on the model organism. At the same time, the results are likely to be transferable to human. In addition, conserved modules carry a stronger signal than individual species modules because they integrate the signal of the individual data sources. Finding conserved active modules, however, is a difficult task. Separately computing species-specific active modules generally results in modules that are not conserved, which partially explains why experimental results are so often not transferable. Conversely, the largest conserved modules, as established, for example, with methods for network alignment, are not necessarily active. A computational model for finding conserved active modules requires thus a notion of both, activity and conservation (see Fig. 1).

Several authors already identified the benefits of combining and comparing cross-species experiments. At the single gene level, van Noort et al. (2003) have demonstrated that conserved co-expression is a strong co-evolutionary signal. More recent studies suggested to identify conserved biological processes. Lu et al. (2010) analyzed transcriptomics profiles of human and mouse macrophages and dendritic cells to derive common response genes involved in innate immunity. Kristiansson et al. (2013) proposed a method for the analysis of gene expression data that takes the homology structure between the different species into account. Berthier et al. (2012) found that murine and human responses to lupus nephritis involves similar gene networks. They first derived species-specific networks of significantly differentially expressed genes and then determined common subnetworks using a graph matching algorithm. Waltman et al. (2010) presented a multi-species integrative method to heuristically identify conserved biclusters. In their setting, a conserved bicluster is a subset of orthologous genes and a subset of conditions that achieve a high score with respect to co-expression, motif co-occurrence and network density. Dede and Ojul (2014) introduced a method that finds triclusters consisting of genes that are coexpressed across a subset of samples and a subset of species.

Deshpande et al. (2010) suggested the neXus algorithm for finding conserved active subnetworks. The authors use average fold

Fig. 1. Conserved active modules. Given two species-specific protein networks and, for each species, two sets of expression profiles of many different samples measured under two different conditions (A), we can annotate the nodes in the networks with activity scores (B), and identify modules that are at the same time highly differentially expressed and well-conserved (C). Cross-species conservation is indicated by dotted lines. Note that the best active module is not necessarily the best conserved active module.
change of genes in a module as a measure for activity. To deal with conservation, they collapse paralogous genes into a cluster of orthologous genes (COG) (Tatusov et al., 1997) into single nodes in the respective networks. They find modules using a seed-and-extend greedy heuristic that starts from a pair of orthologous seed nodes and then tries to simultaneously grow the two subnetworks by including pairs of neighboring orthologous genes. This strategy enforces a very stringent conservation policy: only modules whose genes are fully conserved are found. In addition, the locality of the greedy search strategy impairs the ability to find larger conserved modules and extending the search space around the seed genes drastically increases the runtime. In recent work, Zinman et al. (2015) introduce ModuleBlast, a method that, similarly to neXus, represents groups of orthologous proteins as single nodes in a combined network and tries to find connected subnetworks that are differentially expressed. The novelty of the method is the classification of the found modules according to the sign of the fold change expression values. By doing so, the authors are able to assess whether conserved active modules show consistent or inconsistent expression patterns. Like neXus, ModuleBlast requires strict conservation of module genes.

Here, we propose a mathematical model for identifying conserved active modules for two species. It builds upon a model for single-species expression patterns. Like neXus, ModuleBlast requires strict conservation of module genes.

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The model allows a trade-off between conservation and activity. If no conservation is enforced ($\alpha = 0$), the solution will correspond to two independent maximum-weight connected subgraphs. Conversely, if complete conservation is required ($\alpha = 1$), the solution can only consist of conserved nodes, which results in lower overall activity. The user controls this trade-off by varying the value of the parameter $\alpha$ from 0 to 1. The activity score monotonically decreases with increasing $\alpha$ (see Fig. 2).

Since the maximum-weight connected subgraph problem, which occurs as a subproblem for $\alpha = 0$, is NP-hard (Johnson, 1985), the problem of finding conserved active modules is NP-hard as well.

### 2.2 Integer linear programming approach

We formulate the conserved active modules problem as an integer programming (IP) problem in the following way.

$$\max \sum_{v \in V_1 \cup V_2} w_v x_v$$

subject to:

$$m_v = \max_{u \in V_1} \{ x_u x_v \} \quad u \in V_1$$

$$m_v = \max_{u \in V_2} \{ x_u x_v \} \quad v \in V_2$$

$$\sum_{v \in V_1 \cup V_2} m_v \geq \alpha \sum_{v \in V_1 \cup V_2} x_v$$

$$G_1[x]$$ and $$G_2[x]$$ are connected

Variables $x \in \{0, 1\}^{V_1 \cup V_2}$ encode the presence of nodes in the solution, i.e. for all $v \in V_1 \cup V_2$ we have $x_v = 1$ if $v \in V^*$ and $x_v = 0$ otherwise.

### 2.1 Mathematical model

We consider the conserved active modules problem in the context of two species networks, which we denote by $G_1 = (V_1, E_1)$ and $G_2 = (V_2, E_2)$. Nodes in these networks are labeled by their activity—defined by $w \in \mathbb{R}^{V_1 \cup V_2}$ and conserved node pairs are given by the symmetric relation $R \subseteq V_1 \times V_2$. The aim is to identify two maximal-scoring connected subnetworks, one in each network, such that a given fraction $\alpha$ of module nodes are conserved. The formal problem statement is as follows:

**Problem 1 (Conserved active modules).** Given $G_1 = (V_1, E_1)$, $G_2 = (V_2, E_2)$, $w \in \mathbb{R}^{V_1 \cup V_2}$ and $R \subseteq V_1 \times V_2$, the task is to find a subset of nodes $V^* = V_1^* \cup V_2^*$ with $V_1^* \subseteq V_1$ and $V_2^* \subseteq V_2$ such that the following properties hold:

- **Activity:** Node activity scores are given by $w \in \mathbb{R}^{V_1 \cup V_2}$, where positive scores correspond to significant differential expression. For details see Section 3.2. We require that the sum $\sum_{v \in V} w_v$ is maximal.

- **Conservation:** Conserved node pairs are given by the relation $R \subseteq V_1 \times V_2$. We require that at least a certain fraction $\alpha$ of the nodes in the solution must be conserved, that is, $|U^*| \geq \alpha \cdot |V^*|$ where $U^* := \{ u \in V_1^* | w \in V_2 : w \in R \} \cup \{ v \in V_2^* | w \in V_1 : w \in R \}$.

- **Modularity:** We require that the induced subgraphs $G_1[V_1]$ and $G_2[V_2]$ are connected.

![Fig. 2. Trade-off between activity and conservation. Three optimal solutions (indicated in yellow) for varying conservation ratios $\alpha$ in a toy example instance. Node activities are given next to the nodes, conserved node pairs are linked by dotted lines. The activity of a conserved module is the sum of the activities of its comprising nodes. The parameter $\alpha$ denotes the minimum fraction of nodes in a solution that must be conserved, i.e. connected by a dotted line](https://academic.oup.com/bioinformatics/article-abstract/31/19/3147/210875/2713149?highres=true)
otherwise. The objective function (1) uses these variables to express the activity of the solution, which we aim to maximize. Variables \(m \in \{0, 1\}^{V_1 \times V_2}\) encode the presence of conserved nodes in the solution. Constraints (2) encode that a node \(u \in V_1\) that is present in the solution \((x_u = 1)\) is conserved if there exists a related node \(v \in V_2\) \((av \in R)\) that is also present in the solution \((x_v = 1)\). Similarly, constraints (3) define conserved nodes in \(V_2\) that are present in the solution. The fraction of conserved nodes in the solution is at least \(\alpha\) as captured by Constraint (4). In addition, we satisfy the modularity property by requiring in Constraint (5) that \(G_1[x]\) and \(G_2[x]\) are connected. In Supplementary Text A.1 we give further details on how to model Constraints (2), (3) and (5) as linear inequalities and on the implementation that solves this formulation.

3 Material and methods

3.1 Experimental procedure

We summarize here the experimental procedure followed by Tuomela et al. (2012) and Yosef et al. (2013) to generate transcriptomic profiles. In (Tuomela et al., 2012), CD4+ T-cells were isolated from umbilical cord blood of several healthy neonates, arranged in three different pools, then activated with anti-CD3 and anti-CD28. Cells from each pool were then divided in two batches, one to be polarized toward Th17 direction, and one serving as control (Th0). Th17 differentiating cytokines consisted of IL6 (20 ng/mL), IL1B (10 ng/mL) and TGFβ (10 ng/mL), along with neutralizing anti-IFNG (1 µg/mL) and anti-IL4 (1 µg/mL). Three biological replicates of human cells, for both conditions (coming from each pool), were collected between 0.5 and 72 h (at time points: 0.5, 1, 2, 4, 6, 12, 24, 48, 72 h time points) and hybridized on Illumina Sentrix HumanHT-12 Expression BeadChip Version 3. The microarray data were analyzed using the beadarray Bioconductor package (Dunning et al., 2007). In (Yosef et al., 2013), CD4+ T-cells were purified from spleen and lymph nodes from wild type C57BL/6 mice, then activated with anti-CD3 and anti-CD28. For Th17 differentiation, cells were cultured with TGFb (2 ng/mL), IL6 (20 ng/mL), IL23 (20 ng/mL) and IL1B (20 ng/mL) during 0.5–72 h (at time points 0.5, 1, 2, 4, 6, 8, 10, 12, 16, 20, 24, 30, 42, 48, 50, 52, 60, 72 h), and finally hybridized on an Affymetrix HT_MG-430 A.

3.2 Microarray processing, statistical analysis and node scoring

Preprocessed and quantile normalized data sets were downloaded from GEO under the accession numbers GSE43955 and GSE35103. As downloaded from GEO, both the human and the mouse time-series were already filtered by retaining only the probes with detection \(P\)-values < 0.05 in at least one time point and one condition. Following the original studies, we further only retained probes having a standard deviation > 0.15 over all the conditions and time points; as well as being annotated by a single ENSEMBL gene. Finally, a single probe was selected for each gene by taking, for each ENSEMBL gene, the probe having the largest variance across all samples. In total, 12 307 and 18 497 probes passed the filters for the human and mouse data set, respectively.

Differential expression between Th17 and Th0 conditions were estimated using the limma package (Smyth, 2005). Human samples were indicated as paired according to the experimental design so as to account for the pooled human samples. For mouse samples, calling was performed on all Th0 versus Th17 samples, regardless of the mouse donor. To determine which genes were differentially expressed at a given time point, we used a linear model to estimate the interaction between the treatment and the time effect. The linear models used for the human and mouse studies include one interaction term for each time point and exclude the intercept (In R, the formula reads: ~ 0 + treat × time). Differential expression at any time point \(K\) of interest were determined by the contrasts Th17.time\(_K\)–Th0.time\(_K\). We report in this study results for the following time points: 2, 4, 24, 48, 72 h.

Following (Dittrich et al., 2008), we computed positive and negative scores for each gene at each time point by fitting a beta-uniform mixture model using the implementation in the BioNet package (Beisser et al., 2010). For a detailed description of this procedure, see Supplementary Text A.2. Throughout this study, FDR = 0.1 was used for all samples and species.

Due to the experimental noise and paired design, the human samples have much higher intra-group variance, resulting in significant calls having \(P\)-values orders of magnitude higher than the mouse calls. This results in a range of scores that is much narrower for human than for mouse, possibly imbalancing results towards mouse modules. To correct for this effect, scores of mouse genes were rank normalized to the scores of the human genes as follows: the scores were sorted, and for each gene the score of the rth mouse gene was set to the score of the rth human gene. Comparison of the distribution of scores before and after normalization showed that compared to usual Benjamini-Hochberg FDR and log fold change cut-offs (\(|\log FC|\geq1\)), the loss in statistical power was inconsequential and that this procedure ensured that mouse and human genes had comparable score distributions.

3.3 Network and orthology databases

The human and mouse background networks were downloaded from STRING v9.1, protein.actions.detailed.v9.1.txt (Franceschini et al., 2013), which is a database that contains experimentally verified direct protein interactions. Note that this network also contains interactions predicted based on orthology, so-called interologs. Ideally, we would prefer to use only experimentally predicted interactions, but currently, for mouse, such available data is too incomplete to result in a meaningful background network. Outlier nodes with a degree above 40 times the interquartile range plus the 75th percentile of the distribution of all node degrees were removed (ELAVL1, UBC, Ubb, Ubc). The resulting mouse network has 16 821 nodes and 483 532 edges and the human network has 16 235 nodes and 315 442 edges.

Orthology information was downloaded from Ensembl release 59 (Flicek et al., 2013) and all human and mouse orthologs were kept, regardless of the identity scores. The orthology mapping corresponds to a bipartite graph involving 67 304 human proteins and 43 953 mouse proteins linked by 104 007 edges, grouped in 16 552 bicliques with an average size of 6.72 proteins (SD: 5.34).

3.4 Implementation, input and output

xHeinz is implemented in modern C+++, using the boost libraries and the LEMON graph library (Desső et al., 2011). CPLEX 12.6 is used to solve the ILP. The source code is publicly available in a git repository linked to from http://software.cwi.nl/xheinz.

xHeinz takes as input (i) two species-specific networks, (ii) an orthology mapping between the nodes of the two networks, (iii) scores associated to each of the nodes, e.g. derived from the \(P\)-value of the moderated t-test, (iv) the threshold value \(z\) and (v) an optional time limit.
We performed a preprocessing step where we retained the subgraphs of the input networks induced by the genes that meet the microarray filtering criteria. This reduced the number of nodes to 8453 human nodes, 6882 mouse nodes and 14779 nodes in the orthology mapping. Among these, up to 250 nodes (depending on the time point) have positive scores. The rank normalization as described in Section 3.2 ensured that the number of positive human nodes is in the order of the number of positive mouse nodes.

\texttt{xHeinz} returns two node sets corresponding to a solution found within the time limit together with an upper bound on the optimal solution value. In case the solution value equals this upper bound, the computed solution is provably optimal.

### 4 Results and discussion

#### 4.1 \texttt{xHeinz} identifies conserved modules at different levels of conservation

We applied \texttt{xHeinz} on samples from the Th17 human and mouse data sets for time points 2, 4, 24, 48 and 72h. We solved these instances for different values of $\alpha \in [0,1]$ with a step size of 0.1. All computations were done in single-thread mode on a desktop computer (Intel XEON e5 3 Ghz) with 16 Gb of RAM and a time limit of 12 000 CPU seconds. After this timeout, the best feasible solution is returned by the solver.

Figure 3 shows for the five time points and eleven values of the $\alpha$ parameter, the human and mouse scores of the found modules as well as the distribution of the module contents. For 26 of the 55 instances we solved the conserved active modules problem to provable optimality within the time and memory limit. The optimality gap of a solution is defined as $\frac{UB - LB}{LB}$, where LB and UB are the value of the best solution and the lowest upper bound as identified by the branch-and-cut algorithm, respectively. Of the 29 instances that are not solved to optimality, 22 have a gap smaller than 5%.

Any feasible solution for a conservation ratio of $\alpha$ is also a solution for any $\alpha' \leq \alpha$. We indeed see in Figure 3 that this property holds, the solution values decrease monotonically with increasing $\alpha$. Also the solutions for $\alpha = 0$ (no conservation constraints) are identical to the solutions obtained by running the single species method Heinz (Dittrich et al., 2008) separately on the two networks.

There is a sharp decrease in module size for $\alpha = 1$. Indeed, this is the most restrictive setting since it enforces that all the nodes in a module must be conserved. We also observe that as $\alpha$ increases, both positive and negative conserved nodes are added, indicating that we manage to retrieve informative nodes in a gradual manner. See also Supplementary Text A.8 for a detailed analysis of module overlap for all combinations of $\alpha$ values.

When we compare solutions across time points, we see that the conserved active modules capture two phases of the differentiation process. We observe high activity at 2h as well as at the late time points. Several authors reported such biphasic behavior during early Th17 differentiation, both in mouse (Ciofani et al., 2012; Yosef et al., 2013) and human (Tuomela et al., 2012). The low activity score observed at the 4 h time point is in line with previous mouse studies, which suggest that after the initial induction sustained by Stat3 and Stat1 in the first four hours, a phase of Rorc induction takes place and lasts until the 20h time point, after which the effective protein level of Rorc starts to increase and to trigger the cytokine production phase (Yosef et al., 2013). Our model and the solutions obtained suggest that these dynamics are conserved between the two organisms.

#### 4.2 Early regulation of Th17 differentiation is conserved between human and mouse

In the following, we study the two phases of the Th17 differentiation process in more detail. We focus on the 2 and 48h time points. We selected for this evaluation $\alpha = 0.8$ for both time points, as this value provides a balance between conservation and activity and

![Module score by alpha](https://academic.oup.com/bioinformatics/article-abstract/31/19/3147/210875)

![Distribution of node classes by alpha](https://academic.oup.com/bioinformatics/article-abstract/31/19/3147/210875)

Fig. 3. Statistics of \texttt{xHeinz} solutions. The conserved active module problem was solved for five time points (columns) over a sequence of 11 consecutive values of the $\alpha$ conservation parameter ($\alpha$-axis). We report in the top row the score of the best solution ($y$-axis) and whether optimality was proven by our algorithm (circles). The second row illustrates how module contents vary as $\alpha$ increases. The height of each bar indicates the size of the respective module, colors indicate the fraction of positive and conserved nodes.
produces modules of interpretable size. All results at all time points are available on the accompanying website. Figure 4 reports the resulting human and mouse modules for the two time points.

We assess statistical significance of the resulting modules by performing 100 runs on randomized networks for each value of ζ, and additional 400 runs for the selected ζ = 0.8. We do this using two randomization methods: (i) permuting the node weights while keeping the graph fixed, and (ii) permuting the network topology while keeping the node weights and the node degrees fixed as described in Mihail and Zegura (2003). With the exception of a few extreme cases at the 48 h time point, all modules were found to be highly significant. For details see Supplementary Text A.8.

At the 2 h time point, xHeinz identifies a conserved module consisting of 38 human and 50 mouse proteins. Interestingly, both the human and mouse modules are centered around STAT3/Stat3. STAT3 is a signal transducer having transcription factor activity and was shown to play a key role in the differentiation process of Th17 (Harris et al., 2007). Once activated by Th17 polarizing cytokines (such as IL6 in our case), it eventually binds to the promoter regions of IL17A/Il17a and IL17F/Il17f cytokines and activates transcription. These cytokines are the hallmark cytokines produced by activated Th17 cells. It is worth noting that IL17A/IL17 cytokines and associated receptors are not in the 2 h modules, as these proteins have been shown to be expressed only at later time points (Tuomela et al., 2012). Moreover, STAT1/Stat1, another member of the STAT family, is part of the solution and belongs to the central core of the human and mouse modules, which is consistent with its major role during the early phases of Th17 differentiation (Yosef et al., 2013).

We also observe that the STAT3/BATF/IL6ST/SOCS3 region of the 2 h module is well-conserved. Batf has been shown to directly control Th17 differentiation in mouse (Schraml et al., 2009) and BATF proteins are detected as early as after 12 h of polarization in human (Tuomela et al., 2012). Similarly, SOCS3 is a known IL6 and IL21-induced negative regulator of Th17 polarization, that is eventually down-regulated by TGB and IL6ST at a later phase in order to prolong STAT3 activation (Qin et al., 2009; Zhu et al., 2008). Overall, these modules show highly conserved and significant enrichment for response to cytokine stimulus (Benjamini-Hochberg BH FDR 4.8 e-4), JAK-STAT (BH FDR 4.8 e-4) cascade and transcription regulator activity (BH FDR 2.3 e-4), computed using the DAVID functional annotation chart (Huang et al., 2009). This indicates that the identified module matches expected biological mechanisms observed at early phases (Ciofani et al., 2012). Furthermore, comparison of the dynamics of expression shows that genes differentially expressed in both species change expression in the same direction (cf. Supplementary Text A.3).

We also applied xHeinz to find a conserved module at a later time point (48 h). Kinetics analysis of Th17 differentiation showed that the effective secretion of Th17 hallmark cytokines only happens after several days of polarization (Tuomela et al., 2012; Yosef et al., 2013) and we do observe in these modules a significant enrichment for interleukin related proteins present in both species, which was absent for the 2 h modules, such as up-regulation of IL9/Il9. Secretion of IL9 by Th17 cells have been demonstrated both in mouse and human cells (Beriou et al., 2010), IL9 is know to be induced by Bcl3 (Richard et al., 1999), and Bcl3 inhibition has been recently shown to affect the function of Th17 cells in mouse

Fig. 4. Conserved active Th17 differentiation modules in human and mouse at 2 and 48 h. We obtained node activity scores capturing the significance of differential gene expression between the Th17 and Th0 conditions in human and mouse using the BUM model with FDR = 0.1. xHeinz uses these scores to search for conserved active modules in the STRING protein action network. The first row shows the human counterparts of the best scoring conserved modules for the 2 h (left) and 48 h (right) samples. The second row depicts the mouse counterparts. Rounded squares depict genes for which a homolog—as defined by Ensembl—is present in the counterpart, whereas triangles denote non-conserved genes. Node color gradually indicates activity scores. Orange: larger than 2; white: between ~2 and 2; violet: smaller than ~2. Node labels and sizes are proportional to betweenness centrality and edge width to edge-betweenness—both centralities are with respect to the subnetwork module. Only nodes having a degree larger than 2 (resp. 3) are displayed for the 2 h (resp. 48 h) module. The full networks are available on the accompanying website and in Supplementary Text A.3.

We also observe the conserved down-regulation of GATA3/Gata3, which is known to be the master regulator of Th2 cells (Zheng and Flavell, 1997), and is likely to constrain the Th17 lineage (Yang et al., 2008), and have been implicated in both species (Crome et al., 2009). Interestingly, these regulators are linked to the up-regulation of the vitamin-D receptor (VDR/Vdr), whose role in Th17 differentiation and several human auto-immune related disease have been recently studied (Chang et al., 2013).

In summary, our findings show the relevance of the identified conserved active modules with regard to the biological process of interest. By requiring the active modules to contain a certain fraction of conserved nodes, xHeinz identifies the main core proteins involved in the differentiation of Th17. Our analysis confirms that these proteins are very likely to have similar roles in both species.

4.3 Comparison to neXus

We compare the 48 h xHeinz modules (cf. Fig. 4) with subnetworks computed by neXus version 3 (Deshpande et al., 2010). neXus uses a heuristic technique to grow subnetworks from seed nodes simultaneously in two species. This is done in an iterative fashion. Neighborhoods of the two current modules are determined using a depth-first search. This search is restricted to only consider nodes that have a path to the seed node with a confidence larger than the user-specified parameter dfscutoff. The confidence of a path is defined as the product of the confidences of the edges comprising that path. The modules are extended to include the most active pair of orthologous nodes in the neighborhoods—where activity is defined as normalized log fold change and thus differs from the definition of activity used in xHeinz. This whole procedure is repeated until either the cluster coefficient drops below the user-specified parameter cc, or the average activity scores of one of the two modules drops below the parameter scorecutoff. We ran neXus with the default parameters $cc = 0.1$, $0.2$, $scorecutoff = 0.15$ and $dfscutoff = 0.3$, $0.8$ for mouse and human respectively for all time points. Table 1 gives the resulting module sizes for human and mouse.

<table>
<thead>
<tr>
<th>Solution</th>
<th>0.5 h</th>
<th>1 h</th>
<th>2 h</th>
<th>4 h</th>
<th>48 h</th>
<th>avg.</th>
<th>#sols</th>
</tr>
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<tbody>
<tr>
<td>0.5 h</td>
<td>7 (6)</td>
<td>15 (10)</td>
<td>15 (17)</td>
<td>6 (9)</td>
<td>3 (5)</td>
<td>5.25 (4.73)</td>
<td>4</td>
</tr>
<tr>
<td>1 h</td>
<td>7 (6)</td>
<td>15 (10)</td>
<td>15 (17)</td>
<td>6 (9)</td>
<td>3 (5)</td>
<td>5.25 (4.73)</td>
<td>4</td>
</tr>
<tr>
<td>2 h</td>
<td>7 (6)</td>
<td>15 (10)</td>
<td>15 (17)</td>
<td>6 (9)</td>
<td>3 (5)</td>
<td>5.25 (4.73)</td>
<td>4</td>
</tr>
<tr>
<td>4 h</td>
<td>7 (6)</td>
<td>15 (10)</td>
<td>15 (17)</td>
<td>6 (9)</td>
<td>3 (5)</td>
<td>5.25 (4.73)</td>
<td>4</td>
</tr>
<tr>
<td>48 h</td>
<td>7 (6)</td>
<td>15 (10)</td>
<td>15 (17)</td>
<td>6 (9)</td>
<td>3 (5)</td>
<td>5.25 (4.73)</td>
<td>4</td>
</tr>
</tbody>
</table>

Note: Shown are the sizes in number of nodes of the first 15 representative solutions and the average sizes for the human subnetwork and for the mouse subnetwork in brackets. The last column lists the number of solutions for each time point. No solutions were obtained for time points 24 and 72 h.
FDR 0.48, score -4.01, logFC 0.65). JUNB is a known partner of BATF with which it heterodimerizes preferentially during Th17 differentiation (Schraml et al., 2009), indicating its relevance. Both important genes would have been missed by a more restrictive conservation setting. Indeed, both nXus and xHeinz at $z \approx 1$ fail to find these genes showing that a more flexible view on conservation is required to adequately deal with transferability.

5 Conclusion

We introduce a mathematical model for the problem of finding active subnetwork modules that are conserved between two species and thus contribute to formalizing the notion of conserved active modules. A key feature of our model is a flexible notion of conservation, which is controlled by a parameter $z \in [0,1]$: We require that at least a fraction $z$ of the nodes are conserved between the species-specific modules of a solution. Note that in case of more distantly-related species a smaller $z$ value may be more appropriate. We have translated our model into an integer linear programming formulation and have devised and implemented an exact branch-and-cut algorithm that computes provably optimal or near-optimal conserved active modules in our model.

Our computational experiments for understanding the mechanisms underlying Th17 T cell differentiation in both mouse and human demonstrate that the flexibility in the definition of conservation is crucial for the computation of meaningful conserved active modules. We have found two conserved Th17 modules at time points 2 h ($z = 0.8$) and 48 h ($z = 0.8$) that thoroughly encompass the biphasic Th17 differentiation process. This result can not be revealed by requiring full conservation ($z = 1$) or by independent modules without requiring conservation ($z = 0$). Likewise, nXus, an alternative approach based on a stringent conservation model, is not able to capture the key regulatory program of the differentiation process.

A key characteristics of our model is its flexibility. This allows its extension to multiple species and time points, which we will address in future work. For this reason, however, realistic instances will be harder to compute to optimality and will require the development of powerful algorithm engineering techniques.

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References


Wei,L. et al. (2007) IL-21 is produced by Th17 cells and drives IL-17 production in a STAT3-dependent manner. J. Biol. Chem., 282, 34605–34610.


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