On-Line Supplement to:
The Misalignment of Product Architecture and Organizational Structure in Complex Product Development

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Following are four appendices which provide further details to the data analysis discussed in the body of the article. The appendices are:

- Appendix A: Descriptive Categorical Data Analysis

- Appendix B: *Log-linear p_1* Statistical Analysis

- Appendix C: *Logit p** Statistical Modeling of the Alignment Matrix

- Appendix D: Threats to Validity

Appendix A. Descriptive Categorical Data Analysis

The objective of our analysis is to study how certain factors such as organizational/system boundaries, design interface strength, indirect ties, and system modularity influence the alignment of design interfaces and team interactions characterized by the four states illustrated in **Figure 6**. We first complete a descriptive categorical data analysis (See **Table A1**) based on chi-square tests of independence and homogeneity which make the strong assumption of independence between cells of both the design interface matrix and team interaction matrix. (See Sosa 2000 for details.) Hence, the conclusions listed are only preliminary. In order to effectively test whether the observed differences are larger than what one would expect from random variation in the data, we need to control for other factors that are typically embedded in network data.

Additional References

Sosa, M.E. 2000. *Analyzing the Effects of Product Architecture on Technical Communication in Product Development Organizations*. Doctoral Thesis. MIT. Cambridge, MA.

Table A1. Results of Descriptive Categorical Data Analysis

Hypothesis	Sample	Results	χ^2	Preliminary Conclusion
H1a: Effect of organizational boundaries	569 design interfaces	81% of the 231 <u>within-boundary</u> design interfaces were matched by team interactions, whereas 48% of the 338 <u>cross-boundary</u> design interfaces were matched by team interactions	63.101	H1 tentatively supported [a]
H1b: Effect of systems boundaries	423 team interactions	90% of the 208 <u>within-boundary</u> team interactions were predicted by design interfaces, whereas 75% of the 215 <u>cross-boundary</u> team interactions were predicted by design interfaces	15.517	H1 tentatively supported [a]
H2: Effect of design interface strength	569 design interfaces	72% of the 250 <u>strong</u> design interfaces were matched by team interactions, whereas 53% of the 319 <u>weak</u> design interfaces were matched by team interactions	21.385	H2 tentatively supported [a]
H3: Moderating effects of boundaries on design interface strength	338 cross-boundary design interfaces	54% of the 115 <u>strong</u> cross-boundary design interfaces were matched by team interactions, whereas 45% of the 223 <u>weak</u> cross-boundary design interfaces were matched by team interactions	2.501	H3 tentatively NOT supported [a]
H4: Effect of indirect team interactions	2439 potential cases for indirect team interactions	20% of the 459 cases with <u>more than one potential indirect team interaction</u> corresponded to unmatched design interfaces, whereas 10% of the 579 cases with <u>one potential indirect team interactions</u> corresponded to unmatched design interfaces, and only 5% of the 1401 cases with <u>no potential indirect interactions</u> corresponded to unmatched design interfaces	93.911	H4 tentatively supported [b]
H5: Effect of indirect design interfaces	2293 potential cases for indirect interfaces	7% of the 645 cases with <u>more than three potential indirect interfaces</u> corresponded to unmatched team interactions, whereas 4% of the 643 cases with <u>less than three potential indirect interfaces</u> corresponded to unmatched team interaction, and less than 1% of the 1005 cases with <u>no indirect interfaces</u> corresponded to unmatched team interaction.	51.561	H5 tentatively supported [b]
H6a: Moderating effect of system modularity on organizational boundaries	338 cross-boundary design interfaces	54% of the 228 cross-boundary design interfaces <u>with integrative systems</u> were matched by team interactions, whereas 36% of the 110 cross-boundary design interfaces <u>between modular systems</u> were matched by team interactions	8.740	H6 tentatively supported [a]
H6b: Moderating effect of system modularity on system boundaries	215 cross-boundary team interactions	81% of the 150 cross-boundary team interactions <u>with integrative teams</u> were predicted by design interfaces, whereas 62% of the 65 cross-boundary team interaction <u>between modular teams</u> were predicted by design interfaces	9.566	H6 tentatively supported [a]

a: The null hypothesis is rejected when χ^2 is greater than the critical $\chi^2_{(0.99,1)}$=6.635
b: The null hypothesis is rejected when χ^2 is greater than the critical $\chi^2_{(0.99,2)}$=9.210

Appendix B. *Log-linear p_1 Statistical Analysis*

The statistical models described in this appendix are based on the p_1 distribution introduced by Holland and Leinhardt (1981). In order to introduce the p_1 distribution, let us consider the four-dimensional **Y**-array whose component Y_{ijkl} describes the interaction between element i and element j. The third and fourth dimensions of the **Y**-array are binary and describe the state of dyad ij of a network. Hence, $k=1$ if element i interacts with element j, and $l=1$ if element j interacts with element i. Fienberg and Wasserman (1981) show that Holland and Leinhardt's distribution, p_1, can be expressed in a log-linear format, as follows:

$$\ln \mathrm{P}\{Y_{ijkl}=1\} = \lambda_{ij} + (k+l)\theta + k \cdot \alpha_i + l \cdot \beta_i + l \cdot \alpha_j + k \cdot \beta_j + (kl)\rho \tag{B1}$$

The $\{\alpha_i\}$ parameters measure the *expansiveness* of the elements of the network, indicating how likely an element is to generate relational ties (non-zero cells in row i of the matrices). The $\{\beta_j\}$ parameters measure the *attraction* of the elements of the network, indicating how likely an element is to receive relational ties (non-zero cells in column j of the matrices). The "reciprocity" parameter, ρ, measures the overall tendency in the network to reciprocate interactions. The θ parameter indicates the overall volume of interaction in the network. Finally, the λ_{ij} parameters are "dyadic" effects that ensure that the probabilities sum to one for each dyad (equation B1); they have no substantive meaning. For a more detailed description of these parameters, refer to Holland and Leinhardt (1981).

Similar to our *logit p** approach, we build our log linear models in two stages. First, we model our alignment matrix considering binary design interfaces to test H1 and H6. Then, we extend our log-linear models to consider trichotomous design interfaces in order to test H2 and H3.

1. Log-linear p_1 models of alignment matrix with binary design interfaces

Similar to Van den Bulte and Moenaert (1998) we build log-linear models of our alignment matrix (with binary design interfaces) in five steps:

1.1. Build a p_1 model of the alignment matrix

Fienberg *et al.* (1985) and Wasserman and Iacobucci (1988) extend p_1 to multiple sociometric relations. Based upon these results we develop a log-linear model of the alignment matrix. We consider the joint distribution of both design interfaces and team interactions for a given dyad. That is, each dyad (i,j) of the alignment matrix has 16 states. Four (2 x 2) states are associated with the dyad's design interface relation, and four (2 x 2) states are associated with its team interaction relation, resulting in 16 states. Following the definitions of the variables k and l introduced before, we assign the subscripts (k_1,l_1) to describe the four states

associated with the design interface relation of dyad (i,j), while the subscripts (k_2,l_2) refer to the four states associated with the team interaction relation of dyad (i,j). Hence, the redefined **Y**-array has now six dimensions 54 x 54 x (2 x 2) x (2 x 2), and its characteristic element can be defined as follows:

$Y_{ij\,k1,l1\,k2,l2} = 1$ if dyad (i,j) behaves as described by (k_1,l_1) for their design interfaces AND by (k_2,l_2) for their team interactions.

$Y_{ij\,k1,l1\,k2,l2} = 0$ otherwise.

Considering the joint distribution of design interfaces and team interactions yields a log-linear model which describes simultaneously the behavior of the elements of our network according to two independent relations (design interfaces and team interactions). Hence, the first base log-linear model can be written as follows:

$$\ln P\{Y_{ij\,k_1l_1\,k_2l_2} = 1\} = \lambda_{ij} + (k_1 + l_1)\theta_1 + k_1\alpha_{1i} + l_1\beta_{1i} + l_1\alpha_{1j} + k_1\beta_{1j} + (k_1l_1)\rho_1 +$$
$$(k_2 + l_2)\theta_2 + k_2\alpha_{2i} + l_2\beta_{2i} + l_2\alpha_{2j} + k_2\beta_{2j} + (k_2l_2)\rho_2 \tag{B2}$$

The parameters of this model have the same meaning as in the original p_1 model, but applied to either design interfaces (subscript 1) or team interactions (subscript 2).

1.2. Aggregate physical components and design teams into groups

Fienberg and Wasserman (1981) introduced the approach of placing actors into subsets using relevant actor characteristics such that actors within a subset are assumed to behave similarly. Based on this approach we aggregate the 54 elements of the **Y**-array into 8 subsets according to the system boundaries of the product and the organizational boundaries of the development organization, respectively. By doing so, we obtain a much smaller **W**-array whose dimensions are 8 x 8 x (2 x 2) x (2 x 2), with elements $\{W_{rs\,k1,l1\,k2,l2}\}$ to be equal to the number of dyads between groups r (G_r) and s (G_s) whose design interfaces are described by (k_1,l_1) and whose team interactions are described by (k_2,l_2). Hence,

$$w_{rs\,k_1l_1\,k_2l_2} = \sum_{i \in G_r} \sum_{j \in G_s} y_{ij\,k_1l_1\,k_2l_2} \tag{B3}$$

Therefore, we can rewrite the model in equation (B2) to specify the expected number of dyads between groups r and s that behave as $(k_1,l_1,\,k_2,l_2)$ as follows:

$$\ln E(W_{rs\,k_1l_1\,k_2l_2}) = \lambda_{rs} + (k_1 + l_1)\theta_1 + k_1\alpha_{1r} + l_1\beta_{1r} + l_1\alpha_{1s} + k_1\beta_{1s} + (k_1l_1)\rho_1 +$$
$$(k_2 + l_2)\theta_2 + k_2\alpha_{2r} + l_2\beta_{2r} + l_2\alpha_{2s} + k_2\beta_{2s} + (k_2l_2)\rho_2 \tag{B4}$$

It is important to note that even though we have grouped components and teams into groups to facilitate the estimation and statistical inference of the models, the unit of analysis is still the dyad.

1.3. Capture the alignment of design interfaces and team interactions

The base model specified in equation (B4) assumes that design interfaces and team interactions are two independent relations of the same network of elements. However, we need to consider second-order interaction effects between design interfaces and team interactions to capture the association between the design interface matrix and the team interaction matrix. Following the notation of Wasserman and Iacobucci (1988), we define the following two association parameters, $\theta_{1,2}$ and ρ_{12}. $\theta_{1,2}$ measures any tendency toward conformity across relationships. That is, component i depends on component j, AND team i reports interaction with team j (the "#" cells of the alignment matrix). On the other hand, ρ_{12} measures tendency toward flow reversal. That is, component i depends upon component j, AND team j reports interaction with team i. These two parameters correspond to *association* and *exchange* parameters included in our *logit p** formulation. By including these two parameters, we extend our base model (equation B4) as follows:

$$
\begin{aligned}
\ln E\,(W_{rs\,k_1 l_1\,k_2 l_2}) = \lambda_{rs} + (k_1 + l_1)\theta_1 + k_1\alpha_{1r} + l_1\beta_{1r} + l_1\alpha_{1s} + k_1\beta_{1s} + (k_1 l_1)\rho_1 + \\
(k_2 + l_2)\theta_2 + k_2\alpha_{2r} + l_2\beta_{2r} + l_2\alpha_{2s} + k_2\beta_{2s} + (k_2 l_2)\rho_2 + (k_1 k_2 + l_1 l_2)\theta_{1,2} + (k_1 k_2 + l_1 l_2)\rho_{1,2}
\end{aligned}
\tag{B5}
$$

1.4. Extend the model with structural parameters: *ACROSS* and *MODULAR*

To explicitly represent organizational and system boundary effects, we define the following indicator variable:

ACROSS = 1 if elements (i.e. component and team) i and j are in the different groups ($r \neq s$)

ACROSS = 0 if $r = s$

By expanding the dimension of the **W**-array with *ACROSS* as the seventh dimension, we can estimate parameters associated with the second-order interaction terms *ACROSS* x k_1, and *ACROSS* x k_2, due to symmetry of the **W**-array identical to *ACROSS* x l_1 and *ACROSS* x l_2, respectively. These terms capture the within-boundary effects exhibited in both the design interface matrix and team interaction matrix. Indeed, we expect these terms to be significantly negative indicating that it is less likely to encounter design interfaces across system boundaries and team interactions across organizational boundaries.

In order to include the effects due to system modularity into the model we define another indicator variable, *MODULAR*, as follows:

MODULAR=1 if both components of a dyad belong to modular systems (r<7 and s<7)

MODULAR=0 if one of the components of a dyad belongs to integrative systems (r≥7 or s≥7)

Having defined the indicator variables *ACROSS* and *MODULAR*, we proceed to define third-order and fourth-order interaction effects that allow us to test the effects due to group boundaries (H1) and the moderating effects due to system modularity (H6).

We estimate the parameter associated with the third-order interaction effect *ACROSS* x k_1 x k_2 (due to symmetry of the **W**-array identical to *ACROSS* x l_1 x l_2). Thus, $\theta_{ACROSS,1,2}$ captures whether the occurrence of dyads across boundaries with design interfaces matched by team interactions is significantly less than the occurrence of those dyads within boundaries. Hence, a formal hypothesis testing for H1 can be specified as follows:

H1: $\theta_{ACROSS,1,2} < 0$

We also estimate the parameter associated with the fourth-order interaction effect *MODULAR* x *ACROSS* x k_1 x k_2 (due to symmetry of the **W**-array identical to *MODULAR* x *ACROSS* x l_1 x l_2). Thus, $\theta_{MODULAR,ACROSS,1,2}$ captures whether the effect due to organizational/system boundary is significantly different for modular systems than for integrative systems. We expect this effect to be significantly negative, which corresponds to fewer cross-boundary design interfaces (matched by team interactions) between modular systems than to integrative systems (H6). Hence, a formal hypothesis testing for H6 is expressed as follows:

H6: $\theta_{MODULAR,ACROSS,1,2} < 0$

After extending the model with indicator variables, *ACROSS* and *MODULAR*, to include the high-order interaction effects, we write our final log-linear model as follows:

$$\ln E\left(W_{rs\,k_1 l_1\,k_2 l_2}\right) = \lambda_{rs} + (k_1 + l_1)\theta_1 + k_1\alpha_{1r} + l_1\beta_{1r} + l_1\alpha_{1s} + k_1\beta_{1s} + (k_1 l_1)\rho_1 +$$
$$(k_2 + l_2)\theta_2 + k_2\alpha_{2r} + l_2\beta_{2r} + l_2\alpha_{2s} + k_2\beta_{2s} + (k_2 l_2)\rho_2 + (k_1 k_2 + l_1 l_2)\theta_{1,2} + (k_1 k_2 + l_1 l_2)\rho_{1,2} +$$
$$(ACROSS \cdot k_1 + ACROSS \cdot l_1)\theta_{ACROSS,1} + (ACROSS \cdot k_2 + ACROSS \cdot l_2)\theta_{ACROSS,2} +$$
$$(ACROSS \cdot k_1 \cdot k_2 + ACROSS \cdot l_1 \cdot l_2)\theta_{ACROSS,1,2} + \qquad\qquad (B6)$$
$$(MODULAR \cdot k_1 + MODULAR \cdot l_1)\theta_{MODULAR,1} + (MODULAR \cdot k_2 + MODULAR \cdot l_2)\theta_{MODULAR,2} +$$
$$(MODULAR \cdot k_1 \cdot k_2 + MODULAR \cdot l_1 \cdot l_2)\theta_{MODULAR,1,2}$$
$$(MODULAR \cdot ACROSS \cdot k_1 \cdot k_2 + MODULAR \cdot ACROSS \cdot l_1 \cdot l_2)\theta_{MODULAR,ACROSS,1,2}$$

1.5. Fit models to data and test hypotheses H1 and H6

Fitting a model to data means finding the best (maximum likelihood) estimates of all parameters in the model that could produce the interaction data represented in the aggregated alignment matrix (**W**-array). To test the significance of the parameters we ask how much the expected and observed matrices differ. We do so by using conventional rules for likelihood-ratio and conditional likelihood-ratio tests for log-linear models for categorical data (Bishop *et al.* 1975). Based on results presented by Fienberg and Wasserman (1981) we use

standard iterative proportional fitting computer programs for contingency tables (We used SPSS) to fit the models to data (**W**-array).

Table B1 shows the estimates of the parameters for five log-linear models with their respective likelihood-ratio statistics, G^2, and their numbers of degrees of freedom. The first model (Model 0, independent) does not include the association parameters between design interfaces and team interactions. (This model corresponds to equation B4.) Model 1 (base, which corresponds to equation B5) includes $\theta_{1,2}$ which substantially improves the goodness-of-fit of the independent model ($\Delta G^2 = 943.71$, $\Delta df = 1$) indicating, as expected, that there is significantly strong association of design interfaces and team interactions. Model 1 also includes the exchange parameter, ρ_{12}, which is not statistically significant. Including the second-order interaction effects with *ACROSS* greatly improves the goodness of fit of the base model ($G^2 = 3719.18$, $df = 5688$, model not shown). The inclusion of these effects resulted in significantly negative parameters indicating, as expected, that significantly smaller portions of design interfaces and team interactions take place across boundaries.

Consistent with our *logit p** analysis, model 2 (across) includes a significantly positive $\theta_{ACROSS,1,2}$ parameter indicating that the "pure" alignment of design interfaces and team interactions are more likely to take place across boundaries. Yet, due to strong clustering effects model 2 still predicts a lower probability of finding aligned design interfaces and team interactions across boundaries.

When adding second-order and third-order interaction effects with *MODULAR,* the log-linear model does not significantly improve its goodness-of-fit (see Model 3), which indicates that system modularity does not have a direct effect on the alignment of design interfaces and team interactions. Finally, Model 4, corresponding to equation B6, includes the fourth-order interaction parameter $\theta_{MODULAR,ACROSS,1,2}$, whose value is significantly negative, indicating that cross-boundary design interfaces matched by team interactions are less likely to occur between modular systems (supporting H6).

2. Log-linear p_1 models of the alignment matrix with valued design interfaces

In order to test the effects of design interface strength (H2 and H3) we need to consider non-binary design interfaces. By using the metric $STRENGTH_{ij}$, defined in section 5.1, a cell of the design interface matrix can have three possible states (i.e. NULL design interface, WEAK design interface, or STRONG design interface). Therefore, a dyad of the design interface matrix would have nine possible states and a dyad of the alignment matrix would have 36 possible states (nine states corresponding to the design interface dyad times four states corresponding to the binary team interaction dyad).

Wasserman and Iacobucci (1986) extended p_1 models for statistical analysis of discrete relational data. Using their notation, we can write a p_1 model that estimates the probability that dyad (i,j) of the design interface matrix will behave as the newly defined (k_1, l_1) as follows:

$$\ln P\ (Y_{ij\,k_1 l_1}) = \lambda_{ij} + \theta_{k_1} + \theta_{l_1} + \alpha_{i(k_1)} + \alpha_{j(l_1)} + \beta_{j(k_1)} + \beta_{i(l_1)} + \rho_{k_1,l_1} \tag{B7}$$

The most important difference between this model and the one described by equation (B1) is that this model includes *expansiveness* $\{\alpha_{i(kl)}\}$, *popularity* $\{\beta_{j(kl)}\}$, and *reciprocity* $\{\rho_{kl,\,ll}\}$ parameters associated with each non-zero design interface strength (i.e. WEAK and STRONG).

Following the same rationale as in the previous sub-section, we extend the model described by equation (B7) to a model that describes the joint probability distribution of trichotomous design interfaces and binary team interactions including higher-order interaction effects at specific strengths. Hence, the equivalent model to equation (B5) using trichotomous design interfaces can be expressed as follows:

$$\ln E\ (W_{rs\,k_1 l_1 k_2 l_2}) = \lambda_{rs} + \theta_{k_1} + \theta_{l_1} + \alpha_{r(k_1)} + \alpha_{s(l_1)} + \beta_{s(k_1)} + \beta_{r(l_1)} + \rho_{k_1,l_1} +$$
$$\theta_{k_2} + \theta_{l_2} + \alpha_{r(k_2)} + \alpha_{s(l_2)} + \beta_{s(k_2)} + \beta_{r(l_2)} + \rho_{k_2,l_2} + \theta_{1,2} + \rho_{1,2} \tag{B8}$$

The $\{\theta_{1,2}\}$ parameters are associated with the second-order interaction effects k_1 x k_2 (which due to symmetry are identical to l_1 x l_2). Since k_1 and l_1 have two non-zero states (WEAK and STRONG), including these effects results in estimating two $\theta_{1,2}$ parameters, $\theta_{WEAK,2}$ and $\theta_{STRONG,2}$. $\theta_{WEAK,2}$ captures the level of association of the design interface matrix and team interaction matrix at $k_1=WEAK$ whereas $\theta_{STRONG,2}$ captures the level of association at $k_1=STRONG$. Hence, a formal hypothesis testing of H2 can be expressed as follows:

   H2: $\theta_{STRONG,2}$ - $\theta_{WEAK,2} > 0$

In order to test the moderating effects of organizational and systems boundaries on the effects of design interface strength (H3) we extend our model with structural parameter *ACROSS* to examine the third-order interaction effects *ACROSS* x k_1 x k_2 (due to symmetry identical to *ACROSS* x l_1 x l_2). As before, including this interaction effect means estimating two parameters (one for each non-zero strength). Hence, we estimate $\theta_{ACROSS,WEAK,2}$ and $\theta_{ACROSS,STRONG,2}$. However, we are interested in testing whether the level of association is stronger (across boundaries) for cases with strong design interfaces (H3). Hence, a formal hypothesis testing of H3 is formulated as follows:

   H3: $\theta_{ACROSS,STRONG,2}$ - $\theta_{ACROSS,WEAK,2} > 0$

In order to test H2 and H3 we follow a similar procedure to the one described in step 5 of the previous sub-section, fitting the newly defined log-linear models to data. For the purpose of brevity, Table B2 shows only the estimates of relevant parameters of the models used to test H2 and H3 with their respective likelihood-ratio statistics, G^2, and their numbers of degrees of freedom.

Model 1 (exchange) includes second-order exchange parameters and serves as our base model. Model 2 (clustering) includes parameters to capture tendencies to cluster design interfaces and team interactions within boundaries which, as expected, are all significantly negative. Model 3 (association) includes association parameters between design interfaces and team interaction for both WEAK and STRONG design interfaces. Note that both $\theta_{WEAK,2}$ and $\theta_{STRONG,2}$ are significantly positive ($\Delta G^2 = 224.70$, $\Delta df = 2$, $p < 0.001$), indicating that there is a strong association between design interfaces and team interaction at both levels. To test whether the difference of these parameters is significantly positive we estimate a reduced model that includes a single parameter to capture the association of design interfaces and team interactions. Since this reduced model exhibits a significantly worse goodness-of-fit than model 3, we can conclude that $\theta_{STRONG,2}$ is significantly greater than $\theta_{WEAK,2}$ (supporting H2).

Model 4 includes third-order interaction effects with *ACROSS* (i.e. $\theta_{ACROSS,STRONG,2}$ and $\theta_{ACROSS,WEAK,2}$). Consistent with our binary log-linear models, these parameters are significantly positive ($\Delta G^2 = 17.89$, $\Delta df = 2$, $p < 0.001$) indicating that the *pure* tendency for alignment is stronger across boundaries for both WEAK and STRONG interface strengths. Yet, we are interested in testing whether there is a significance difference between the newly included parameters. To do so, we estimate a reduced model that captures, with a single parameter, the association of design interfaces and team interactions across boundaries. Since the reduced model does NOT exhibit a significantly worse goodness-of-fit than model 4, we cannot conclude that $\theta_{ACROSS,STRONG,2}$ is significantly different than $\theta_{ACROSS,WEAK,2}$, hence H3 is not supported.

Finally, we ran additional models including the indicator variable *MODULAR* to test whether there was a moderating effect of system modularity on the effect of design interface strength and found no evidence of such effect (models not included in Table B2).

3. Additional References

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Table B1. Results of Log-Linear Analysis (Binary Relations)

Parameters	Model 0 (Independent)	Model 1 (Base)	Model 2 (ACROSS)	Model 3 (MODULAR)	Model 4 (FINAL)
Parameters for the design interface matrix					
α_{1FAN}	0.4321	0.3632	0.3743	0.2598	0.3128
α_{1LPC}	0.2090	0.3632	0.3161	0.2603	0.2562
α_{1HPC}	-0.0120	0.1061	0.0517	0.0108	-0.0129
α_{1BD}	-0.0172	-0.2137	-0.1407	-0.2924	-0.2042
α_{1HPT}	-0.5653	-0.5731	-0.5401	-0.6408	-0.6033
α_{1LPT}	-0.0771	-0.0533	-0.0621	-0.1451	-0.1301
α_{1MC}	-0.2567	-0.1496	-0.1596	0.0862	0.0280
α_{1EC}	0.2869	0.1575	0.1606	0.4612	0.3535
β_{1FAN}	-0.7416	-0.6587	-0.6993	-0.7507	-0.7918
β_{1LPC}	-0.0672	0.1355	0.0896	0.0263	0.0284
β_{1HPC}	0.0509	0.2169	0.1834	0.1045	0.1177
β_{1BD}	-0.0957	-0.4262	-0.3557	-0.5249	-0.3993
β_{1HPT}	0.4363	0.3360	0.3757	0.2159	0.3253
β_{1LPT}	-0.3862	-0.2229	-0.2226	-0.3289	-0.3016
β_{1MC}	0.3176	0.1773	0.1667	0.4843	0.3522
β_{1EC}	0.4856	0.4420	0.4624	0.7738	0.6691
θ_1	-2.1306	0.2063	0.1198	1.0958	0.3526
ρ_1	3.9891	3.5224	3.4502	3.5083	3.4532
Parameters for the team interaction matrix					
α_{2FAN}	0.2779	0.2312	0.2269	0.0776	0.1370
α_{2LPC}	0.0062	-0.2327	-0.2088	-0.3657	-0.3203
α_{2HPC}	-0.0313	-0.1437	-0.1321	-0.2783	-0.2500
α_{2BD}	0.0009	0.2323	0.2945	0.0904	0.2538
α_{2HPT}	-0.3079	-0.0678	-0.0237	-0.1989	-0.1104
α_{2LPT}	-0.0197	0.0706	0.1023	-0.0797	-0.0017
α_{2MC}	-0.3880	-0.3491	-0.4667	0.0249	-0.1738
α_{2EC}	0.4620	0.2595	0.2076	0.7297	0.4655
β_{2FAN}	-0.5182	-0.2337	-0.3480	-0.4008	-0.4945
β_{2LPC}	-0.1838	-0.3553	-0.3426	-0.5244	-0.4493
β_{2HPC}	-0.1618	-0.3120	-0.3185	-0.4837	-0.4220
β_{2BD}	0.2767	0.5694	0.6579	0.3802	0.6202
β_{2HPT}	0.3069	0.2591	0.3355	0.0683	0.2941
β_{2LPT}	-0.5070	-0.3638	-0.3993	-0.5360	-0.5222
β_{2MC}	0.4625	0.4057	0.4521	0.9271	0.6903
β_{2EC}	0.3249	0.0307	-0.0371	0.5690	0.2834
θ_2	-2.1239	-0.4895	-0.8373	0.9959	-0.3599
ρ_2	3.5191	2.5124	2.206	2.4583	2.1749
Second-order, third-order and fourth-order interaction parameters					
$\theta_{1,2}$		**3.2314[a]**	3.2902	3.2318	2.9670
ρ_{12}		-0.2101[a]	-0.3290	-0.2453	-0.3603
$\theta_{ACROSS,1}$			**-0.2081**		-0.6137
$\theta_{ACROSS,2}$			**-1.0284**		-1.4850
$\theta_{ACROSS,1,2}$			**0.9016[b]**		0.5645
$\theta_{MODULAR,1,2}$				**0.0547[c]**	-0.4831
$\theta_{MODULAR,ACROSS,1,2}$					**-0.3487[d]**
Goodness-of-fit					
G^2 [†]	5243.00	4298.70	3705.60	4134.61	3670.23
df	5692	5690	5687	5687	5683

† G^2 provided by statistical packages is incorrect because the unit of analysis is still the dyad rather than the group of dyads. We calculate G^2 as follows (Fienberg and Wasserman 1981):

$$G^2 = 2\sum_{i<j}\sum_{k_1,l_1,k_2,l_2} y_{ijk_1l_1k_2l_2} \log(y_{ijk_1l_1k_2l_2}/\hat{y}_{ijk_1l_1k_2l_2}) = -2\left[\sum_{r<s}\sum_{k_1,l_1,k_2,l_2} w_{rsk_1l_1k_2l_2}\log(\hat{w}_{rsk_1l_1k_2l_2}/[G_rG_s]) + \sum_r\sum_{k_1,l_1,k_2,l_2} w_{rrk_1l_1k_2l_2}\log(\hat{w}_{rrk_1l_1k_2l_2}/[G_r(G_r-1)])\right]$$

a: The unconstrained model against which significance of $\theta_{1,2}$ was assessed is model 1. Hence, $\Delta G^2 = 943.71$, $\Delta df = 1$, $p < .001$. Model 2 does not significantly improve its goodness-of-fit when the term ρ_{12} is added ($\Delta G^2 = 0.59$, $\Delta df = 1$, hence $p > 0.1$)

b: The unconstrained model against which the hypothesis (H1) is tested includes second-order parameters with ACROSS ($G^2 = 3719.18$, $df = 5688$). Hence, $\Delta G^2 = 13.58$, $\Delta df = 1$, $p < 0.001$.

c: The unconstrained model against which the significance is assessed includes the second-order parameters with MODULAR ($G^2 = 4134.90$, $df = 5688$). Hence, $\Delta G^2 = 0.29$, $\Delta df = 1$, $p > 0.1$

d: The unconstrained model against which the hypothesis (H6) is tested includes second and third-order interaction terms with both ACROSS and MODULAR ($G^2 = 3706.68$, $df = 5684$). Hence, $\Delta G^2 = 36.45$, $\Delta df = 1$, $p < .001$)

Table B2. Results of Log-linear Analysis with Valued Design Interfaces

Parameters	Model 1 (Exchange)	Model 2 (Clustering)	Model 3 (Association)	Model 4 (Association across)
Second order exchange parameters				
$\rho_{WEAK,2}$	2.0508 [a]	1.8575	-0.3786	-0.3099
$\rho_{STRONG,2}$	2.6590 [a]	2.2256	-0.5228	-0.4705
Second-order interaction parameters with ACROSS				
$\theta_{ACROSS,WEAK}$		-0.8299 [b]	-0.7179	0.0204
$\theta_{ACROSS,STRONG}$		-1.3483 [b]	-1.2106	-0.6157
$\theta_{ACROSS,2}$		-1.2892 [b]	-1.2596	-1.1904
Second-order association parameters				
$\theta_{WEAK,2}$			2.9187 [c,c1]	3.1348
$\theta_{STRONG,2}$			3.5711 [c,c1]	3.6950
Third-order interaction parameters with ACROSS				
$\theta_{ACROSS,WEAK,2}$				1.1398 [d,d1]
$\theta_{ACROSS,STRONG,2}$				0.74.18 [d,d1]
Goodness-of-fit				
G^2 [†]	5399.20	4739.95	4515.25	4497.36
df	8535	8532	8530	8528

[†] G^2 is determined as indicated in Table B1.

[a]: The unconstrained model against which the significance is assessed is the independent model (equation B7) whose G^2 =6112.07, df = 8537. Hence, ΔG^2 =712.87, Δdf = 2, $p < 0.001$

[b]: The unconstrained model against which the significance is assessed is Model 1. Hence, $\Delta G^2 = 659.25$, $\Delta df = 3$, $p < 0.001$

[c]: The unconstrained model against which the significance is assessed is Model 2. Hence, $\Delta G^2 = 224.70$, $\Delta df = 2$, $p < 0.001$

[c1]: The model against which the significance of the parameters difference is assessed is a reduced model with a single association parameter, $G^2 = 4522.63$, $df = 8531$. Hence, $\Delta G^2 = 7.38$, $\Delta df = 1$, $p < 0.01$

[d]: The unconstrained model against which the significance is assessed is Model 3. Hence, $\Delta G^2 = 17.89$, $\Delta df = 2$, $p < 0.001$

[d1]: The model against which the significance of the parameters difference is assessed is a reduced model with a single association parameter across boundaries, $G^2 = 4498.85$, $df = 8527$. Hence, $\Delta G^2 =1.49$, $\Delta df = 1$, $p > 0.1$

Appendix C. *Logit p** **Statistical Modeling of the Alignment Matrix**

The general log-linear form of *p** can be expressed as (Wasserman and Pattison, 1996):

$$\Pr(\mathbf{X} = \mathbf{x}) = \frac{\exp\{\theta' z(\mathbf{x})\}}{\kappa(\theta)} = \frac{\exp\{\theta_1 z_1(\mathbf{x}) + ... + \theta_n z_n(\mathbf{x})\}}{\kappa(\theta)} \qquad (C1)$$

where **x** is the observed *matrix* of the network of interest. The response variable is the probability of the observed **x**. θ is a vector of *n* model parameters and **z(x)** is the vector of the *n* explanatory variables. The θ parameters are unknown "regression-type" coefficients that must be estimated. The function $\kappa(\theta)$ is a constant that ensures a proper probability distribution (i.e., the sum of $\Pr(\mathbf{X}=\mathbf{x})$ over all possible **X** is unity). The problem with this formulation is that the constant κ is very difficult to determine analytically and computationally for most networks (except for very small ones). Hence, a logit formulation for *p** models that does not depend on the normalizing constant has been developed for single dichotomous relation networks (Strauss and Ikeda 1990, Wasserman and Pattison 1996). As a result, Wasserman and Pattison (1996) define the log of conditional odds as follows:

$$\varpi_{ij} = \log\left\{\frac{\Pr(X_{ij} = 1 \mid X_{ij}^c)}{\Pr(X_{ij} = 0 \mid X_{ij}^c)}\right\} = \theta'\left[z(x_{ij}^+) - z(x_{ij}^-)\right] = \theta'\delta(x_{ij}) \qquad (C2)$$

This expression is discussed at length by Wasserman and Pattison (1996). Of interest is the term $\delta(x_{ij})$, which is the vector of explanatory variables that surfaces when the tie *ij* changes from 1 to 0. As indicated by Wasserman and Pattison (1996, p. 407), "to specify a *logit p** model, one chooses *a priori* a collection of network statistics that is supposed to affect the log odds of a tie being present to absent". Hence, the model depends on the network effects that one believes to have a significant tendency of being present in the network. For each network effect (such as expansiveness, reciprocation, or transitivity), there is a corresponding network statistic and a corresponding explanatory variable in the logit model. It is important to emphasize that the explanatory variable is the change in the network statistic when the tie from element *i* to element *j* (X_{ij}) changes from being present to absent. Wasserman and Pattison (1996) describe how by explicitly assuming a dependence structure between the ties in a network the independence dyad assumption is no longer needed. Extensions of the *logit p** model for multivariate and valued relations are presented by Pattison and Wasserman (1999) and Robins *et al.* (1999), respectively.

Having introduced the *logit p** model for single dichotomous relation, our next task is to build specific members of the *logit p** family to properly model our alignment matrix and test our hypotheses. We carry out this task in two stages. First, based on Pattison and Wasserman (1999), we rewrite equation (C2) for two binary

relations by considering the dichotomous random variable X_{ijm} which records whether tie ij of type m is present. In our case, $m=1$ corresponds to design interfaces while $m=2$ corresponds to team interactions. With such models, we test hypotheses H1, H4, H5, and H6. We can express our *logit p** for two binary relations as follows (Pattison and Wasserman 1999):

$$\varpi_{ijm} = \log\left\{\frac{\Pr(X_{ijm} = 1 \mid X_{ijm}^c)}{\Pr(X_{ijm} = 0 \mid X_{ijm}^c)}\right\} = \theta'\left[z(x_{ijm}^+) - z(x_{ijm}^-)\right] = \theta'\delta(x_{ijm}) \tag{C3}$$

In the second stage, we extend our formulation to incorporate the effects of design interface strength (to test hypotheses H2 and H3) based on Robins *et al.* (1999). When considering trichotomous design interfaces, our original X_{ijm} array will have *1s* and *2s* for $m=1$. As a result, we need to transform our newly defined trichotomous X_{ijm} array into a three-way binary array, $Y_{ij,m}$, in which the third dimension has three states ($m=1$w, $m=1$s, and $m=2$). That is, $m=1$w corresponds to WEAK design interfaces, while $m=1$s corresponds to STRONG design interfaces, and $m=2$ corresponds to team interactions. Hence, the transformation takes the following form:

$Y_{ij,2} = X_{ij2}$ If $X_{ij1} = 0$, then $Y_{ij,1w} = Y_{ij,1s} = 0$

If $X_{ij1} = 1$, then $Y_{ij,1w} = 1$ and $Y_{ij,1s}$ is undefined

If $X_{ij1} = 2$, then $Y_{ij,1s} = 1$ and $Y_{ij,1w}$ is undefined

As a result of such a transformation, we can write the *logit p** model using our newly defined $Y_{ij,m}$ which purposely excludes "response" variables for which $Y_{ij,m}$ is undefined. Hence, we write the expression for the *logit p** for the $Y_{ij,m}$ array as follows:

$$\varpi_{ij,m} = \log\left\{\frac{\Pr(Y_{ij,m} = 1 \mid Y_{ij,m}^c)}{\Pr(Y_{ij,m} = 0 \mid Y_{ij,m}^c)}\right\} = \gamma'\left[z(y_{ij,m}^+) - z(y_{ij,m}^-)\right] = \gamma'\delta(y_{ij,m}) \tag{C4}$$

Additional References

Strauss, D. and M. Ikeda. 1990. Pseudolikelihood estimation for social networks. *J. Amer. Statist. Assoc.* 85, 204-212.

Table C1. Network effects included in *logit p** models

Network effect label	Description	Graphical configuration	Parameters	Network statistic $z(\mathbf{x})$
Dyadic effects				
Choice	For m=1, propensity of components to have a design interface with others For m=2, propensity of teams to report interactions with others		$\theta_1 \quad \theta_2$	$L_m = \sum_{ij} X_{ij,m}$
Reciprocation (or mutuality)	Configurations in which ties ij and ji are both present for each network of type m		$\rho_1 \quad \rho_2$	$M_m = \sum_{i<j} X_{ij,m} X_{ji,m}$
Triadic effects				
2-In-star (overall attractiveness)	Configurations in which two separate ties are directed towards the same element. This effect captures the overall tendency for each element to attract ties of type m		$\sigma_{I,1} \quad \sigma_{I,2}$	$S_{I,m} = \sum_{i,j,k} X_{ji,m} X_{ki,m}$
2-Out-star (overall expansiveness)	Configurations in which two separate ties are directed away from the same element. This effect captures the overall tendency for each element to generate ties of type m		$\sigma_{O,1} \quad \sigma_{O,2}$	$S_{O,m} = \sum_{i,j,k} X_{ij,m} X_{ik,m}$
2-mixed-star	Configurations in which a tie is directed away from an element to which another tie is directed to		$\sigma_{M,1} \quad \sigma_{M,2}$	$S_{M,m} = \sum_{i,j,k} X_{ji,m} X_{ik,m}$
Transitivity	Configurations in which three elements form a transitive triad (such as ij, jk, and ik) of type m		$\tau_1 \quad \tau_2$	$T_{T,m} = \sum_{i,j,k} X_{ij,m} X_{jk,m} X_{ik,m}$
Cyclicity	Configurations in which three ties of type m form an intransitive cycle such as ij, jk, and ki		$\zeta_1 \quad \zeta_2$	$T_{C,m} = \sum_{i,j,k} X_{ij,m} X_{jk,m} X_{ki,m}$
Bivariate effects				
Exchange	Configurations in which a design interface is present and it is reciprocated by a team interaction, or vice versa		ρ_{12}	$M_{1,2} = \sum_{i<j} X_{ij,1} X_{ji,2}$
Association	Configurations in which both design interface and team interactions are present		θ_{12}	$L_{1,2} = \sum_{ij} X_{ij,1} X_{ij,2}$
Indirect team interactions	Configurations in which a transitive triad is formed by two subsequent team interactions with a design interface		τ_{221}	$T_{221} = \sum_{i,j,k} X_{ij,2} X_{jk,2} X_{ik,1}$
Indirect design interfaces	Configurations in which a transitive triad is formed by two subsequent design interfaces with a team interaction		τ_{112}	$T_{112} = \sum_{i,j,k} X_{ij,1} X_{jk,1} X_{ik,2}$

Table C2. Results of *logit p** analysis (dichotomous relations)

Params.	Model 0 Independent	Model 1 Assoc.	Model 2 Across	Model 3 Indirect	Model 4 Ind. Within	Model 5 Modular	Model 6 All
Design interface effects							
θ_1	-2.446 (91.259)	-3.046	-2.490	-2.547	-1.703	-2.701	-1.877
ρ_1	3.246 (360.035)	2.871	2.846	2.826	2.735	2.819	2.711
$\sigma_{I,1}$	021 (.890)	.000	.002	-.029	-.028	.003	-.028
$\sigma_{O,1}$	.020 (.754)	-.017	-.015	.034	.043	-.013	.043
$\sigma_{M,1}$	-.129 (35.304)	-.084	-.074	-.086	-.090	-.072	-.089
τ_1	.267 (111.052)	.262	.259	.283	.280	.259	.280
ζ_1	-.134 (3.903)	-.176	-.195	-.171	-.147	-.192	-.144
Team interaction effects							
θ_2	-3.319(177.838)	-4.178	-3.056	-3.020	-3.198	-3.753	-3.948
ρ_2	3.815 (362.516)	3.231	3.021	3.001	2.977	2.972	2.944
$\sigma_{I,2}$	-.004 (.028)	-.023	.000	-.081	-.088	.012	-.079
$\sigma_{O,2}$	.063 (15.965)	.090	.111	.139	.142	.121	.152
$\sigma_{M,2}$	-.092 (27.383)	-.072	-.045	-.037	-.033	-.038	-.029
τ_2	.334 (113.162)	.249	.212	.229	.225	.212	.222
ζ_2	-.389 (20.849)	-.366	-.421	-.392	-.439	-.408	-.442
Alignment effects							
ρ_{12}		**-.242** (2.124)	-.224 (1.740)	-.242 (1.970)	-.196 (1.282)	-.198 (1.343)	-.166 (.900)
θ_{12}		**2.769** (329.614)	1.917 (46.185)	2.121 (54.088)	2.203 (56.673)	1.807 (22.092)	2.227 (29.711)
Clustering effects and boundary effects (H1)							
$\theta_{ACROSS,1}$			**-.803** (9.864)	-.860 (10.522)	-1.807 (20.093)	-.771 (9.050)	-1.738 (18.194)
$\theta_{ACROSS,2}$			**-1.895** (35.314)	-1.908 (35.209)	-1.659 (15.251)	-1.816 (31.969)	-1.462 (11.508)
$\theta_{ACROSS,12}$			**1.013** (10.681)	1.077 (11.721)	.977 (9.315)	1.375 (11.924)	1.265 (8.937)
Effects of indirect team interactions and indirect design interfaces (H4, H5)							
τ_{221}				**-.004** (.004)	-.004 (.004)		.000 (.000)
τ_{112}				**-.082** (2.732)	-.061 (1.490)		-.059 (1.392)
$\tau_{WITHIN,221}$					**.228** (5.746)		.258 (7.183)
$\tau_{WITHIN,112}$					**-.330** (11.809)		-.337 (12.004)
Effects between modular systems (H6)							
$\theta_{MOD,1}$						**.230** (1.359)	.196 (.941)
$\theta_{MOD,2}$						**.681** (6.866)	.701 (7.034)
$\theta_{MOD,12}$						**.117** (0.086)	-.089 (.045)
$\theta_{ACR,MOD,1,2}$						**-.749** (3.003)	-.687 (2.283)
N. Params.	14	16	19	23	25	23	29
G_{PL}^2	2451.659	2021.192	1984.473	1955.779	1944.521	1974.203	1934.936

Wald$_{PL}$ statistics are shown between parentheses. For approximate statistical inference we compare Wald$_{PL}$ against χ^2.
Hence, $p < 0.1$ if Wald$_{PL} > 2.706$

Models 3, 4 and 6 also include lower order parameters $\sigma_{I,12}$ and $\sigma_{O,12}$. For models 4 and 6, we define *WITHIN$_{ij}$* to capture whether tie *ij* is within boundaries.

Appendix D. **Threats to Validity**

Although we have carefully studied the significance of some effects to explain the mismatches between design interfaces and team interactions, we have not included all potentially contributing factors. Of particular concern would be omitted factors that correlate with one or more of the independent variables included in our statistical models. We briefly discuss here the possible impact of two such effects: team interactions with system integration teams and design interface carry-over.

We expect the effects of interactions with system integration teams (i.e., the last six teams in the team interaction matrix) to be insignificant because these teams interact with almost every other team in the organization. We found no significant evidence of indirect team interactions through system integration teams (Sosa 2000). This is consistent with our results which suggest that design teams tend to use indirect interactions to exchange technical information only within group boundaries.

In cases of incremental innovation such as with derivative products, many design interfaces may not change from one generation of a product to the next. This "carry-over effect" could result in unaddressed design interfaces as long as the current organization "remembers" the state of those unchanged interfaces and needs no interaction to verify them. During follow-up data collection with the high-pressure turbine and low-pressure turbine design teams, we found that some unchanged design interfaces were still addressed by team interactions due to the high level of criticality of the interface and/or the presence of new design participants (Sosa 2000). Although we believe it an important factor to consider when planning team interactions, we do not expect carry-over effects to significantly impact the significance of effects studied in this paper.