High-dimensional Adaptive Minimax Sparse Estimation with Interactions

Chenglong Ye, Yuhong Yang

School of Statistics
University of Minnesota
313 Ford Hall, 224 Church St SE
Minneapolis, MN 55455, USA
e-mail: yexxx323@umn.com; yangx374@umn.edu

Abstract: High-dimensional linear regression with interaction effects is broadly applied in research fields such as bioinformatics and social science. In this paper, we first investigate the minimax rate of convergence for regression estimation in high-dimensional sparse linear models with two-way interactions. We derive matching upper and lower bounds under three types of heredity conditions: strong heredity, weak heredity and no heredity. From the results: (i) A stronger heredity condition may or may not drastically improve the minimax rate of convergence. In fact, in some situations, the minimax rates of convergence are the same under all three heredity conditions; (ii) The minimax rate of convergence is determined by the maximum of the total price of estimating the main effects and that of estimating the interaction effects, which goes beyond purely comparing the order of the number of non-zero main effects $r_1$ and non-zero interaction effects $r_2$; (iii) Under any of the three heredity conditions, the estimation of the interaction terms may be the dominant part in determining the rate of convergence for two different reasons: 1) there exist more interaction terms than main effect terms or 2) a large ambient dimension makes it more challenging to estimate even a small number of interaction terms. Second, we construct an adaptive estimator that achieves the minimax rate of convergence regardless of the true heredity condition and the sparsity indices $r_1, r_2$.

MSC 2010 subject classifications: Primary 62C20; secondary 62J05.
Keywords and phrases: Minimax rate of convergence, sparsity, high-dimensional regression, quadratic model, interaction selection, heredity condition, hierarchical structure, adaptive estimation.

1. Introduction

High-dimensional data are increasingly prevalent in various areas such as bioinformatics, astronomy, climate science and social science. When the number of variables $p$ is larger than the sample size $n$ in the linear regression setting, statistical estimation of the regression function often requires some crucial conditions. One common condition is the sparsity of the data generating model, under which only a small portion of the variables are important to affect the response variable. Under this condition, both sparse estimation of high-dimensional linear regression functions and variable selection have been well studied with fruitful theoretical understandings in the recent decade. Minimax estimation of the regression function with main effects only are well investigated under $l_q$-
sparsity constraints with $0 \leq q \leq 1$ (e.g., van de Geer 2007, Candes & Tao 2007, Bunea et al. 2007, Zhang & Huang 2008, van de Geer 2008, van de Geer & Bhlmann 2009, Bickel et al. 2009, Zhang 2010a, Knight & Fu 2000, Raskutti et al. 2011, Rigollet & Tsybakov 2011, Wang et al. 2014); model selection consistency results are also obtained for various model selection procedures (e.g., Fan & Li 2001, Zhao & Yu 2006, Zhang & Huang 2008, Zou & Yuan 2008, Lv & Fan 2009).

However, models with only main effects are often not adequate to fully capture the nature of the data. Interaction terms may be necessary to not only improve the prediction performance but also enhance the understanding of the relationships among the variables, especially in areas such as genetics, medicine and behavioristics, where interaction effects between the covariates are of enormous interest. Hierarchical constraints are often imposed to describe the underlying structure of models with interaction effects, such as the marginality principle (Nelder 1977), the effect heredity principle (Hamada & Wu 1992) and the “well-formulated models” (Peixoto 1987). We follow a popular naming convention of heredity conditions as adopted in Chipman (1996): strong heredity and weak heredity. Strong heredity assumes that if an interaction term is in the model, then both of its corresponding main effects should also be included, while weak heredity only requires that at least one of its main effects should be included. In practice, it is possible that, compared to the interaction terms, some main effects are so small that including them in modeling may not be beneficial from the perspective of estimation variability. Thus, in this work we take into consideration the additional case where no heredity condition is imposed at all, also for the purpose of theoretical comparison with the other two heredity conditions.

Many approaches are proposed for interaction selection, most of which can be categorized into two types: joint selection and stage-wise selection. The joint selection approach selects the main and interaction terms simultaneously by searching over all possible models with interactions. A typical way of joint selection is to use regularization methods with specially designed penalty terms. For example, Yuan et al. (2009) introduced a family of shrinkage estimators, which incorporate the hierarchical structures through linear equality constraints on the coefficients and possess both selection consistency and root-$n$ estimation consistency under fixed $p$. Choi et al. (2010) re-parameterized the regression model with interactions and applied an adaptive $L_1$-norm penalty. The estimators have the oracle property (Fan & Li 2001) when $p = o(n^{1/10})$. Hao et al. (2017) proposed a computationally efficient regularization algorithm under marginality principle (RAMP) that simultaneously selects the main effects, interaction effects and quadratic effects for high-dimensional data $p \gg n$. They also verified the interaction selection consistency property of the two-stage LASSO under some sensible conditions. The stage-wise selection procedure first performs a main effect selection (by excluding the interaction terms) to reduce the dimension of variables and then carries out a joint selection on the reduced dimension of variables, which is computationally feasible and effective. For example, viewing the sliced inverse regression (Li 1991) from a likelihood perspective, Jiang & Liu (2014) suggested a stage-wise variable selection algorithm (SIRI)
via inverse regression, which is able to detect higher order interactions without imposing any hierarchical structures. Hao & Zhang (2014) proposed two stage-wise interaction selection procedures, IFORT and IFORM, both of which enjoy sure screening property in the first stage. Fan et al. (2016) proposed a method, named the interaction pursuit, that incorporates both screening and variable selection in ultra-high dimensions. The method possesses both the sure screening property and the oracle property in the two stages respectively. For some other works on interaction selection, see Zhao et al. 2009, Li et al. 2012, Bien et al. 2013, Hall & Xue 2014. While having the aforementioned good properties, both types of interaction selection approaches have their own disadvantages as well. The joint selection is usually computational infeasible (insufficient storage) when $p$ is large; the stage-wise selection, as pointed out in Hao & Zhang (2014), may be very difficult to be theoretically justified under general conditions.

Although there have been many novel developments on selection of interaction terms as described above, little work has been done on the estimation of the regression function when interactions exist. In this paper, we present some theoretical results on the minimax rate of convergence for estimating the high-dimensional regression function with interaction terms under three different hierarchical structures. Regardless of the heredity condition, our results show that the minimax rate is determined by the maximum of the total estimation price of the main effects and that of the interaction effects. Heredity conditions enter the minimax rate of convergence in terms of the estimation price of the interaction effects, namely $r_2(1 + \log(K/r_2))/n$, where $r_2$ is the number of non-zero interaction effects and $K$ is the number of eligible candidate interaction terms under the different heredity conditions. Consequently, a stronger heredity condition leads to possibly faster minimax rate of convergence. For example, when the underlying model has no more than $r_1$ non-zero main effects, at most $K = \binom{r_1}{2}$ interaction terms are allowed to enter the model under strong heredity, compared to $K = r_1(p_n - (r_1 + 1)/2)$ under weak heredity. As will be seen, only in certain situations is the minimax rate improved by imposing the strong heredity, although strong heredity allows fewer eligible interaction terms than the other two heredity conditions. Also, from the perspective of estimation, there may be no difference in rate of convergence between weak heredity and no heredity in many situations. Our results provide a complete characterization and comparison of the minimax rates of convergence under the three heredity conditions.

In real applications, since one does not know the true heredity condition behind the data (or practically the best heredity condition to describe the data at the given sample size), it is desirable to construct an estimator that performs optimally no matter which of the three heredity conditions holds. Such an estimator that adapts to the true heredity condition as well as the unknown number of main and interaction effects will be obtained in this paper.

The remainder of the paper is organized as follows. In Section 2, we introduce the model setup, the loss function and the heredity conditions for the problem. In Section 3, after stating the required assumption, we present our main results of the minimax rate of convergence under strong heredity. The theoretical results
under weak heredity and no heredity are presented in Section 4. Section 5.1 provides detailed rates of convergence under different heredity conditions in relation to the sparsity indices, the ambient dimension and the sample size, followed by Section 5.2 where we present some interesting implications of the detailed results. In Section 6, we extend our results to quadratic models in which both quadratic and interaction effects are considered. In Section 7, we construct an adaptive estimator that achieves the minimax rate of convergence without knowledge of the type of the heredity condition or the sparsity indices ($r_1$ and $r_2$). The proofs of our results and some technical tools are presented in the Appendix.

2. Preliminaries

Model Setup Suppose the dataset is composed of $(X,Y)$, where $X = (x_1, ..., x_p)$ is a $n \times p$ matrix with $n$ observations on $p$ covariates and $Y = (y_1, ..., y_n)^T$ is the response vector. We start by considering a linear regression model with both main effects and two-way interaction effects:

$$Y = Z\beta + \epsilon,$$

where $\beta = ((\beta^{(1)})^T, (\beta^{(2)})^T)^T$ is the overall coefficient vector, $Z = (X_{(XX)}) \in \mathbb{R}^{n \times (p^2+p)}$ is the full design matrix, and the random noise vector $\epsilon \sim N(0, \sigma^2 I_n)$ with known $\sigma$. More specifically, $\beta^{(1)} \in \mathbb{R}^p$ and $\beta^{(2)} \in \mathbb{R}^\binom{p}{2}$ are the coefficients of the main effects and the two-way interaction effects respectively. Here we define $[XX] = (x_1 \otimes x_2, ..., x_1 \otimes x_p, ..., x_{p-1} \otimes x_p)^T$ as the $n \times \binom{p}{2}$ matrix that contains all the two-way interaction terms, where $\otimes$ denotes the point-wise product of two vectors.

In this paper, our focus is on the fixed design, i.e., the covariates are considered given. Our goal is to estimate the mean regression function by a linear combination of the covariates and interaction terms.

Loss Function Denote $h(\cdot) : \mathbb{R}^{(p^2+p)/2} \rightarrow \mathbb{R}$ as the mean regression function, i.e., $h(z) = z^T \beta$ for $z \in \mathbb{R}^{(p^2+p)/2}$. Denote $\hat{h}(z) = z^T \hat{\beta}$ as an estimated function of $h(z)$. In our fixed design setting, we focus on the prediction loss (or the Averaged Squared Error) $L(h, \hat{h}) := \frac{1}{n}\|Z\beta - Z\hat{\beta}\|^2_2$, where $\|\cdot\|_2$ is the Euclidean norm. Set the index sets for the main effects and the interaction effects as $I_{\text{main}} = \{1, ..., p\}$ and $I_{\text{int}} = \{(i, j) : 1 \leq i < j \leq p\}$ respectively.

Let $I = (I_1, I_2) \subset I_{\text{main}} \otimes I_{\text{int}}$ (\otimes is the Cartesian product) be the index set of a model with $|I_1|$ non-zero main effects and $|I_2|$ non-zero interaction effects. In this paper, we consider the data generating model (2.1) with at least two main effects and one interaction effect purely for convenience, which does not affect the conclusions. Let $Z_I$ be the $n \times |I|$ submatrix of $Z$ that corresponds to the model index $I$. Its corresponding least squares estimator $P_I Y$ is used to estimate $Z \beta$, where $P_I$ is the projection matrix onto the column space of $Z_I$. The loss function of using model $I$ is denoted as $L(I) := \frac{1}{n}\|P_I Y - Z \beta\|^2_2$. 
Heredity Conditions  Denote the space of all the $p + \binom{p}{2}$-dimensional vectors with a hierarchical notation of the subscripts as
\[ \mathbb{R}_p^p = \{ \beta \in \mathbb{R}^p | \beta = (\beta_1, ..., \beta_p, \beta_{1,2}, ..., \beta_{p-1,p}) \}. \]
We refer to $\beta^{(1)} = (\beta_1, ..., \beta_p)$ as the subvector consisting of the first $p$ elements in $\beta$, and $\beta^{(2)} = (\beta_{1,2}, ..., \beta_{p-1,p})$ as the subvector containing the rest of the elements. We introduce the following two vector spaces:
\[ \mathbb{R}^p_{\text{weak}} = \{ \beta \in \mathbb{R}^p | 1_{\beta_{i,j} \neq 0} \leq 1_{\beta_i \neq 0} \vee 1_{\beta_j \neq 0}, 1 \leq i < j \leq p \} \]
and
\[ \mathbb{R}^p_{\text{strong}} = \{ \beta \in \mathbb{R}^p | 1_{\beta_{i,j} \neq 0} \leq 1_{\beta_i \neq 0} \wedge 1_{\beta_j \neq 0}, 1 \leq i < j \leq p \}. \]
The space $\mathbb{R}^p_{\text{strong}}$ captures the strong heredity condition that if the interaction term is in the model, then both of its corresponding main effects should also be included. The space $\mathbb{R}^p_{\text{weak}}$ characterizes the weak heredity condition that if the interaction is in the model, then at least one of its main effects should be included. As pointed out in Hao & Zhang (2016), the sign of the main effect coefficients are not invariant of linear transformation of the covariates individually due to the existence of the interaction terms. Heredity conditions are consequently meaningless without the specification of the model parametrization.
In our paper, we stick to the parameterization $Z$ and include the no heredity condition by considering the vector space $\mathbb{R}^p$. Define the $l_0$-norm of a vector $a = (a_1, ..., a_p)$ as the number of its non-zero elements, i.e., $\|a\|_0 = \sum_{i=1}^p 1_{a_i \neq 0}$.
For a vector space $S \in \{ \mathbb{R}^p_{\text{strong}}, \mathbb{R}^p_{\text{weak}}, \mathbb{R}^p \}$, define the corresponding $l_0$-ball and $l_0$-hull of $S$ as
\[ B_0(r_1, r_2; S) = \{ \beta = (\beta^{(1)}, \beta^{(2)}) \in S, \left\| \beta^{(1)} \right\|_0 \leq r_1, \left\| \beta^{(2)} \right\|_0 \leq r_2 \} \]
and
\[ F_0(r_1, r_2; S) = \{ h : h(x) = x^T \beta, \beta \in B_0(r_1, r_2; S) \} \]
respectively. Note that $B_0(r_1, r_2; S)$ represents the collection of coefficients $\beta$ with at most $r_1$ non-zero main effects and $r_2$ non-zero interaction effects under a certain hierarchical constraint $S$. And $F_0(r_1, r_2; S)$ denotes the collection of linear combinations of the covariates with coefficients $\beta \in B_0(r_1, r_2; S)$.
Throughout this paper, we assume that $r_1 + r_2 \leq n$ (otherwise the minimax risk may not converge or the rate may not be optimal), $r_1 \geq 2$ and $r_2 \geq 1$.

Minimax Risk  It is helpful to consider the uniform performance of a modeling procedure when we have plentiful choices of modeling procedures during the analysis of a statistical problem. The minimax framework seeks an estimator that minimizes the worst performance (in statistical risk) assuming that the truth belongs to a function class $\mathcal{W}$. The minimax risk we consider is
\[ \min_{\hat{h}} \max_{h \in \mathcal{W}} EL(\hat{h}, h), \]
where \( \hat{h} \) is over all estimators, and min and max may refer to \( \inf \) and \( \sup \), more formally speaking. In our work, we assume that the true mean regression function has a hierarchical structure by imposing \( W = F_0(r_1, r_2; S) \), with \( S \in \{ \mathbb{R}_{\text{strong}}, \mathbb{R}_{\text{weak}} \} \).

In this paper, we will use the notation \( b_n \succeq a_n \) or \( a_n \preceq b_n \) to represent \( a_n = O(b_n) \). If both \( b_n \succeq a_n \) and \( a_n \preceq b_n \) hold, we denote \( a_n \asymp b_n \) to indicate that \( a_n \) and \( b_n \) are of the same order. If \( a_n \succeq b_n \) holds without \( a_n \asymp b_n \), we use the notation \( a_n \succ b_n \) or \( b_n \prec a_n \).

3. Minimax Rate of Convergence under Strong Heredity

3.1. Assumption

We start by stating an assumption required for our result of the minimax rate of convergence under strong heredity. In this paper, we use \( p_n \) to indicate that the number of main effects \( p \) can go to infinity as \( n \) increases. We also allow \( r_1 \) and \( r_2 \) to increase with the sample size \( n \) as well.

Sparse Reisz Condition (SRC) For some \( l_1, l_2 > 0 \), there exist constants \( b_1, b_2 > 0 \) (not depending on \( n \)) such that for any \( \beta = (\beta^{(1)}, \beta^{(2)}) \) with \( \|\beta^{(1)}\|_0 \leq \min(2l_1, p_n) \) and \( \|\beta^{(2)}\|_0 \leq \min(2l_2, (p_n)^2) \), we have

\[
 b_1 \|\beta\|_2 \leq \frac{1}{\sqrt{n}} \|Z\beta\|_2 \leq b_2 \|\beta\|_2. \tag{3.1}
\]

The SRC assumption requires that the eigenvalues of \( Z^T Z \) for any sparse submatrix \( Z_I \) of \( Z \) are bounded above and away from 0. It was first proposed by Zhang & Huang (2008). It is similar to the sparse eigenvalue conditions in Zhang (2010b), Raskutti et al. (2011), quasi-isometry condition in Rigollet & Tsybakov (2011); it is also related to the more stringent restricted isometry property (which requires the constants \( b_1, b_2 \) are close to 1) in Candes & Tao (2007). Such assumptions are standard in the \( l_1 \)-regularization analysis like LASSO and the Dantzig selector. See Bickel et al. (2009), Meinshausen & Yu (2009), van de Geer (2007), Koltchinskii (2009) for more references.

3.2. Minimax Rate

Now we present our main result of the minimax rate of convergence under strong heredity. A simple estimator is enough for an effective minimax upper bound. Let \( \hat{I} = \arg\min_{I \in \mathcal{I}^{\text{strong}}_{r_1, r_2}} \sum_{i=1}^n (Y_i - \tilde{Y}_I^i)^2 \) be the model that minimizes the residual sum of squares over all the models that have exactly \( r_1 \) non-zero main effects and \( r_2 \) non-zero interaction effects under strong heredity, denoted as \( \mathcal{I}^{\text{strong}}_{r_1, r_2} \), where \( \tilde{Y}_I^1 = P_I Y \) is the projection of \( Y \) onto the column space of
the design matrix $Z_1$. For lower bounding the minimax risk, the information- theoretical tool of using Fano’s inequality with metric entropy understanding (Yang & Barron 1999) plays an important role in the proof.

**Theorem 3.1.** Under the Sparse Reisz Condition with $l_1 = r_1 \leq p_n \land n$, $l_2 = r_2 \leq \binom{r_1}{2} \land n$ and the strong heredity condition $W = F_0(r_1, r_2; \mathbb{R}_{strong}^p)$, the minimax risk is upper bounded by

$$\min_{h} \max_{\hat{h} \in W} EL(\hat{h}, h) \leq \sup_{\hat{h} \in W} E(\mathcal{L}(\hat{h})) \leq \frac{c\sigma^2}{n} \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right),$$

where $c$ is a pure constant; the minimax risk is lower bounded by

$$\min_{h} \max_{\hat{h} \in W} EL(\hat{h}, h) \geq c_1 \frac{\sigma^2}{n} \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) \lor r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right)$$

for some positive constant $c_1$ that only depends on the constants $b_1$ and $b_2$ in the SRC assumption.

From the theorem, under the SRC and the strong heredity condition, the minimax rate of convergence scales as: $\min_{h} \max_{\hat{h} \in W} EL(\hat{h}, h) \asymp \frac{\sigma^2}{n} (r_1 (1 + \log \frac{p_n}{r_1}) \lor r_2 (1 + \log (\binom{r_1}{2}/r_2)))$.

**Remark 1.** The term $r_1 (1 + \log (p_n/r_1))/n = \frac{r_1}{n} + \frac{p_n}{n} \log (p_n/r_1)$ reflects two aspects in the estimation of the main effects: the price of searching among $\binom{p_n}{r_1}$ possible models, which is of order $r_1 \log (p_n/r_1)/n$, and the price of estimating the $r_1$ main effect coefficients after the search. Thus $r_1 (1 + \log (p_n/r_1))/n$ is the total price of estimating the main effects. Similarly, $r_2 (1 + \log (\binom{r_1}{2}/r_2))/n$ is the total price of estimating the interaction effects.

**Remark 2.** Our result of the upper bound is general and does not require the sparsity condition of $r_1 \prec p_n$, although it may be needed for fast rate of convergence.

4. Minimax Rate of Convergence under Weak Heredity and No Heredity

Similar results are obtained under weak heredity and no heredity. The minimax rate of convergence is still determined by the maximum of the total price of estimating the main effects and that of the interaction effects. When the heredity condition changes, the total price of estimating the interaction effects may differ, possibly substantially.

**Theorem 4.1.** Under the Sparse Reisz Condition with $l_1 = r_1 \leq p_n \land n$, $l_2 = r_2 \leq (r_1 p_n) \land n$ and the weak heredity condition $W = F_0(r_1, r_2; \mathbb{R}_{weak}^p)$, the minimax risk is of order

$$\min_{h} \max_{\hat{h} \in W} EL(\hat{h}, h) \asymp \frac{\sigma^2}{n} \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) \lor r_2 \left( 1 + \log \frac{r_1 \cdot p_n}{r_2} \right) \right).$$  (4.1)
Theorem 4.2. Under the Sparse Reisz Condition with $l_1 = r_1 \leq p_n \land n$, $l_2 = r_2 \leq \left(\frac{p_n}{r_1}\right) \land n$ and the no heredity condition $W = \mathcal{F}_0(r_1, r_2; \mathbb{R}^p)$, the minimax risk is of order
\[
\min_{\hat{h}} \max_{h \in W} \text{EL}(\hat{h}, h) \preceq \frac{\sigma^2}{n} \left( r_1 \left(1 + \log \frac{p_n}{r_1}\right) \lor r_2 \left(1 + \log \frac{p_n}{r_2}\right) \right). \tag{4.2}
\]

5. Comparisons and Insights

In this section, we summarize the consequences of our main results in three scenarios for an integrated understanding. For brevity, we introduce the following notation. For $a, b \in \mathbb{N}^+$ and $a \geq b$, define the quantity
\[
\xi_{ab} := \frac{b}{1 + \log \left( \frac{a}{b} \right)}.
\]
The total price of estimating the main effects and the interaction effects are then denoted as $\sigma^2 n \xi_{p_n r_1}$ and $\sigma^2 n \xi_{K r_2}$ respectively, where $K$ depends on $p_n, r_1$ and the heredity condition. We also use the notation $K_S$ (7.5) to indicate that $K$ depends on the heredity condition $S$. Let
\[
\mathcal{M}(S) := \min_{\hat{h}} \max_{h \in \mathcal{F}_0(r_1, r_2; S)} \text{EL}(\hat{h}, h)
\]
denote the minimax risk under the heredity condition $S$.

5.1. Detailed Rates of Convergence

Since the minimax rate of convergence depends on the maximum of $\xi_{p_n r_1}$ and $\xi_{K r_2}$, we discuss the cases where one of the two quantities is greater than the other.

Scenario 1: $r_2 \preceq r_1$

When there are more main effects than interaction effects in the sense that $r_2 \preceq r_1$, the minimax rate of convergence is not affected by the heredity conditions. When $\log\left(\frac{p_n}{r_1}\right) \preceq \log r_1$, we always have $\xi_{p_n r_1} \geq \xi_{K r_2}$ regardless of the heredity conditions. When $\log\left(\frac{p_n}{r_1}\right) \prec \log r_1$, it depends on the order of $r_2$ to further decide which estimation price is larger. When $\log\left(\frac{p_n}{r_1}\right) \prec \log r_1$, let $r_*$ be such that $\xi_{p_n r_1} \prec \xi_{K r_*}$. If $r_* \preceq r_2$, we have $\xi_{p_n r_1} \geq \xi_{r_2}$; otherwise $\xi_{p_n r_1} \prec \xi_{K r_2}$.

In summary, given that $r_2 \preceq r_1$, the minimax risk is of order
\[
\mathcal{M}(S) \preceq \begin{cases} \frac{\sigma^2}{n} \xi_{p_n r_1}^2, & \text{if } r_* \preceq r_2 \preceq r_1 \text{ and } \log \frac{p_n}{r_1} \prec \log r_1, \\ \frac{\sigma^2}{n} \xi_{K r_*}^2, & \text{otherwise,} \end{cases}
\]
for $S \in \left\{ \mathbb{R}^p_{\text{strong}}, \mathbb{R}^p_{\text{weak}}, \mathbb{R}^p \right\}$.

Remark 3. This scenario also includes the special case when $p_n = O(1)$, where we must have $r_1 = O(1)$ and $r_2 = O(1)$. The minimax rate of convergence is of the standard parametric order $1/n$ regardless of the heredity conditions.
Scenario 2: \( r_1 \leq r_2 \) and \( \log p_n \leq r_1 \) When there exist more interaction terms, i.e., \( r_1 \leq r_2 \), under weak or no heredity, the quantity \( \xi_{r_2}^n \) is always no less than (in order) \( \xi_{r_1}^n \).

For strong heredity, we discuss case by case. When \( \log(p_n/r_1) < \log r_1 \), we always have \( \xi_{r_1}^n \leq \xi_{r_2}^n \). When \( \log(p_n/r_1) \geq \log r_1 \), it depends on the order of \( r_2 \) to decide which estimation price is larger in terms of order. When \( \log(p_n/r_1) \geq \log r_1 \), let \( r'_2 \) be such that \( \xi_{r_1}^n \leq \xi_{r'_2}^n \). If \( r_2 \geq r'_2 \), we have \( \xi_{r_1}^n \leq \xi_{r_2}^n \); otherwise \( \xi_{r_1}^n > \xi_{r_2}^n \). In summary, given that \( r_1 \leq r_2 \) and \( \log p_n \leq r_1 \), the minimax risk is of order

\[
\mathcal{M}(\hat{\beta}_{\text{strong}, r_n}) \approx \begin{cases} 
\frac{\sigma^2}{n} \xi_{r_1}^n, & \text{if } r_1 \leq r_2 \leq r'_2 \text{ and } \log p_n \geq \log r_1, \\
\frac{\sigma^2}{n} \xi_{(r_2 \wedge r_1)}^n, & \text{otherwise},
\end{cases}
\]

\[
\mathcal{M}(\hat{\beta}_{\text{weak}, r_n}) \approx \frac{\sigma^2}{n} \xi_{(r_2 \wedge r_1, r_n)}^n,
\]

\[
\mathcal{M}(\hat{\beta}_{r_n}) \approx \frac{\sigma^2}{n} \xi_{r_2}^n.
\]

Remark 4. The term \( \xi_{(r_2 \wedge K)}^n \), deals with the case where \( r_2 \) is inactive in the sense that \( r_2 \) exceeds \( K \) under the specific heredity condition. For example, with \( r_2 \geq \left( \frac{r_1}{2} \right) \), the upper bound \( r_2 \) in (2.2) does not provide any new information of the number of non-zero interaction effects for strong heredity. Thus the \( l_0 \)-ball \( B_0(r_1, r_2; \hat{\beta}_{\text{strong}, r_n}) \) is automatically reduced to a subset \( B_0(r_1, \left( \frac{r_1}{2} \right); \hat{\beta}_{\text{strong}, r_n}) \).

Scenario 3: \( r_1 \leq r_2 \) and \( \log p_n \geq r_1 \) When the number of the main effects \( p_n \) is at least exponentially as many as the non-zero main effects in the sense that \( \log p_n \geq r_1 \), \( \xi_{r_1}^n \) is always no less than \( \xi_{r_2}^n \) in terms of order. In fact, in this scenario, the results of the minimax rates under weak or no heredity are exactly the same as those in Scenario 2. For completeness, we still present the results. Specifically, the minimax risk is of order

\[
\mathcal{M}(\hat{\beta}_{\text{strong}, r_n}) \approx \frac{\sigma^2}{n} \xi_{r_1}^n,
\]

\[
\mathcal{M}(\hat{\beta}_{\text{weak}, r_n}) \approx \frac{\sigma^2}{n} \xi_{(r_2 \wedge r_1, r_n)}^n,
\]

\[
\mathcal{M}(\hat{\beta}_{r_n}) \approx \frac{\sigma^2}{n} \xi_{r_2}^n.
\]

5.2. Interesting Implications

1. Comparing the results for weak heredity and no heredity, we may or may not have distinct rates of convergence. When there exists a small constant \( c > 0 \) such that \( \log r_2 \leq (1 - c) \cdot \log (r_1 p_n) \) for large enough \( n \), there is
no difference between weak heredity and no heredity from the perspective of rate of convergence in estimation. It still remains an open question how they are different for the problem of model identification. Without the above relationship between \( r_1 \) and \( r_2 \), there is no guarantee that the rates of convergence are the same under weak heredity and no heredity. For example, when \( r_2 = r_1 p_n / \log r_1 \), if in addition we have \( r_1 = p_n \leq n^{1/2} \), the minimax rates are the same under weak and no heredity, at \( \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \asymp \mathcal{M}(\mathbb{R}^n_{\text{strong}}) \asymp r_1 p_n \log \log r_1 / (n \log r_1) \). In contrast, if instead we have \( r_1 = \sqrt{p_n} \), then the minimax rates are different, with \( \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \asymp r_1 p_n \log \log r_1 / (n \log r_1) \) and \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) \asymp r_1 p_n \).

2. Heredity conditions do not affect the rates of convergence in some situations. For example, when there exist more main effects than interaction effects (Scenario 1), the minimax rates of convergence are the same under all three heredity conditions.

3. From the detailed rates of convergence, under any of the three heredity conditions, the estimation of the interaction terms \( \xi_{r_2} / n \) may become the dominating part. There are two different reasons why the price of estimating the interaction terms becomes higher than that for the main effect terms. One is that the number of interaction terms is more than that of the main effect terms. The other reason is that although the main effect terms outnumber the interaction terms, the ambient dimension is so large that even estimating a small number of the interaction terms is more challenging than estimating the main effects.

4. How much can the rate of convergence be improved by imposing strong heredity? We quantify this improvement by taking the ratio of two minimax rates of convergence given the ambient dimension \( p_n \), i.e., \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \) and \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \). In Scenario 2 (\( r_1 \leq r_2 \) and \( \log p_n \leq r_1 \)), we have \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \geq \log p_n / p_n \), where the maximal improvement happens when \( r_1 \approx \log p_n \) and \( r_2 \approx r_1 p_n \). That is, the minimax rate of convergence under strong heredity is up to \( \log p_n / p_n \) times faster than that under weak heredity. Similarly we have \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \geq \log^2 p_n / p_n^2 \), where the maximal improvement \( \log^2 p_n / p_n^2 \) happens at \( r_1 \approx \log p_n \) and \( r_2 \approx p_n^2 \).

5. In Scenario 3 (\( r_1 \leq r_2 \) and \( \log p_n \geq r_1 \)), the improvement \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \geq \log p_n / p_n \), where the maximal improvement happens when \( r_2 \geq r_1 p_n \). In this scenario, the maximal improvement of the minimax rate from weak heredity to strong heredity depends on the ambient dimension \( p_n \). In other words, the larger the ambient dimension is, the more improvement of minimax rate of convergence we have from weak heredity to strong heredity. Similarly we have \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \geq \log p_n / p_n^2 \), where the equality holds if \( r_1 = O(1) \) and \( r_2 \approx p_n^2 \).

6. If \( r_3 \) is active for all three heredity conditions, i.e., \( r_2 \leq \left( \frac{r_3}{2} \right) \), the maximal improvement of minimax rate from weak/no heredity to strong heredity turns out to be consistent. That is, \( \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \asymp \mathcal{M}(\mathbb{R}^n_{\text{strong}}) / \mathcal{M}(\mathbb{R}^n_{\text{weak}}) \geq 1 / \log p_n \), where the maximal improvement hap-
pens at \( r_1 \asymp \log p_n \) and \( r_2 \asymp r_1^2 \).

6. Extension to Quadratic Models

Our aforementioned results do not consider quadratic effects. When both quadratic and two-way interaction effects are included in a model (called a quadratic model), it is easy to see the rates of convergence in the theorems still apply under both strong heredity and weak heredity. However, in the case of no heredity, the number of quadratic terms enters into the minimax rate. Assume one model has at most \( r_3 \) extra non-zero quadratic terms. We need the following assumption.

**Sparse Reisz Condition 2 (SRC2)** For some \( l_1, l_2, l_3 > 0 \), there exist constants \( b_1, b_2 > 0 \) (not depending on \( n \)) such that for any \( \beta = (\beta^{(1)}, \beta^{(2)}, \beta^{(3)}) \) with \( \|\beta^{(1)}\|_0 \leq \min(2l_1, p_n) \), \( \|\beta^{(2)}\|_0 \leq \min(2l_2, (p_n/2)) \) and \( \|\beta^{(3)}\|_0 \leq \min(2l_3, p_n) \), we have

\[
\frac{b_1}{\sqrt{n}} \|Z^* \beta\|_2 \leq b_2 \|\beta\|_2,
\]

where \( Z^* = (X, [XX], X^2) \) is the new design matrix, with \( X^2 \) representing the \( n \times p \) matrix that contains all the quadratic terms.

Next we state the minimax results for quadratic models. Strong heredity and weak heredity are exactly the same condition since a quadratic term has only one corresponding main effect term. That is, both strong and weak heredity require that if a quadratic term \( X_2^1 \) has a non-zero coefficient, then \( X_1 \) must also have a non-zero coefficient. Similarly, under SRC2 with \( l_1 = r_1, l_2 = r_2, l_3 = r_3 \), the minimax rate of convergence under strong/weak heredity for the quadratic model stays the order

\[
\frac{\sigma^2}{n} r_1 (1 + \log \frac{p_n}{r_1}) \vee r_2 (1 + \log \frac{r_1}{r_2}); \quad (6.1)
\]

under no heredity, its order becomes

\[
\frac{\sigma^2}{n} \bar{r} (1 + \log \frac{p_n}{r}) \vee r_2 (1 + \log \frac{p_n}{r_2}), \quad (6.2)
\]

where \( \bar{r} = r_1 \vee r_3 \).

7. Adaptation to Heredity Conditions and Sparsity Indices

In the previous sections, we have determined the minimax rates of convergence for estimating the linear regression function with interactions under different sizes of sparsity indices \( r_1, r_2 \) and heredity conditions \( S \). These results assume
that \( r_1, r_2 \) and \( S \) are known. However, in practice, we usually have no prior information about the underlying heredity condition nor the sparsity constraints. Thus it is necessary and appealing to build an estimator that adaptively achieves the minimax rate of convergence without the knowledge of \( S, r_1 \) and \( r_2 \). We construct such an adaptive estimator as below.

To achieve our goal, we consider one specific model and three types of models together as the candidate models:

\[
\hat{F} = \{ I_{p_n, (p_n^2 - p_n)/2} \} \cup \{ I_{k_1, k_2}^{\text{strong}} \} \cup \{ I_{k_1, k_2}^{\text{weak}} \} \cup \{ I_{k_1, k_2}^{\text{no}} \},
\]

where \( I_{p_n, (p_n^2 - p_n)/2} \) denotes the full model with \( p_n \) main effects and all the \((p_n^2)\) interaction effects. It is included so that the risk of our estimator will not be worse than order \( R_Z/n \), in which \( R_Z \) is the rank of the full design matrix. With a slight abuse of the notation, we use \( I_{k_1, k_2}^{\text{strong}}, I_{k_1, k_2}^{\text{weak}} \) and \( I_{k_1, k_2}^{\text{no}} \) to represent a model with \( k_1 \) main effects and \( k_2 \) interaction effects under strong heredity, weak heredity and no heredity respectively. Note that some models appear more than once in \( \hat{F} \), which does not cause any problem for the goal of estimating the regression function. The details of the range of \( k_1 \) and \( k_2 \) for each model class are shown in (7.2), (7.3) and (7.4).

To choose a model from the candidate set, we apply the ABC criterion in Yang (1999). For a model \( \mathcal{I} \) in \( \hat{F} \), the criterion value is

\[
ABC(\mathcal{I}) = \sum_{i=1}^{n} (Y_i - \hat{Y}_i^\mathcal{I})^2 + 2r_1\sigma^2 + \lambda \sigma^2 C_1,
\]

where \( \hat{Y}_i^\mathcal{I} = P_1 Y \) is the projection of \( Y \) onto the column space of the design matrix \( Z \) with rank \( r_1 \), \( C_1 \) is the descriptive complexity of model \( \mathcal{I} \) and \( \lambda > 0 \) is a constant. The model descriptive complexity satisfies \( C_1 > 0 \) and \( \sum_{\mathcal{I} \in \hat{F}} \exp(-C_1) \leq 1 \).

The model descriptive complexity is crucial in building the adaptive model. Let \( \pi_0, \pi_1, \pi_2, \pi_3 \in (0, 1) \) be four constants such that \( \pi_0 + \pi_1 + \pi_2 + \pi_3 = 1 \). Set \( C_{I_{p_n, (p_n^2 - p_n)/2}} = -\log \pi_0 \) for the full model,

\[
C_{I_{k_1, k_2}^{\text{strong}}} = -\log \pi_1 + \log(p_n \wedge n) + \log \binom{k_1}{2} + \log \binom{p_n}{k_1} + \log \binom{k_2}{2},
\]

for \( 1 \leq k_1 \leq p_n \wedge n \) and \( 0 \leq k_2 \leq \binom{k_1}{2} \wedge n \),

\[
C_{I_{k_1, k_2}^{\text{weak}}} = -\log \pi_2 + \log(p_n \wedge n) + \log(K \wedge n) + \log \binom{p_n}{k_1} + \log \binom{K}{k_2},
\]

with \( K = k_1p_n - \binom{k_1}{2} - k_1 \) for \( 1 \leq k_1 \leq p_n \wedge n \) and \( 0 \leq k_2 \leq K \wedge n \), and

\[
C_{I_{k_1, k_2}^{\text{no}}} = -\log \pi_3 + \log(p_n \wedge n) + \log \binom{p_n}{2} + \log \binom{p_n}{k_1} + \log \binom{p_n}{k_2},
\]
for $1 \leq k_1 \leq p_n \wedge n$ and $0 \leq k_2 \leq \binom{p_n}{2} \wedge n$. This complexity assignment recognizes that there are three types of models under the different heredity conditions.

Let $\hat{I} = \arg\min_{I \in \mathcal{F}} ABC(I)$ denote the model that minimizes the ABC criterion over the candidate model set $\mathcal{F}$ and $\hat{Y}^\dagger := P_{\hat{I}} Y$ denote the least squares estimate of $Y$ using the model $\hat{I}$. Then we have the following oracle inequality.

**Theorem 7.1.** When $\lambda \geq 5.1 / \log 2$, the worst risk of the ABC estimator $\hat{Y}$ is upper bounded by

$$
\sup_{h \in \mathcal{F}_0(r_1, r_2; S)} E(\mathcal{L}^{\dagger}(\hat{I})) \leq \frac{c \sigma^2}{n} \left[ R_Z \wedge \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{K_S}{r_2} \right) \right) \right],
$$

with

$$
K_S = \begin{cases} 
\binom{r_1}{2}, & \text{if } S = \mathbb{R}^p_{\text{strong}}, \\
r_1 p_n, & \text{if } S = \mathbb{R}^p_{\text{weak}}, \\
\binom{p_n}{2}, & \text{if } S = \mathbb{R}^p,
\end{cases}
$$

where $R_Z$ is the rank of the full design matrix $Z$ and the constant $c$ only depends on the constant $\lambda$.

From the theorem, without any prior knowledge of the sparsity indices, the constructed ABC estimator adaptively achieves the minimax upper bound regardless of the heredity conditions. The result also indicates a major difference between estimation and model identification. For estimation, from the result, we are able to achieve adaptation with respect to the heredity condition without any additional assumption. For model identification, although we are not aware of any work that addresses the task of adaptation over the unknown heredity nature, it seems certain that much stronger assumptions than those for consistency under an individual heredity condition will be necessary to achieve adaptive selection consistency. Achieving adaptive model selection consistency under different types of conditions remains an important open problem on model selection theory and methodology.

**Remark 5.** We do not require any assumptions on the relationship among the variables for the upper bound in the theorem. In particular, the variables may be arbitrary correlated.

**Remark 6.** The order $R_Z/n$ is achievable when we use the projection estimator from the full model. Thus the minimax rate of convergence is no slower than the order $R_Z/n$. As is known, the rank of the design matrix plays an important role in determining the minimax rate of convergence under fixed design (Yang 1999, Rigollet & Tsybakov 2011, Wang et al. 2014). For our result, when $p_n$, $r_1$ and $r_2$ together make the total estimation price of the true model small enough, the upper bound will be improved from $R_Z/n$ to $(r_1 (1 + \log(p_n/r_1)) \lor r_2(1 + \log((r_1^2)/r_2)))/n$.

**Remark 7.** The ABC estimator may not be practical when $p_n$ is large. In such case, stochastic search instead of all subset selection can be used for implementation.
Remark 8. The term “$R_Z \land$” automatically applies to the lower bound under whichever heredity condition, since under the SRC assumption, it intrinsically requires that $r_1(1+\log(p_n/r_1))\lor r_2(1+\log((r_1^2)/r_2))$ is no larger than $R_Z$ in terms of order. Otherwise, the lower bound $(r_1(1+\log(p_n/r_1))\lor r_2(1+\log((r_1^2)/r_2)))/n$ by our proof will exceed the upper bound $R_Z/n$, which leads to a contradiction. We give a specific example in Appendix F to illustrate this requirement.

Appendix A: Proof of the upper bound in Theorem 3.1

Proof of (3.2)

Recall that $h(z) = z^T \beta$ and $\hat{h}(z) = z^T \hat{\beta}$. Set $h_I := P_I h$ as the estimator by model $I$, where we use the bold-face $h = (h(z^T_1), ..., h(z^T_n))^T$ to denote the mean regression function vector and $z_i$ is the $i$-th row of the full design matrix $Z$. We first prove that $\hat{I}$ is equivalently an ABC estimator over the candidate set we consider. The SRC assumption with $l_1 = r_1$, $l_2 = r_2$ assures that $r_1 + r_2 \leq n$. It follows that, for any model $I = (I_1, I_2)$ with $|I_1|_0 = r_1$, $|I_2|_0 = r_2$, the corresponding submatrix $Z_I$ is full rank, i.e., $r_1 = r_1 + r_2$. Thus,

\[ \hat{I} = \arg \min_{I \in F} \sum_{i=1}^{n} (Y_i - \hat{Y}_I)^2, \]

where $F$ is the collection of models that have $r_1$ non-zero main effects and $r_2$ non-zero interaction effects with $0 \leq r_1 \leq p_n$, $1 \leq r_2 \leq \binom{r_1^2}{r_2}$, and all the models in $F$ share the same model descriptive complexity

\[ C_{I, r_1, r_2}^{\text{strong}} = \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{\binom{r_1^2}{r_2}}{r_2} \right). \]

The ABC criterion and the model descriptive complexity are introduced near (7.1). Therefore, $\hat{I}$ is an ABC estimator over the candidate set $F$.

Next we prove the upper bound. Since $\hat{I}$ is an ABC estimator over the candidate set $F$, by Theorem 1 in Yang (1999), we have:

\[ E(\mathcal{L}(\hat{I})) \leq c \inf_{I \in F} \left( \frac{1}{n} \| h_1 - h \|_2^2 + \sigma^2 r_1 + \frac{\lambda \sigma^2 C_I^1}{n} \right), \quad (A.1) \]

where $c$ is a positive constant that depends on the constant $\lambda$ only. When $h \in W = F_0(r_1, r_2; \mathbb{R}^{p_n}_{\text{strong}})$, there exists a specific model in $F$ such that the projection estimator of this model is equal to $h$. We consider the RHS of (A.1)
evaluated at such a model, where we still denote it as $I_{r_1, r_2}$ for convenience. Thus,

$$E(L(\hat{I})) \leq c \left( \|h_{I_{r_1, r_2}} - h\|^2 + \frac{\sigma^2 r_{1}, r_2}{n} + \frac{\lambda \sigma^2 C_{I_{r_1, r_2}}}{n} \right)$$

$$= \frac{c}{n} \left( \sigma^2 r_{1}, r_2 + \lambda \sigma^2 C_{I_{r_1, r_2}} \right).$$

The term $(i)$ is bounded as follows:

$$(i) \leq \frac{c_1 \lambda}{n} \sigma^2 \left( \frac{1}{\lambda} (r_1 + r_2) + \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{r_1}{r_2} \right) \right)$$

$$\leq \frac{c_1 \lambda}{n} \sigma^2 \left( \frac{1}{\lambda} (r_1 + r_2) + r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right)$$

$$\leq \frac{c_2}{n} \sigma^2 \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right).$$

Therefore,

$$E(L(\hat{I})) \leq \frac{c_2 \cdot \sigma^2}{n} \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right).$$

Thus we have

$$\min_{\hat{h}} \max_{h \in W} E(L(\hat{h}, h)) \leq \max_{h \in W} E(L(\hat{I})) \leq \frac{c_2 \cdot \sigma^2}{n} \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1}{r_2} \right) \right),$$

where the above $c_1, c_2$ are universal constants.

**Appendix B: Proof of the lower bound in Theorem 3.1**

Before stating the proof of (3.3), we introduce the local metric entropy, two important sets that aid the understanding of the metric entropy of the regression function space, together with the lemmas in relation to these two sets.

**B.1. Metric Entropy**

Metric entropy plays a central role in minimax theory, through the concepts of packing and covering. It provides a way to understand the “cardinality” of a set with infinitely many elements. In deriving the lower bound, information theoretic techniques play a key role, such as the local metric entropy, Fano’s inequality, Shannon’s mutual information and Kullback–Leibler divergence. We begin by introducing the definition of the local metric entropy.
Definition 1 (Local Metric Entropy). Given a metric space \((\mathcal{X}, \rho)\), let \(B(x, \epsilon) = \{x' \in \mathcal{X} | \rho(x, x') \leq \epsilon\}\) be an \(\epsilon\)-ball around \(x\). For \(0 < a < 1\), the \(a\)-local \(\epsilon\)-entropy at \(x\), denoted as \(\log M_x^a(\epsilon; \mathcal{X}, \rho)\), is defined as the \(a\epsilon\)-packing entropy of \(B(x, \epsilon)\).

The \(a\)-local \(\epsilon\)-entropy, denoted as \(\log M_x^a(\epsilon; \mathcal{X}, \rho)\), is then defined as the maximum (or supremum if maximum does not exist) of \(\log M_x^a(\epsilon; \mathcal{X}, \rho)\) over all \(x\) in \(\mathcal{X}\), i.e., \(\log M_x^a(\epsilon; \mathcal{X}, \rho) = \max_{x \in \mathcal{X}} \log M_x^a(\epsilon; \mathcal{X}, \rho)\).

B.2. Important Subsets

Set the Hamming distance between any two vectors \(v, v' \in \mathbb{R}^d\) as \(d_H(v, v') = \sum_{i=1}^{d} I_{v_i \neq v_i'}\). Consider the set

\[
\mathcal{H} = \left\{ \beta \in \mathbb{R}^{p_n}_{\text{strong}} : \beta \in \{-1, 0, 1\}^{p_n + \binom{p_n}{2}}, \left\| \beta^{(1)} \right\|_0 \leq r_1, \left\| \beta^{(2)} \right\|_0 \leq r_2 \right\}
\]

and let \(\mathcal{H}_1\) denote a subset of \(\mathcal{H}\) where the first \(r_1\) coordinates are fixed, i.e.,

\[
\mathcal{H}_1 = \left\{ \beta \in \mathcal{H} : \beta^{(1)} = (1, \ldots, 1, 0, \ldots, 0), \left\| \beta^{(2)} \right\|_0 = r_2 \right\}
\]

Let \(\mathcal{H}_2\) denote another subset of \(\mathcal{H}\) where no interaction effect exists, i.e.,

\[
\mathcal{H}_2 = \left\{ \beta \in \mathcal{H} : \left\| \beta^{(1)} \right\|_0 = r_1, \left\| \beta^{(2)} \right\|_0 = 0 \right\}
\]

The following two lemmas of the metric entropy of the subsets \(\mathcal{H}_1\) and \(\mathcal{H}_2\) are needed in the proof of (3.3).

Lemma 1. If \(r_2 \leq \frac{2}{3} \binom{r_1}{2}\), then there exists a subset of \(\mathcal{H}_1\) with its cardinality no less than \(\exp \left( \frac{n}{d} \log \frac{\binom{r_1}{2} - r_2}{r_2} \right)\) such that the pairwise Hamming distance of the points in this subset is greater than \(r_2/2\).

Proof. The proof is presented in Appendix B.4.

Lemma 2. If \(r_1 \leq 2p_n/3\), then there exists a subset of \(\mathcal{H}_2\) with its cardinality no less than \(\exp \left( \frac{n}{d} \log \frac{p_n - r_1/2}{r_1} \right)\) such that the pairwise Hamming distance of the points in this subset is greater than \(r_1/2\).

Proof. The proof is similar to that of Lemma 1.

B.3. Proof of (3.3)

It suffices to prove under \(r_2 \leq \left( r_1^2 - r_1 \right)/4 \). Since \(r_2(1 + \log((r_1^2)/r_2)) \approx (r_1^2)/2\) for \(r_1^2/2 \leq r_2 \leq (r_1^2)/2\), the monotonicity of the minimax risk in the function class reduces the proof to the case \(r_2 \leq \left( r_1^2 - r_1 \right)/4 \). Similarly it suffices to prove under \(r_1 \leq p_n/2\).
Recall that \(B_0(r_1, r_2; \mathbb{R}_n^{\text{str}}) = \{\beta \in \mathbb{R}_n^{\text{str}} : \|\beta(1)\|_0 \leq r_1, \|\beta(2)\|_0 \leq r_2\}\) is the coefficient space of interest and \(\mathcal{F}_0(r_1, r_2; \mathbb{R}_n^{\text{str}}) = \{h : h(z) = z^T \beta, \beta \in B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})\}\) is the mean regression function space. For convenience, let \(h_\theta, h_\vartheta\) denote the regression functions with coefficients \(\theta, \vartheta\) respectively, i.e., \(h_\theta(z) = z^T \theta, h_\vartheta(z) = z^T \vartheta\). Let

\[
B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})(\epsilon) = \{\beta : \beta \in B_0(r_1, r_2; \mathbb{R}_n^{\text{str}}), \|\beta\|_2 \leq \epsilon\}
\]

be an \(l_2\)-ball of radius \(\epsilon\) around \(0\) in \(B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})\) and

\[
\mathcal{F}_0(r_1, r_2; \mathbb{R}_n^{\text{str}})(h, \epsilon_0) = \{h' : h'(z) = z^T \beta, \beta \in B_0(r_1, r_2; \mathbb{R}_n^{\text{str}}), d(h', h) \leq \epsilon_0\}
\]

be the ball of radius \(\epsilon_0\) around the underlying regression function \(h\). Without loss of generality, we assume \(h = 0\). The square root of the empirical \(l_2\)-norm loss

\[
d(h_\theta, h_\vartheta) := \sqrt{\frac{1}{n} \sum_{i=1}^{n} (h_\theta(z_i) - h_\vartheta(z_i))^2} = \frac{1}{\sqrt{n}} \|Z(\theta - \vartheta)\|_2
\]

is used to measure the distance between any two functions \(h_\theta, h_\vartheta\). We prove the following two cases separately.

Case 1: \(\frac{\epsilon}{2} \log((p_n - r_1/2)/r_1) \leq \frac{\epsilon}{2} \log(((r_2/2) - r_2/2)/r_2)\). We consider the subset \(\mathcal{H}_1 = \{\epsilon \circ \beta : \beta \in \mathcal{H}_1\}\) of the \(l_2\)-ball \(B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})(\epsilon)\), where \(\epsilon\) is the point-wise product of two vectors,

\[
\epsilon = \epsilon \left(\frac{1}{\sqrt{r_1}}, \ldots, \frac{1}{\sqrt{r_1}}, \frac{1}{\sqrt{r_2}}, \ldots, \frac{1}{\sqrt{r_2}}\right)
\]

and

\[
\mathcal{H}_1 = \left\{\beta \in \mathcal{H} : \beta(1) = (1, \ldots, 1, 0, \ldots, 0), \|\beta(2)\|_0 = r_2\right\}.
\]

From Lemma 1, there exists a subset \(\mathcal{H}_{\text{sub}}\) of \(\mathcal{H}_1\) such that \(|\mathcal{H}_{\text{sub}}| \geq \exp(\frac{\epsilon^2}{2} \log((\frac{r_2}{r_1}) - \frac{r_2}{2}))\) and the pairwise Hamming distance of the elements within \(\mathcal{H}_{\text{sub}}\) is greater than \(r_2/2\). Set \(\mathcal{H}'_{\text{sub}} := \{\epsilon \circ \beta : \beta \in \mathcal{H}_{\text{sub}}\}\). For any \(\theta', \vartheta' \in \mathcal{H}'_{\text{sub}}\), there exist \(\theta, \vartheta \in \mathcal{H}_{\text{sub}}\) such that \(\|\theta' - \vartheta'\|_2 = \|\epsilon \circ \theta - \epsilon \circ \vartheta\|_2 \geq \sqrt{2} \frac{\epsilon \sqrt{p_n}}{\sqrt{r}} \sqrt{\rho H(\theta, \vartheta)} \geq \frac{\epsilon \sqrt{p_n}}{\sqrt{r}} \sqrt{r_2/2} = \frac{\epsilon}{2}\). We also have \(|\mathcal{H}'_{\text{sub}}| = |\mathcal{H}_{\text{sub}}|\) since it is a one-to-one mapping from \(\mathcal{H}_{\text{sub}}\) to \(\mathcal{H}'_{\text{sub}}\). Thus, we have \(\mathcal{H}'_{\text{sub}} \subseteq B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})(\epsilon)\) and the pairwise \(l_2\)-distance of the elements in \(\mathcal{H}'_{\text{sub}}\) is greater than \(\epsilon/2\).

For any \(\theta', \vartheta' \in \mathcal{H}'_{\text{sub}} \subseteq B_0(r_1, r_2; \mathbb{R}_n^{\text{str}})(\epsilon)\), let \(h_{\theta'}, h_{\vartheta'}\) be such that \(h_{\theta'}(z) = z^T \theta', h_{\vartheta'}(z) = z^T \vartheta'\). By SRC assumption with \(l_1 = r_1, l_2 = r_2\), we have

\[
b_1 \frac{\epsilon}{2} \leq b_1 \|\theta' - \vartheta'\|_2 \leq d(h_{\theta'}, h_{\vartheta'})
\]

\[
d(h, h_{\vartheta'}) \leq b_2 \|\theta' - \vartheta'\|_2 \leq b_2 \epsilon.
\]
Let $\epsilon_0 = b_2 \epsilon$, it follows that $\mathcal{F}_0(r_1, r_2; \mathbb{R}^{\bar{p}_n}_{\text{strong}})(h, \epsilon_0)$ has a subset

$$\mathcal{F}_{\text{sub}} := \{ h' : h'(z) = z^T \beta, \beta \in \mathcal{H}_{\text{sub}}, d(h', h) \leq \epsilon_0 \},$$

in which the pairwise distance (in terms of $d$) of the functions are no less than $\frac{1}{2} b_2 \epsilon_0$. This implies that the $\frac{1}{2} b_2 \epsilon_0$-local $\epsilon_0$-packing entropy of $\mathcal{F}_0(r_1, r_2; \mathbb{R}^{\bar{p}_n}_{\text{strong}})(h, \epsilon_0)$ is lower bounded by $\log |\mathcal{F}_{\text{sub}}| = \log |\mathcal{H}_{\text{sub}}| \geq \frac{1}{2} b_2 \epsilon_0 \log \left( \frac{r_1 - r_2}{r_2} \right)$. So $\log M_{\text{local}}(\epsilon_0)$ of $\mathcal{F}_0(r_1, r_2; \mathbb{R}^{\bar{p}_n}_{\text{strong}})$ is no less than $\frac{1}{2} b_2 \log((\frac{r_1^2}{2} - r_1 - r_2)/2r_2)$. Then by (7) in Yang & Barron (1999), the minimax risk is lower bounded by

$$c_1 \frac{\sigma^2 r_2}{n} \log \left( \frac{r_1 - r_2}{2r_2} \right) = c_1 \frac{\sigma^2}{n} \left( \frac{r_1}{2} \log \frac{p_n - r_1/2}{r_1} \lor \frac{r_2}{2} \log \frac{r_2}{r_2} \right),$$

where $c_1 > 0$ is a constant that depends on $b_1$ and $b_2$ only.

Case 2: $\frac{1}{2} b_2 \epsilon_0 \log((\frac{r_1^2}{2} - r_1 - r_2)/2r_2)$. We consider the subset $\mathcal{H}_2 = \epsilon'_1 \mathcal{H}_2$ of $B_0(r_1, r_2; \mathbb{R}^{\bar{p}_n}_{\text{strong}})(\epsilon)$, where $\epsilon'_1 = \epsilon/\sqrt{r_1}$ and

$$\mathcal{H}_2 := \{ \beta \in \mathcal{H} : \| \beta(1) \|_0 = r_1, \| \beta(2) \|_0 = 0 \}.$$

Following the same arguments above, we conclude that the minimax is lower bounded by

$$c_2 \frac{\sigma^2}{n} r_1 \frac{p_n - r_1/2}{r_1} = c_2 \frac{\sigma^2}{n} \left( \frac{r_1}{2} \log \frac{p_1 - r_1/2}{r_1} \lor \frac{r_2}{2} \log \frac{r_2}{r_2} \right),$$

where $c_2 > 0$ is a constant that depends on $b_1$ and $b_2$ only.

Notice that when $p_n/r_1 \geq 2$, we have $\log(p_n/r_1 - \frac{1}{2}) \geq \frac{1}{10} (1 + \log(p_n/r_1))$. Similarly, we have $\log((\frac{r_1^2}{2} - r_1 - \frac{1}{2}) \geq \frac{1}{10} (1 + \log((\frac{r_1^2}{2} - r_1 - \frac{1}{2})/2 r_2))$ when $(\frac{r_1^2}{2} - r_1 - r_2)/2 r_2 \geq 2$. Together with the fact that the lower bounds for the two cases are the same, the minimax risk is lower bounded by

$$c \frac{\sigma^2}{n} \left( r_1 (1 + \log \frac{p_n}{r_1}) \lor r_2 (1 + \log \frac{r_2}{r_2}) \right).$$

Thus the desired lower bound holds.

Remark 9. One way to interpret the imposition of the SRC assumption is that $\| Z \theta - Z \beta \|^2_2$ is indeed up to a constant of the Kullback-Leibler divergence between two joint densities (the joint distribution of the response variable $y$ under fixed design) parameterized with $\theta$ and $\beta$ respectively. To see this, let $z_i$ be the $i$-th row of $Z$ and we have the joint density $P_0 = (2\pi)^{-n/2} \sigma^{-n} \prod_{i=1}^n \exp(-\frac{1}{2}(y_i - z_i \theta)^2/\sigma^2)$ with parameter $\theta$. The K-L distance is then $D(P_0\|P_\beta) = \frac{1}{2\sigma^2} \sum_{i=1}^n (z_i \beta - z_i \theta)^2 = \frac{1}{2\sigma^2} \| Z \theta - Z \beta \|^2_2$. 


B.4. Proof of Lemma 1

First we have $|H_1| = \left(\frac{r_1^2 - r_1}{r_2}\right)2^{r_2}$ since the main effects are fixed. Fix $z \in H_1$, let $A$ denote the collection of all the points in $H_1$ that are within $\frac{r_2}{2}$ Hamming distances to $z$, i.e., $A = \{z' \in H_1 : \rho_H(z, z') \leq r_2/2\}$. It follows that the cardinality of $A$ is bounded above:

$$|A| \leq \left(\frac{r_1}{r_2/2}\right)^{3^{r_2/2}}.$$

For this upper bound, since the main effects are fixed for any point in $H_1$, we only need to pick $r_2/2$ positions of the interaction effects where $z'$ is different from $z$. In the remaining interaction effect positions, $z'$ is the same as $z$. It gives us at most $\left(\frac{r_1}{r_2/2}\right)$ possible choices of the $r_2/2$ positions out of the $\left(\frac{r_1}{r_2}\right)$ coordinates. For these $r_2/2$ positions, $z'$ can take any values in $\{-1, 1, 0\}$, thus the desired upper bound follows.

Let $B$ be a subset of $H_1$ such that $|B| \leq m := \left(\frac{r_1}{r_2}\right)/\left(\frac{r_1}{r_2/2}\right)$. Consider the collection of the points in $H_1$ that are within $r_2/2$ Hamming distance to some element in $B$, i.e., $\{z \in H_1 : \rho_H(z, z') \leq \frac{r_2}{2} \text{ for some } z' \in B\}$. We have

$$\left|\left\{z \in H_1 : \rho_H(z, z') \leq \frac{r_2}{2} \text{ for some } z' \in B\right\}\right| \leq \frac{|B| |A|}{\left(\frac{r_1}{r_2/2}\right)^{3^{r_2/2}}} < \left(\frac{r_1}{r_2}\right)2^{r_2} = |H_1|.$$

The strictly less inequality implies that for any set $B \subset H_1$ with $|B| \leq m$, $\exists z \in H_1$ such that $\rho_H(z, z') > \frac{1}{2}r_2$ for all $z' \in B$. By induction, we can create a set $B \subset H_1$ with $|B| > m$ such that Hamming distance between any two elements in $B$ exceeds $\frac{1}{2}r_2$. Next, we introduce one useful inequality. When $0 \leq B \leq \frac{4}{3}A$ for $A, B \in \mathbb{N}$, we have

$$\frac{(A)}{(B)} = \frac{(A - \frac{B}{2})!(\frac{B}{2})!}{(A - B)!B!} \geq \prod_{j=1}^{B/2} \frac{A - B + j}{\frac{B}{2} + j} \geq \prod_{j=1}^{B/2} \frac{A - B + \frac{B}{2}}{\frac{B}{2} + \frac{B}{2}} = \left(\frac{A - B}{B}\right)^{B/2}.$$

When $r_2 \leq (r_1^2 - r_1)/3$, we have

$$m = \frac{\left(\frac{r_1}{r_2}\right)}{\left(\frac{r_1}{r_2/2}\right)} \geq \left(\frac{r_1}{r_2}\right)^{r_2/2}.$$
Thus,
\[
\log m \geq \frac{r_2}{2} \log \left( \frac{r_1}{r_2} \right) - \frac{r_2}{2}. 
\]
The desired result follows.

**Appendix C: Proof of Theorem 4.1**

*Proof.* The proofs are similar to the arguments for strong heredity with slight differences.

To prove the upper bound under weak heredity, we instead consider the model \( \hat{I} = \arg\min_{I \in I_{weak}} \sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2 \) that minimizes the residual sum of squares over all the models that have \( r_1 \) non-zero main effects and \( r_2 \) non-zero interaction effects under weak heredity. The model descriptive complexity is thus different from the strong heredity. In this case, \( C_{I_{weak}} = \log \left( \frac{p_n}{r_2} \right) + \log \left( \frac{K}{r_2} \right) \) with \( K = r_1(p_n - (r_1 + 1)/2) \) for \( 1 \leq r_1 \leq p_n \wedge n \) and \( 0 \leq r_2 \leq (r_1 p_n - \left( \frac{r_1}{2} \right) - r_1) \wedge n \). The ABC criteria for the models are defined as in (7.1). The same arguments in the proof of (3.2) can then be used.

To prove the lower bound under weak heredity, we consider the set
\[
\mathcal{H}_{weak} = \left\{ \beta \in \mathbb{R}^{p_n}_{weak} : \beta \in \{-1, 0, 1\}^{p_n + \left( \frac{r_2}{2} \right)}, \left\| \beta^{(1)} \right\|_0 \leq r_1, \left\| \beta^{(2)} \right\|_0 \leq r_2 \right\}. 
\]
Then the two important subsets are instead
\[
\mathcal{H}_1 = \left\{ \beta \in \mathcal{H}_{weak} : \beta^{(1)} = (1, \ldots, 1, 0, \ldots, 0), \left\| \beta^{(2)} \right\|_0 = r_2 \right\}
\]
and
\[
\mathcal{H}_2 = \left\{ \beta \in \mathcal{H}_{weak} : \left\| \beta^{(1)} \right\|_0 = r_1, \left\| \beta^{(2)} \right\|_0 = 0 \right\}.
\]

Similar metric entropy results of the above two subsets can be derived in the same fashion as in Lemmas 1 and 2. Other arguments are the same as in the proof of (3.3). \(\square\)

**Appendix D: Proof of Theorem 4.2**

*Proof.* For the upper bound under no heredity, we consider the model \( \hat{I} = \arg\min_{I \in I_{no}} \sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2 \) with the model descriptive complexity \( C_{I_{no}} = \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{r_2}{r_2} \right) \) for \( 1 \leq r_1 \leq p_n \wedge n \) and \( 0 \leq r_2 \leq \left( \frac{r_2}{2} \right) \wedge n \). The ABC criteria for the models are defined as in (7.1).

For the lower bound under no heredity, we consider the set
\[
\mathcal{H}_{no} = \left\{ \beta \in \mathbb{R}^{p_n} : \beta \in \{-1, 0, 1\}^{p_n + \left( \frac{r_2}{2} \right)}, \left\| \beta^{(1)} \right\|_0 \leq r_1, \left\| \beta^{(2)} \right\|_0 \leq r_2 \right\}. 
\]
Then the two important subsets are instead
\[
H_1 = \left\{ \beta \in H_{\text{no}} : \beta^{(1)} = (1, \ldots, 1, 0, \ldots, 0), \begin{bmatrix} \beta^{(2)} \end{bmatrix} = r_2 \right\}
\]
and
\[
H_2 = \left\{ \beta \in H_{\text{no}} : \begin{bmatrix} \beta^{(1)} \end{bmatrix} = r_1, \begin{bmatrix} \beta^{(2)} \end{bmatrix} = 0 \right\}.
\]
Similar metric entropy results of the above two subsets can be derived in the same fashion as Lemmas 1 and 2.

Other arguments are the same as in the proofs of (3.2) and (3.3).

Appendix E: Proof of Theorem 7.1

The model descriptive complexity term \( \lambda \sigma^2 C_1 \) plays a fundamental role in model selection theory (Barron & Cover 1991, Barron et al. 1999, Yang 1999, Wang et al. 2014). Since we are considering models with interaction terms, the model descriptive complexity \( C_1 \) reflects our comprehension of the model complexity other than the total number of parameters only. The detailed designation of the descriptive complexity usually depends on the class of models of interest. Instead of interpreting \( C_1 \) as the code length (or description length) of describing the model index, one can also treat \( \exp(-C_1) \) as the prior probability assigned to the model from a Bayesian viewpoint.

Proof. The candidate set can be represented as the union of the candidate sets under three heredity conditions, i.e., \( \mathcal{F} = \mathcal{F}_{\text{strong}} \cup \mathcal{F}_{\text{weak}} \cup \mathcal{F}_{\text{no}} \), with
\[
\mathcal{F}_{\text{strong}} := \left\{ I_{p_n,(p_n^2-p_n)/2} \right\} \cup \left\{ I_{k_1,k_2}^{\text{strong}} \right\},
\]
\[
\mathcal{F}_{\text{weak}} := \left\{ I_{p_n,(p_n^2-p_n)/2} \right\} \cup \left\{ I_{k_1,k_2}^{\text{weak}} \right\},
\]
\[
\mathcal{F}_{\text{no}} := \left\{ I_{p_n,(p_n^2-p_n)/2} \right\} \cup \left\{ I_{k_1,k_2}^{\text{no}} \right\}.
\]
When \( h \in \mathcal{F}_0(r_1, r_2; \mathbb{R}^{p_n}_{\text{strong}}) \), there exists a specific model in \( \mathcal{F}_{\text{strong}} \) such that the projection estimator of this model is equal to \( h \). Also, the projection of \( h \) onto the full design matrix is still \( h \). We denote the two models as \( I_{r_1,r_2} \) and
Therefore, we have
\[ E(\mathcal{L}(\hat{Y}^\tau)) \leq \inf_{I \in \mathcal{F}} \left( \frac{1}{n} \| h_1 - h \|_2^2 + \frac{\sigma^2 r_1}{n} + \frac{\lambda \sigma^2 C_1}{n} \right) \]
\[ \leq \inf_{I \in \mathcal{F}_{\text{strong}}} \left( \frac{1}{n} \| h_1 - h \|_2^2 + \frac{\sigma^2 r_1}{n} + \frac{\lambda \sigma^2 C_1}{n} \right) \]
\[ \leq c \left( \| h_{I_{1,r_2}} - h \|_2^2 + \frac{\sigma^2 r_{1,r_2}}{n} + \frac{\lambda \sigma^2 C_{1,r_2}}{n} \right) \]
\[ \wedge c \left( \| h_{I_{p_1,p_2(p_n - 1)/2}} - h \|_2^2 + \frac{\sigma^2 R_Z}{n} + \frac{-\lambda \sigma^2 \log \pi_0}{n} \right) \]
\[ = \frac{c}{n} \left( \sigma^2 r_{1,r_2} + \lambda \sigma^2 C_{1,r_2} \right) \wedge \frac{c}{n} \left( \sigma^2 R_Z - \lambda \sigma^2 \log \pi_0 \right), \quad \text{(E.2)} \]

where \( R_Z \) is the rank of the full design matrix, the first inequality follows from (A.1), the second inequality follows from \( \mathcal{F}_{\text{strong}} \subseteq \mathcal{F} \) and the third inequality results from the evaluation of (E.1) at \( I_{1,r_2} \) and \( I_{p_1,p_2(p_n - 1)/2} \). The two terms \( (i) \) and \( (ii) \) are bounded as follows:

\[(i) \leq \frac{c_1 \lambda}{n} \sigma^2 \left( \frac{r_1 + r_2}{\lambda} - \log \pi_1 + \log p_n + \log \left( \frac{r_1}{2} \right) + \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{r_1}{2} \right) \right) \]
\[ \leq \frac{c_1 \lambda}{n} \sigma^2 \left( \frac{r_1 + r_2}{\lambda} - \log \pi_1 + r_1 \left( 1 + \log \frac{p_n}{r_1} \right) \right. \]
\[ \left. \quad + \log r_1^2 + r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1^2}{r_2^2} \right) \right) \]
\[ \leq \frac{c_2}{n} \sigma^2 \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1^2}{r_2^2} \right) \right), \]

and

\[(ii) \leq \frac{c}{n} \left( \sigma^2 R_Z - \lambda \sigma^2 \log \pi_0 \right) \]
\[ \leq \frac{c_3}{n} \sigma^2 R_Z. \]

Therefore, we have
\[ E(\mathcal{L}(\hat{Y}^\tau)) \leq \max\left( \frac{c_2}{n} \cdot \sigma^2 \right) \left[ \left( r_1 \left( 1 + \log \frac{p_n}{r_1} \right) + r_2 \left( 1 + \log \frac{r_1^2}{r_2} \right) \right) \wedge R_Z \right] \]

where \( c_1, c_2, c_3 \) are some constants that depend only on the constant \( \lambda \). Thus the desired minimax upper bounded follows.

When \( h \in \mathcal{F}_0(r_1, r_2; \mathbb{R}^{p_n}) \) or \( h \in \mathcal{F}_0(r_1, r_2; \mathbb{R}^{p_n}) \) with \( I \in \mathcal{F}_{\text{weak}} \) or \( I \in \mathcal{F}_{\text{no}} \) replacing \( I \in \mathcal{F}_{\text{strong}} \) in (E.1), the quantity \( (i) \) in (E.2) will instead be no greater
than
\[
\frac{c_1 \lambda}{n} \sigma^2 \left( \frac{r_1 + r_2}{\lambda} - \log \pi_2 + \log p_n + \log K + \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{K}{r_2} \right) \right)
\]
with \( K = r_1 p_n - \binom{r_1}{2} - r_1 \) under weak heredity \( h \in \mathcal{F}_0(r_1, r_2; \mathbb{R}^{p_n}) \), or
\[
(i) \leq \frac{c_1 \lambda}{n} \sigma^2 \left( \frac{r_1 + r_2}{\lambda} - \log \pi_3 + \log p_n + \log \left( \frac{p_n}{2} \right) + \log \left( \frac{p_n}{r_1} \right) + \log \left( \frac{p_n}{r_2} \right) \right)
\]
under no heredity \( h \in \mathcal{F}_0(r_1, r_2; \mathbb{R}^{p_n}) \). The different constants \( \pi_2, \pi_3 \) does not affect the conclusion in terms of order. Following the same arguments in the proof of strong heredity, the desired results follow when the underlying heredity condition is weak heredity or no heredity.

\[\square\]

Appendix F: An Example When SRC is not Satisfied

For simplicity, let us consider an example where the regression mean function includes only one main effect term, i.e., \( r_1 = 1, r_2 = 0 \). The corresponding SRC assumption with \( l_1 = r_1 = 1, l_2 = r_2 = 0 \) will be that there exist constants \( b_1, b_2 > 0 \) (not depend on \( n \)) such that for any \( \beta \in \mathbb{R}^{p_n} \) with \( \| \beta \|_0 \leq 2 \), we have
\[
b_1 \| \beta \|_2 \leq \frac{1}{\sqrt{n}} \| Z \beta \|_2 \leq b_2 \| \beta \|_2, \tag{F.1}
\]
where the design matrix \( Z = X \) is the matrix that contains the main effects.

Assume the first \( R_Z \) columns of \( Z \) are linearly independent and denote \( Z = (Z^1, Z^2) \), where \( Z^1 = (Z_{11}, \ldots, Z_{1R_Z}) \) is the \( n \times R_Z \) submatrix with \( \text{rank}(Z^1) = R_Z \). Suppose the submatrix \( Z^1 \) satisfies the SRC assumption. Assume that \( \| Z_0 \|_2 = f(n) \) for \( 1 \leq i \leq p_n \). For the purpose of illustration, we set \( f(n) = \sqrt{n} \).

Let \( A \) be the collection of all columns in \( Z^2 \): \( A = \{ z | z = Z^1 \alpha, \alpha \in \mathbb{R}^{R_Z}, \| z \|_2 = f(n) \} \). Then \( A \) should satisfy that \( \forall z, z' \in A \), we have \( b_1 \leq \frac{1}{\sqrt{n}} \| a_1 z + a_2 z' \|_2 \leq b_2 \) for all \( a_1, a_2 \in \mathbb{R} \) and \( a_1^2 + a_2^2 = 1 \). We know
\[
\frac{1}{\sqrt{n}} \| a_1 z + a_2 z' \|_2 = \frac{1}{\sqrt{n}} \sqrt{a_1^2 \| z \|_2^2 + a_2^2 \| z' \|_2^2 + 2a_1 a_2 \| z \|_2 \| z' \|_2 \cos \theta},
\]
where \( \theta \) is the angle between two \( n \)-dimensional vectors \( z \) and \( z' \).

Thus we have
\[
\frac{1}{\sqrt{n}} \sqrt{a_1^2 \| z \|_2^2 + a_2^2 \| z' \|_2^2 + 2a_1 a_2 \| z \|_2 \| z' \|_2 \cos \theta} = \frac{f(n)}{\sqrt{n}} \sqrt{a_1^2 + a_2^2 + 2a_1 a_2 \cos \theta} = \sqrt{1 + 2a_1 a_2 \cos \theta}.
\]

Then \( \sqrt{1 + 2a_1 a_2 \cos \theta} \geq b_1 \) for all \( a_1^2 + a_2^2 = 1 \) (otherwise \( \frac{1}{\sqrt{n}} \| a_1 z + a_2 Z \|_2 \) is less than \( b_1 \), which violates the SRC assumption). Since \( -1 \leq 2a_1 a_2 \leq 1 \)
for \( a_1^2 + a_2^2 = 1 \), we have \( b_1 \leq \sqrt{1 - |\cos \theta|} \), which implies \( |\cos \theta| \leq 1 - b_2^2 \). That means the pairwise \( l_2 \) distance between any two elements in \( A \) should be greater than \( \sqrt{2b_1} \) and less than \( \sqrt{4 - 2b_1^2} \). It is well known that the \( \epsilon \)-covering entropy of the \( R_Z \)-dimensional unit ball \( B \) is of order \( R_Z \log(1/\epsilon) \). We denote \( \sqrt{n}B \) as a ball of radius \( \sqrt{n} \). Let \( \epsilon = \sqrt{2b_1} / 2 \), there exists a positive constant \( c_1 \) such that \( \log N(\epsilon; \sqrt{n}B, l_2) \leq c_1 R_{\bar{Z}} \log(\sqrt{2n}/b_1) \). Since \( A \) is a \( 2\epsilon \)-packing set of a ball of radius \( f(n) = \sqrt{n} \), its cardinality satisfies \( \log |A| \leq \log M(2\epsilon; \sqrt{n}B, l_2) \). The covering number and the packing number are closely related as in the well-known inequality \( M(\epsilon; X, \rho) \leq N(\rho/\epsilon; X, \rho) \leq M(\rho; X, \rho) \). Thus we have \( \log |A| \leq \log M(2\epsilon; \sqrt{n}B, l_2) \leq \log N(\epsilon; \sqrt{n}B, l_2) \leq c_1 R_{\bar{Z}} \log(\sqrt{2n}/b_1) \), which implies \( A \) has at most \((\sqrt{2n}/b_1)^{c_1 R_{\bar{Z}}} \) elements under the SRC assumption. Thus, as long as \( p_n > (\sqrt{2n}/b_1)^{c_1 R_{\bar{Z}}} \), the SRC assumption will not be satisfied because the SRC assumption requires that \((F.1)\) must hold for any pair of columns in \( Z \). In this case, the lower bound \( r_1(1 + \log(p_n/r_1))/n \) in our theorems does not apply.

References

Barron, A., Birgé, L. & Massart, P. (1999), ‘Risk bounds for model selection via penalization’, *Probability theory and related fields* **113**(3), 301–413.

Barron, A. R. & Cover, T. M. (1991), ‘Minimum complexity density estimation’, *IEEE transactions on information theory* **37**(4), 1034–1054.

Bickel, P. J., Ritov, Y. & Tsybakov, A. B. (2009), ‘Simultaneous analysis of lasso and dantzig selector’, *The Annals of Statistics* pp. 1705–1732.

Bien, J., Taylor, J. & Tibshirani, R. (2013), ‘A lasso for hierarchical interactions’, *Annals of statistics* **41**(3), 1111.

Bunea, F., Tsybakov, A. B., Wegkamp, M. H. et al. (2007), ‘Aggregation for gaussian regression’, *The Annals of Statistics* **35**(4), 1674–1697.

Candes, E. & Tao, T. (2007), ‘The dantzig selector: Statistical estimation when \( p \) is much larger than \( n \)’, *The Annals of Statistics* pp. 2313–2351.

Chipman, H. (1996), ‘Bayesian variable selection with related predictors’, *The Canadian Journal of Statistics / La Revue Canadienne de Statistique* **24**(1), 17–36.

Choi, N. H., Li, W. & Zhu, J. (2010), ‘Variable selection with the strong heredity constraint and its oracle property’, *Journal of the American Statistical Association* **105**(489), 354–364.

Fan, J. & Li, R. (2001), ‘Variable selection via nonconcave penalized likelihood and its oracle properties’, *Journal of the American statistical Association* **96**(456), 1348–1360.

Fan, Y., Kong, Y., Li, D. & Lv, J. (2016), ‘Interaction pursuit with feature screening and selection’, *arXiv preprint arXiv:1605.08933*.

Hall, P. & Xue, J.-H. (2014), ‘On selecting interacting features from high-dimensional data’, *Computational Statistics & Data Analysis* **71**, 694–708.

Hamada, M. & Wu, C. J. (1992), ‘Analysis of designed experiments with complex aliasing’, *Journal of Quality Technology; (United States)* **24**(3).
Hao, N., Feng, Y. & Zhang, H. H. (2017), ‘Model Selection for High Dimensional Quadratic Regression via Regularization’, Journal of the American Statistical Association 24(4), 0–0.

Hao, N. & Zhang, H. H. (2014), ‘Interaction Screening for Ultrahigh-Dimensional Data’, Journal of the American Statistical Association 109(507), 1285–1301.

Hao, N. & Zhang, H. H. (2016), ‘A note on high dimensional linear regression with interactions’, The American Statistician (just-accepted).

Jiang, B. & Liu, J. S. (2014), ‘Variable selection for general index models via sliced inverse regression’, The Annals of Statistics 42(5), 1751–1786.

Knight, K. & Fu, W. (2000), ‘Asymptotics for lasso-type estimators’, Annals of statistics pp. 1356–1378.

Koltchinskii, V. (2009), ‘The dantzig selector and sparsity oracle inequalities’, Bernoulli 15(3), 799–828.

Li, K.-C. (1991), ‘Sliced inverse regression for dimension reduction’, Journal of the American Statistical Association 86(414), 316–327.

Li, R., Zhong, W. & Zhu, L. (2012), ‘Feature screening via distance correlation learning’, Journal of the American Statistical Association 107(499), 1129–1139.

Lv, J. & Fan, Y. (2009), ‘A unified approach to model selection and sparse recovery using regularized least squares’, The Annals of Statistics pp. 3498–3528.

Meinshausen, N. & Yu, B. (2009), ‘Lasso-type recovery of sparse representations for high-dimensional data’, The Annals of Statistics pp. 246–270.

Nelder, J. A. (1977), ‘A Reformulation of Linear Models’, Journal of the Royal Statistical Society. Series A (General) 140(1), 48–31.

Peixoto, J. L. (1987), ‘Hierarchical variable selection in polynomial regression models’, The American Statistician 41(4), 311–313.

Raskutti, G., Wainwright, M. J. & Yu, B. (2011), ‘Minimax rates of estimation for high-dimensional linear regression over \( \ell_q \)-balls’, IEEE transactions on information theory 57(10), 6976–6994.

Rigollet, P. & Tsybakov, A. (2011), ‘Exponential screening and optimal rates of sparse estimation’, Annals of Statistics 39(2), 731–771.

van de Geer, S. A. (2007), The deterministic lasso.

van de Geer, S. A. (2008), ‘High-dimensional generalized linear models and the lasso’, Ann. Statist. 36(2), 614–645.

van de Geer, S. A. & Bhlmann, P. (2009), ‘On the conditions used to prove oracle results for the lasso’, Electron. J. Statist. 3, 1360–1392.

Wang, Z., Paterlini, S., Gao, F. & Yang, Y. (2014), ‘Adaptive minimax regression estimation over sparse \( \ell_q \)-hulls.’, Journal of Machine Learning Research 15(1), 1675–1711.

Yang, Y. (1999), ‘Model selection for nonparametric regression’, Statistica Sinica pp. 475–499.

Yang, Y. & Barron, A. (1999), ‘Information-theoretic determination of minimax rates of convergence’, The Annals of Statistics 27(5), 1564–1599.

Yuan, M., Joseph, V. R. & Zou, H. (2009), ‘Structured variable selection and
estimation’, *The Annals of Applied Statistics* pp. 1738–1757.
Zhang, C.-H. (2010a), ‘Nearly unbiased variable selection under minimax con-
cave penalty’, *Ann. Statist.* **38**(2), 894–942.
Zhang, C.-H. & Huang, J. (2008), ‘The sparsity and bias of the lasso selection in
high-dimensional linear regression’, *The Annals of Statistics* pp. 1567–1594.
Zhang, T. (2010b), ‘Analysis of multi-stage convex relaxation for sparse re-
gularization’, *Journal of Machine Learning Research* **11**(Mar), 1081–1107.
Zhao, P., Rocha, G. & Yu, B. (2009), ‘The composite absolute penalties fam-
ily for grouped and hierarchical variable selection’, *The Annals of Statistics*
pp. 3468–3497.
Zhao, P. & Yu, B. (2006), ‘On model selection consistency of lasso’, *Journal of
Machine learning research* **7**(Nov), 2541–2563.
Zou, H. & Yuan, M. (2008), ‘Composite quantile regression and the oracle model
selection theory’, *Ann. Statist.* **36**(3), 1108–1126.