We are grateful to the reviewers for their substantive and constructive feedback. We are grateful that there is consensus that this manuscript (R2) "brings together a few different works in an interesting way" to (R3) "move closer to biological plausibility" with sparse coding models in a way that is (R4) "well-backed by both theoretical and experimental results" and (R4) "paves the way for these models to keep making important contributions to our understanding of efficient information coding both in biological and artificial neural networks." We propose revisions and are additional experiments (detailed below) to address reviewer comments, and believe the resulting manuscript will be much stronger.

While we appreciate that (R4) viewed the manuscript favorably, we’re also confident that there are opportunities for improvement. Unfortunately, without listing any weaknesses, we are unclear what changes (R4) could envision that would improve the impact of the work.

1: Connections to related research.

- (R2) We agree that a number of modeling factors affect the dictionary structure and we will improve the manuscript with an explicit discussion of these points. As noted, the goal of our study is not to produce the highest fidelity with biological receptive fields among all possible models, but rather to focus on the role of localized wiring constraints in randomized compression for the sparse coding model (which itself did not perfectly match the width/height distribution). To be explicit, we used the same hyper-parameters across all experiments. While our focus is specifically on the localized wiring, we also note that the prior work introducing learning in the compressed space (with dense wiring) did not report quantitative aspects of coding performance or fits with biological data. Similarly, we will further contextualize our results by including a discussions of the relationship to other papers involving dimensionality reduction and sparse coding (including the works by Hyvarinen and Cottrell).

- (R3) We agree that we can improve the context of the manuscript by highlighting the relationship to other results on structured sparse measurement matrices as well as frame theory from the harmonic analysis literature. This change will be included in the revision.

2: Additional analysis.

- (R2) We agree that the redundancy reduction metrics would be interesting and valuable to add to the manuscript (as another panel in figure 3). In fact, we have already calculated those metrics on the recovered dictionaries and we see qualitatively the same relationship as with the other metrics. Specifically, this analysis shows that multi-information is significantly reduced from the pixel space in all cases, with similar levels of redundancy reduction with all learned dictionaries (with small additional reductions when learned in the compressed space, and further small reductions when wiring is localized).

- (R3) We agree that additional analysis based on the retinal neuroanatomy literature will help place our modeling choices in better context. Specifically, we will include a detailed discussion of photoreceptor density (ranging from 50k-150k cells/mm²), retinal ganglion cell density (peaking at 30k cells / mm²), and degree of photoreceptor innervation of individual retinal ganglion cells (ranging from 1-1000). This analysis will further demonstrate that retinal anatomy generally shows a spatially localized pooling of inputs from photoreceptors in a way that is qualitatively captured by the proposed model (with characteristics that quantitatively reflect many of the basic properties of the biology).

3: Writing clarity.

- (R2) We agree that the material in lines 186-191 and line 154 is less clear than it should be. We will revise this text to be more clear, including adding text and a graphic to the supplement to explain the reshaping procedure.

- (R3) The figures will be revised to increase readability.

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**Figure 1:** New analysis of redundancy reduction showing similar decreases in redundancy for all learned dictionaries.