Wiring Variations That Enable and Constrain Neural Computation in a Sensory Microcircuit

The Harvard community has made this article openly available. Please share how this access benefits you. Your story matters

<table>
<thead>
<tr>
<th>Citation</th>
<th>Tobin, William. 2016. Wiring Variations That Enable and Constrain Neural Computation in a Sensory Microcircuit. Doctoral dissertation, Harvard University, Graduate School of Arts &amp; Sciences.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Citable link</td>
<td><a href="http://nrs.harvard.edu/urn-3:HUL.InstRepos:33840705">http://nrs.harvard.edu/urn-3:HUL.InstRepos:33840705</a></td>
</tr>
<tr>
<td>Terms of Use</td>
<td>This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at <a href="http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA">http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA</a></td>
</tr>
</tbody>
</table>
Wiring Variations That Enable and Constrain Neural Computation in a Sensory Microcircuit

A dissertation presented

by

William Foster Tobin

to

The Division of Medical Sciences

in partial fulfillment of the requirements

for the degree of

Doctor of Philosophy

in the subject of

Neurobiology

Harvard University

Cambridge, Massachusetts

July 2016
Wiring Variations That Enable and Constrain Neural Computation in a Sensory Microcircuit

Abstract

Neural network function can be shaped by varying the strength of synaptic connections. One way to achieve this is to vary connection structure. To investigate how structural variation among synaptic connections might affect neural computation, we examined primary afferent connections in the *Drosophila* olfactory system. We used large-scale serial section electron microscopy to reconstruct all the olfactory receptor neuron (ORN) axons that target a left-right pair of glomeruli, as well as all the projection neurons (PNs) postsynaptic to these ORNs. We find three variations in ORN→PN connectivity. First, we find a systematic co-variation in synapse number and PN dendrite size, suggesting total synaptic conductance is tuned to postsynaptic excitability. Second, we show that PNs receive more synapses from ipsilateral than contralateral ORNs, providing a structural basis for odor lateralization behavior. Finally, we provide evidence of imprecision in ORN→PN connections and show how this can diminish network performance.
Table of Contents

Abstract ...................................................................................................................... iii
Table of Figures ....................................................................................................... vi
Table of Tables......................................................................................................... vii
Acknowledgements ................................................................................................. viii
Attributions ............................................................................................................... x

Chapter 1 General Introduction and Background ............................................... 1
1.1 Anatomical Variability in Identified Cell Types .............................................. 2
1.2 Organization of the Early Olfactory System of Drosophila melanogaster .......... 7
1.3 Development of the Drosophila Glomerular Network ..................................... 9
1.4 Summary of our Approach and its Limitations ............................................... 11

Chapter 2 Wiring Variations Among the Principal Neurons of an
Antennal Lobe Glomerulus .................................................................................... 13
2.1 Introduction ....................................................................................................... 13
2.2 Results .............................................................................................................. 17
  2.2.1 Cells comprising the glomerular micro-circuit ............................................ 17
  2.2.2 Relative abundance of connection types .................................................... 21
  2.2.3 The structure and strength of excitatory connections ............................... 22
  2.2.4 Compensatory variations in dendrite size and synapse number ............... 24
  2.2.5 A basis for odor lateralization in the structure of synaptic connections .......... 32
  2.2.6 Inequalities among olfactory receptor neurons ........................................... 36
  2.2.7 Connection noise in olfactory receptor neuron projections ........................ 42
  2.2.8 Functional implications of connection noise .............................................. 47
2.3 Discussion ......................................................................................................... 53
  2.3.1 Strengths and limitations of our data .......................................................... 53
  2.3.2 Structural correlates of connection strength .............................................. 55
  2.3.3 Co-variation in cell number, dendrite size, and synapse number .............. 56
  2.3.4 Developmental noise in wiring ................................................................. 59
  2.3.6 Variations in the connectome: signal and noise ........................................ 62
2.4 Experimental Procedures........................................................................................................... 63
2.4.1 EM material preparation ........................................................................................................ 63
2.4.2 Large-scale TEM imaging and alignment ............................................................................. 64
2.4.3 Reconstruction and verification ......................................................................................... 65
2.4.4 Labeling DM6 PNs for cell counting .................................................................................... 66
2.4.5 Compartmental models ....................................................................................................... 67
2.4.6 Spike Count Discrimination Classifier ............................................................................... 69
2.4.7 Lateralization Classifier ..................................................................................................... 71
2.4.8 Statistics ............................................................................................................................. 72
2.4.9 Code and Data Availability ............................................................................................... 72

Chapter 3 Conclusion...................................................................................................................... 73

Appendix 1 Supplementary Figures ............................................................................................ 79

Bibliography.................................................................................................................................. 89
Table of Figures

Figure 1: Cells and connections comprising the glomerular micro-circuit. .......................................................... 19

Figure 2: Connectivity compensates for a missing cell. ......................... 25

Figure 3: Dendritic arbor size equalizes average unitary responses. .... 28

Figure 4: A basis for odor lateralization behavior in ORN wiring. ....... 34

Figure 5: Wiring inequalities among sister ORNs................................................................. 37

Figure 6: Correlated and independent variation in ORN wiring. ........ 44

Figure 7: Functional consequences of variability in ORN wiring......... 48

Figure S1: Variations in the number of PNs in glomerulus DM6........ 80

Figure S2: Comparing anatomical features of ipsi- and contralateral
ORN axons in glomerulus DM6................................................................. 83

Figure S3: Axon-dendrite proximity correlates with the number of
synapses per ORN-PN connection............................................................ 85

Figure S4: Comparing model output sensitivity to parameter value
changes........................................................................................................ 87
Table of Tables

Table S1.................................................................82
Acknowledgements

The work presented in this thesis is the product of many individual’s efforts. I have been exceedingly lucky to receive their help and I would like to heartily thank them all.

My advisor, Rachel Wilson, has been a stalwart presence in my life for the last six years. As a manager she strives for honesty, clarity and consistency. Her scientific contributions to this work cannot be overstated; she provided invaluable guidance at each step even when working outside of her realm of expertise. Most importantly, Rachel is a kind person and I will miss her in the years to come.

Wei Lee has served as a second advisor to me in spite of the fact that he was under no obligation to do so. My graduate education has been significantly enriched because of this fact. His work made this project possible and collaborating with him was continually rewarding.

In my time as a Wilson lab member I have had the pleasure of working alongside Quentin Gaudry, Joey Zhou, Brendan Lehnert, Mehmet Fişek, Kathy Nagel, Wendy Liu, Betty Hong, Tony Azevedo, Joe Bell, Allison Baker, Alex Batchelor, Stephen Holtz, Jamie Jeanne, Sasha Rayshubskiy, Asa Barth-Maron, Michael Marquis, Alexandra Moore, Tatsuo Okubo, Paola Patella and John “Coach” Tuthill. These individuals have provided invaluable feedback and taught me much of what I know about how to actually do science. I am particularly grateful to the more senior members of the lab who had great patience with me in the early years.

I have been lucky to have Rick Born, Bob Datta, Mark Andermann, Bruce Bean, Matt Pecot, Mike Do and John Maunsell on my committee at various points in time. They all diligently kept me on track and made sure the science I was doing was as good as it could be.

The Program in Neuroscience has succeeded in ushering me through the various stages of graduate school, ensuring I was not being treated unfairly or exploited unduly along the way. I would like to thank Karen Harmin for her flawless administrative performance. Rick Born, who directed the program for most of my time in it, was always attentive and supportive.

Most of the dataset annotation was painstakingly completed by a number of Northeastern University co-op students. Some of the individuals who devoted an inordinate amount of time to this effort include Rose Caplan, Zachary Tweed, Matthew Johnson, Catharina Dekker, Sirine Bellou and Palmer Starkey among others.

Without the exceptional friendship and unflagging moral support of Alex Wiltshcko, Mehmet Fişek and James Jeanne I would not have stuck it out this long in grad school.
Without my wife, Cara, and my son, Hank, life would be no fun at all and I would not be a functional person.

Finally, my parents, James and Patricia Tobin, and my brothers, Patrick and Eric Albertini, have supported me unconditionally all the years of my life and for that I am unspeakably grateful.
Attributions

I am the sole author of chapter 1. Chapter 2 consists of a manuscript that I authored with Rachel I. Wilson and Wei-Chung Allen Lee. Rachel Wilson and I wrote chapter 3. The author contributions for chapter 2 are as follows:

W.C.L. processed the tissue for EM and sectioned the series. W.T. and W.C.L. imaged it on the TEMCA. W.T. aligned the EM images into a volume. W.T. annotated the EM dataset and supervised the segmentation effort. W.T. and W.C.L. analyzed the EM reconstruction. W.T. performed the compartmental modeling. W.T., R.W., and W.C.L. designed the study and wrote the paper.
Chapter 1

General Introduction and Background

Neurons are network elements that transform synaptic input to spiking output. These transformations are steps in the generation of perceptions and behaviors. The form of the transformation implemented by a neuron depends critically on the nature of its synaptic inputs. Because synaptic connections are not binary, simply knowing that a pair of cells is connected is insufficient to fully describe their relationship. One of several key additional pieces of information is the strength of the connection, which can vary as a result of differences in the anatomy of connections. For example, connection strength can depend on the number of release sites involved, and their position on a postsynaptic cell as well as that cell’s morphology. Therefore, variations in such structural parameters can translate into variations in synaptic physiology. It stands to reason that some anatomical differences between connections have been selected for by evolution or produced by plasticity because of the advantage they confer to system performance. However, because all biological mechanisms have limited precision some anatomical variability likely represents noise and will constrain system performance. Yet other variations may have no significant functional effect and will therefore not be subject to selection. The goal of the work presented here was to characterize anatomical variability among the synaptic connections formed between sensory neurons and their primary excitatory targets in an antennal lobe glomerulus of Drosophila melanogaster. We have attempted to identify what aspects of this variability serve computational goals as well those that represent noise and how these may limit performance.
1.1 Anatomical Variability in Identified Cell Types

A common approach to simplifying nervous system complexity is to classify neurons into types (Masland, 2004). However, this naturally raises the question of how similar neurons of the same type are, both within and across individuals. Of particular relevance to the work presented here is the question of how similar such cells are in terms of their anatomy and synaptic connectivity. Furthermore, any variability that does exist may be either adaptive or represent noise and its significance depends on this distinction. Quantifying the amount of variability among neural connections that represents noise will allow us to place bounds on the optimality of neural wiring.

Invertebrate nervous systems are particularly amenable to addressing these issues. Their identifiable neurons regularly exhibit striking morphological and physiological stereotypy in all individuals of the species. Such clear similarities provide some measure of confidence that classifying these neurons as the same type is warranted.

A number of studies have used light or electron microscopy (EM) to directly measure variability in the morphology and synaptic connectivity of identifiable cells (Couton et al., 2015; Goodman, 1978; Mellert et al., 2016; Ohyama et al., 2015; Randel et al., 2014; Randel et al., 2015; Takemura et al., 2015). Some common themes emerge from this work and suggest the existence of general principles of anatomical variability among cells of the same type.

First, in spite of a high degree of stereotypy, the anatomy and synaptic connectivity of identifiable cells does indeed vary both within and across individuals.
Even when genetic background and environmental exposure is held constant, by making comparisons within the same individual or across isogenic animals raised together, morphology and synaptic connectivity is not completely invariant. The most frequent observation has been that different cells of the same type are strikingly similar in the shape and position of their large gauge processes. The structure of their fine processes, on the other hand, is often unique. Much less frequently, gross anatomical abnormalities are seen, such as mistargeted branches or even missing cells. Furthermore, the presence of major synaptic connections, consisting of more than a few synapses, was also found to be highly consistent across cells. However, the exact number of synapses that comprise these connections varies.

A second general principle that we can glean is that the degree of cell-to-cell variability appears to be cell-type specific. In the Goodman and Mellert et al. studies this was observed as different frequencies of gross morphological abnormalities across the cell types studied. Interestingly, Couton and colleagues found that even in the absence of aberrant morphology, different motor neuron types formed synaptic connections with a specific interneuron at different frequencies. This result suggests that variability not only in gross anatomy but synaptic connectivity may be cell-type specific or even connection type specific. However, the small number of observations in this paper prevents a strong conclusion on this point.

A third general principle might be that a cell type’s susceptibility to morphological variation is controlled, at least in part, by the genome. The Goodman and Couton papers documented strain specific differences in the characteristic frequency with which susceptible cell types actually manifested aberrant morphologies. The latter study
also showed that this frequency is not purely a product of the genetic background but could also be altered by the temperature experienced during development.

Takemura et al. 2015 raises another interesting possibility. That is, structural features may systematically co-vary in the nervous system. These authors found that a column of the *Drosophila* medulla lacking an identified interneuron showed a series of related anatomical abnormalities that likely represent compensation. Some neurons that normally received input from the missing cell formed unusual connections with other members of the same cell type as the missing cell in neighboring columns. Additionally, the column that lacked a cell was invaded by a branch of a neighboring interneuron of the same type as the missing cell. This is striking because these interneurons typically restrict their processes to a single column. These results suggest that variation in one aspect of network structure may cause compensatory modifications to other structural features. The absence of an identified cell and the growth of an unusual branch are rather large variations. However, it is possible that similar relationships exist between finer anatomical features. Furthermore, it could be that the expression of multiple anatomical features is somehow yoked together. This could represent a strategy to maintain robust system performance and would also lead to co-variation.

I think it is instructive to also consider findings from the similar field of functional parameter variability in identified invertebrate neurons. Functional parameters in this context often include the magnitude of synaptic and intrinsic conductances, as well as single-cell ion channel mRNA levels. Much of this work has been conducted in central pattern generating circuits, which offer the benefits of identified neurons, numerical simplicity and ease of experimental access.
Of particular relevance is the general finding that individual neurons and networks can show similar behavior in spite of significant underlying parameter variation (Goldman et al., 2001; Prinz et al., 2004; Roffman et al., 2012; Schulz et al., 2006). One explanation for this is that there are compensatory relationships between parameters (Grashow et al., 2010; MacLean et al., 2003). Alternatively, the system behavior under study may simply be insensitive to the value of some parameters. Indeed, it is interesting to note that the degree of variability itself can vary across parameters and cell types (Schulz et al., 2007). This suggests that some parameters may be more tightly regulated than others, perhaps because system performance is more sensitive to these values.

These results highlight the possibility that differences in anatomy may not straightforwardly translate to differences in neuronal behavior. Some anatomical differences between cells may be compensated for and others may simply have a minimal impact on performance. However, variability that is seemingly inconsequential in one condition may reveal itself to be consequential following a state change. For example, variability in the strength of a synapse in a *Tritonia* swim circuit was shown to have no behavioral effect under normal conditions (Sakurai et al., 2014). Following a lesion, however, the strength of this synapse was correlated with the degree of motor impairment. Additionally, it has been argued that variability with no obvious behavioral effects may result in diverse reactions to neuromodulators and drugs (Grashow et al., 2009).

Another important result of this work is that for a fixed value of one parameter, variation in related parameters can lead to a variety of system behaviors (Prinz et al., 2004). Therefore, knowledge of just one or a limited subset of parameter values is likely
to be insufficient to predict performance. This is a gloomy forecast for an experimentalist who would like to explain system behavior with a reduced set of parameter values. However, because functional parameters are often correlated, characterizing a few can reduce uncertainty about others (Roffman et al., 2012; Schulz et al., 2007; Tobin et al., 2009). A caveat here is that such correlations may change during the life of an animal under the action of neuromodulators or neural activity (Temporal et al., 2012; Temporal et al., 2014). Ultimately, measuring more parameters in each experiment is likely to result in more insight into the mechanistic basis of the preparation’s behavior. This would seem to be as relevant to the subject of anatomy as it is to cellular physiology.

Finally, it is interesting to consider the possibility that compensatory relationships may not be confined to separate functional and structural categories. It may be that variability in functional parameters is compensated for by variability in structural parameters or vice versa.

In summary, identified neurons often show a striking degree of stereotypy in their anatomy, connectivity and physiology. This does not mean, however, that all such cells are identical. Cells with similar anatomy on a gross level often differ in fine details. Cells that behave similarly may generate that behavior with variable underlying components. How variability is distributed in biological systems, the relationships between variability in different components and its significance for system performance are all fascinating avenues for future work.
1.2 Organization of the Early Olfactory System of *Drosophila melanogaster*

The work I describe here is focused on the early olfactory system of *Drosophila melanogaster*. This system offers a number of benefits for the study of variability in the anatomy and connectivity of identified neurons. These benefits include cell types that have been extensively physiologically characterized and whose computational roles are, to some extent, understood. Additionally, the anatomical organization of the system allows cell identification based purely on innervation pattern. Furthermore, there are many genetic tools and reagents that offer good experimental access to these neurons that will facilitate follow up work and future studies. Finally, a full description of the fine-scale anatomy and connectivity of the larval antennal lobe has recently been published (Berck et al., 2016). As our anatomical description of the adult antennal lobe develops this will allow interesting comparisons to be made between homologous structures in these two forms.

Olfaction in *Drosophila* begins in the antennae and maxillary palps. These peripheral sense organs house the cell bodies and dendrites of olfactory receptor neurons (ORNs), the primary sensory cells of the system. As a general rule, each ORN expresses a single type of olfactory receptor (OR) protein and each OR is expressed in many ORNs (Vosshall et al., 2000). These receptors define an ORN’s stimulus selectivity meaning that all ORNs expressing the same OR will respond to odors in a similar fashion (Hallem and Carlson, 2004). The axons of ORNs project bilaterally to innervate a mirror symmetrical pair of brain regions called the antennal lobes. Within each antennal lobe, all
axons from ORNs expressing the same OR target the same neuropil compartment called a glomerulus (Couto et al., 2005). There are approximately 50 glomeruli corresponding to a similar number of OR genes in the genome and functional types of ORN. Importantly, the spatial organization of glomeruli is stereotyped across individual flies. This makes it possible to identify any glomerulus in any fly brain based on its relative position alone. Within the glomerulus, ORNs form synapses on the dendrites of projection neurons (PNs). PNs are the major output cell type of the antennal lobes, projecting axons to higher order olfactory brain regions. Each PN typically restricts its dendrites to a single glomerulus and therefore receives input from only one type of ORN (Jefferis et al., 2001; Stocker et al., 1990). Furthermore, each PN receives input from all the ORNs innervating the same glomerulus (Kazama and Wilson, 2009). A collection of several hundred local neurons also innervates the antennal lobes. Most of these cells extend processes into multiple glomeruli and are GABAergic inhibitory neurons (Chou et al., 2010). An important fact about these interneurons is that their anatomy seems much less stereotyped across individuals than that of ORNs and PNs. These three cell types, ORNs, PNs and local neurons are the three major types found in the antennal lobes. It should, however, be kept in mind that this region contains processes from a diverse array of other neuron types including those that release modulatory substances (Carlsson et al., 2010).

The convergence of many ORNs of the same type onto each PN is a striking feature of the glomerular network architecture. It has been shown that this organization allows PNs to improve their response accuracy by effectively averaging their ORN inputs (Jeanne and Wilson, 2015). One reason this operation is beneficial is that ORNs of the same type show independent spiking activity (Kazama and Wilson, 2009). Thus, PNs are
able to average across many co-tuned inputs that carry independent noise. Another well-documented computation performed by antennal lobe PNs is the encoding of stimulus lateralization. Stimuli that activate ORNs in one antenna more strongly than the other also activate PNs on that side more strongly (Gaudry et al., 2013). This means that the lateral asymmetry of a stimulus can be calculated by comparing spike trains from the same type of PN in opposite brain hemispheres. This allows a walking fly to respond to such stimuli by turning towards the more strongly stimulated side, a behavior called osmotropotaxis.

To summarize, the antennal lobes of *Drosophila melanogaster* are comprised of three major cell types whose physiology, anatomy and organismal roles are relatively well understood. The spatial layout of the system as well as the relatively small number of identifiable cells in each glomerulus make it amenable to a study of anatomical variability among these cells.

### 1.3 Development of the *Drosophila* Glomerular Network

The topic of how the glomerular network develops is closely related to that of the structural variability of its components. Indeed, their variability is a reflection of the precision or regulation of a series of underlying processes that established their anatomy. These are the process of axon/dendrite targeting, morphogenesis and synapse formation. Little is known about how the fine-scale circuitry within a glomerulus forms. However, a picture of how the antennal lobe is patterned and how cognate ORN and PN classes are matched is developing.
The adult *Drosophila* antennal lobe is constructed during the pupal stage of development. During this period, the larval antennal lobe degenerates as the adult lobe begins to form alongside it (Jefferis et al., 2004). Larval ORN axons degenerate completely and persistent larval PNs remodel their dendrites to participate in the adult lobe. The first neurons to innervate the nascent adult lobe are PNs, which target their dendrites to type specific regions of the neuropil (Jefferis et al., 2004). The size of the region occupied by dendrites of a particular PN class is determined by several interactions. Expression of Dscam molecules in PNs promotes diffuse elaboration, likely through a self-repulsion mechanism (Zhu et al., 2006). It seems reasonable that minimizing self-fasciculation is important for maximizing the dendrite area free to interact with other cells with which the PN will form synapses. Conversely, expression of the molecule N-cadherin in PNs acts to restrict their dendrites to a single glomerulus presumably through homophilic dendro-dendritic interaction (Zhu and Luo, 2004). These two mechanisms reflect the need for PNs to both restrict their processes to a single glomerulus and to efficiently fill that space. After PN dendrites have coarsely patterned the developing lobe, ORN axons invade and target their cognate PNs (Jefferis et al., 2004). PN dendrites likely play a role in guiding ORN axon targeting. Evidence for this includes the observation that manipulations that cause dendrite mistargeting can result in a corresponding shift in ORN axons (Zhu et al., 2006). The process of ORN-PN partner matching is unlikely to be influenced by neural activity because it is largely complete before ORNs begin expressing olfactory receptor proteins (Clyne et al., 1999; Jefferis et al., 2004). Interestingly, it also seems likely that partner matching is accomplished before synapses between ORNs and PNs form (Devaud et al., 2003; Hong and Luo, 2014).
These last two observations highlight the possibility that the formation of synaptic connections is constrained by prior events in development. There is little information about the degree of fine-tuning of anatomy and synaptic connectivity that might occur following the onset of activity. Ablation of specific ORN or PN classes after activity onset does not seem to drive large-scale reorganization of the network (Berdnik et al., 2006). However, removal of ipsilateral ORN input to a glomerulus triggers an increase in contralateral axon density suggesting some plasticity is possible.

In summary, the development of a glomerulus in the *Drosophila* antennal lobe occurs in a step-wise fashion. First PNs target a subregion of the developing lobe, then ORN axons invade and target their cognate PN dendrites. This occurs before the onset of odorant receptor driven activity in ORNs and the development of ultrastructurally identifiable synaptic specializations. Thus, key steps in targeting and morphogenesis occur without instruction from the activity the circuit will eventually support. It is therefore likely that synaptic connection formation is constrained by developmental decisions that have already been made.

### 1.4 Summary of our Approach and its Limitations

Our goal in this work was to gain a better understanding of variability among the ORNs and PNs that innervate a glomerulus. Furthermore, we have tried to predict what the functional implications of this variability might be. Our approach was to generate a detailed anatomical description of the cells within a glomerulus using serial section transmission electron microscopy. We collected ~1900 thin sections from a single fly
brain for electron microscopy, a volume that encompassed both antennal lobes. We then chose a single glomerulus to focus on and reconstructed the morphologies and synaptic connectivity of its constituent ORNs and PNs in both hemispheres of the brain. This provided the anatomical information we desired at single synapse resolution. It is important to state that there were costs involved in taking this approach. One is that we were restricted to studying a snapshot of a single brain at the time of fixation. To explore the functional implications of our anatomical findings we build compartmental models of PN dendrites and their ORN inputs. We were able to use published electrophysiological measurements to constrain our model parameters (Gouwens and Wilson, 2009). However, these models were passive and we made no attempt to simulate PN spiking. Therefore, while they were useful tools that allowed us to identify interesting and non-obvious features of our data, they are an explicit simplification. Future work to overcome some of these limitations will be important to further clarify the extent, distribution and significance of structural variation in this system. To aid in this effort, we will make the full EM dataset that we generated in the course of this work public and freely available.
Chapter 2

Wiring Variations Among the Principal Neurons of an Antennal Lobe Glomerulus

2.1 Introduction

The wiring of a neural network is a key determinant of its function. In principle, each synaptic connection might have an optimal strength, as dictated by activity patterns passing through the synapses comprising that connection, as well as the computations that the connection ought to support. The strength of each connection will depend on many structural features, such as the number of presynaptic neurotransmitter release sites it contains, or the diameter of the postsynaptic dendrite. Therefore, it is fundamentally important to understand how the structure of synaptic connections can be systematically varied to enable specific neural computations, as well as the precision of these systematic variations.

A useful way to study this issue is to examine multiple instances of the same connection type. Studies of isogenic grasshoppers and worms, for example, have discovered anatomical variations in connectivity made by an identifiable neuron in different individuals (Goodman, 1978; Ward et al., 1975). These variations were interpreted as evidence of imprecision in developmental wiring programs (“connection noise”).
However, wiring variations may not necessarily reflect noise. For example, wiring variations might be adaptive if they systematically weight inputs according to their reliability. A recent study in the mouse found that an identifiable motor neuron can make structurally different connections on the left and right sides of the body, and this was suggested to be evidence of an adaptive learning rule that can fine-tune wiring based on neural activity patterns (Lu et al., 2009). Adaptive wiring variations might also emerge from homeostatic processes that systematically compensate for variations in neural activity patterns (Roffman et al., 2012). In short, wiring variations can be substrates for neural computations – rather than simply constraining neural computations.

In this study, we investigated wiring variations in an olfactory glomerulus of the *Drosophila* antennal lobe. The glomerulus is the basic unit of organization in the olfactory system (Chen and Shepherd, 2005; Su et al., 2009; Wachowiak and Shipley, 2006). In the adult fly, there are about 50 glomeruli in total. Each glomerulus receives feedforward sensory input from many olfactory receptor neurons (ORNs), and all the ORNs that project to the same glomerulus express the same odorant receptor, meaning they should all have similar odor responses (Hallem and Carlson, 2004; Vosshall et al., 2000). ORNs synapse onto projection neurons (PNs) that carry signals from the antennal lobe to higher brain regions. The dendritic arbor of a PN is typically confined to a single glomerulus (Hallem and Carlson, 2004; Stocker et al., 1990). Because a PN pools strong synaptic inputs from all the ORNs that target its cognate glomerulus, the PN can respond relatively quickly and reliably to odor stimuli (Bhandawat et al., 2007; Jeanne and Wilson, 2015).
ORN→PN connections are an ideal setting for studying wiring variations because there are many such connections per glomerulus, each with the same ostensible function. Moreover, these connections have been extensively studied using in vivo electrophysiological recordings and calcium imaging (Wilson, 2013). To comprehensively visualize the structure of these connections, we generated a serial section electron microscopy (EM) data set comprising both antennal lobes of an adult Drosophila brain. We focused our analysis on a specific glomerulus (DM6) whose cognate ORNs have been well-characterized (Couto et al., 2005; Hallem and Carlson, 2006) and whose postsynaptic PNs have been studied using in vivo intracellular recordings (Gaudry et al., 2013; Kazama and Wilson, 2008; Kazama and Wilson, 2009; Kazama et al., 2011; Nagel et al., 2015). We performed a dense reconstruction of all the ORNs and PNs corresponding to DM6 on the left and right sides of the brain. We then integrated our anatomical data with electrophysiological measurements to construct compartmental models of each reconstructed PN. These models allowed us to understand how structure and function are interrelated at individual connections, and how these relationships affect the specific computations that the PN performs.

We discovered three kinds of variations in ORN→PN synaptic connections. First, we found a systematic variation in the number of synapses per ORN→PN connection that compensates for differences in the size of PN dendrites. We used compartmental models to show how this sort of compensation can tightly regulate the postsynaptic impact of each ORN spike. Second, we found a systematic structural difference in the connections
made by ORNs onto ipsi- and contralateral PNs. Our compartmental models showed that this systematic structural variation can account for the known physiological differences between ipsi- and contralateral connections. This difference is likely critical to the fly’s ability to lateralize odor stimuli. Third, we found some non-systematic structural variation in ORN→PN connections that does not correlate with variation in ORN activity. We argue that this reflects developmental “connection noise” and we show how it can constrain a PN’s ability to count ORN spikes. Taken together, our results imply that certain structural parameters of these synaptic connections are systematically varied to enable specific neural computations, but the limited precision of synaptic structural control also represents a fundamental constraint on network performance.
2.2 Results

2.2.1 Cells comprising the glomerular micro-circuit

We used large-scale serial section transmission EM (Bock et al., 2011; Lee et al., 2016) to collect a volumetric data set comprising the anterior portion of one adult *Drosophila* brain (Figure 1A and 1B, and Movie S1). The series consisted of ~1900 sections acquired at ~4 x 4 x 40 nm/voxel, amounting to ~4 million camera images and ~50 TB of raw data. This data set spans both hemispheres of the brain, and it includes both right and left copies of the antennal lobe.

Three experts independently identified glomerulus DM6 in the EM data set by visual inspection based on a published light-level map (Couto et al., 2005). We then manually reconstructed all the ORNs and PNs targeting glomerulus DM6 (Movie S2) on both sides (Figures 1C-D and S1). In total, 53 ORNs innervated glomerulus DM6. Like most *Drosophila* ORNs, these ORNs project bilaterally (Couto et al., 2005; Stocker et al., 1990; Vosshall et al., 2000). However, we found that one right ORN and one left ORN projected only ipsilaterally. Therefore, each glomerulus contained the axons of 52 ORNs.

Interestingly, we found three “sister” PNs on the left side the brain and two on the right. This is likely to represent a developmental anomaly, because Gal4 lines that label DM6 PNs typically reveal three such cells in each glomerulus (Figure S2). In a later section, we will examine the consequences of this anomaly in more detail.
Profiles not identified as ORNs or PNs are referred to here as multiglomerular neurons. Most of these profiles are probably inhibitory local neurons, because this cell type is the most numerous and broadly-arborizing of the multiglomerular cell types in the antennal lobe (Chou et al., 2010; Lai et al., 2008; Lin et al., 2012; Yu et al., 2010). In addition, some of these profiles may be multiglomerular projection neurons, or neurons that project into the antennal lobe from other regions.

Every segment and synapse of every reconstructed neuron was reviewed by at least two independent annotators. To assess what our reconstructions may be missing, we quantified the percentage of cellular profiles presynaptic to PNs that were “orphans”, i.e. fragments that could not be connected to any neuron. Overall, the percentage of orphans was relatively small (6.8 ± 1.5%, mean ± SEM). This value was lower for the left glomerulus (4.4 ± 0.8%) than for the right glomerulus (10.4 ± 0.4%). Another study using essentially the same reconstruction strategy demonstrated that false continuations between fragments are easily detected and corrected during independent review by a second annotator, and are therefore very rare in the final reconstruction (Schneider-Mizell et al., 2016).
Figure 1: Cells and connections comprising the glomerular micro-circuit.

(A) Electron micrograph of a frontal section (76,000 × 58,000 pixels) from the anterior portion of the brain. Glomerulus DM6 is outlined.

(B) Zoomed-in view of a synapse. Red arrowhead demarcates a presynaptic specialization (T-bar). The long edge of the image measures 2 µm.

(C) Schematic of reconstructed cells. All ORNs and PNs within glomerulus DM6 were fully reconstructed. Not shown in this schematic are multi-gglomerular neurons (cells that interconnect different glomeruli), which were not fully reconstructed.

(D) 3-D rendering of a single ORN→PN cell pair viewed frontally. The ORN axon (blue) makes multiple synapses (red) onto the PN dendrite (green). The approximate region occupied by the DM6 glomerulus is circled with dashed lines. The PN cell body is represented as a sphere for display purposes.

(E) Top: synapses made by ORNs, expressed as a fraction of each ORN’s total pool of output synapses.

Bottom: synapses received by ORNs, expressed as a fraction of each ORN’s total pool of input synapses. “MG” denotes multiglomerular neurons.

(F) Synapses made by PNs and received by PNs, normalized in the same way.

(G) Number of synapses between connected pairs of cells, sorted by connection type. Each symbol represents a unitary connection.
Figure 1 (Continued)
2.2.2 Relative abundance of connection types

In our reconstructions, we identified every connection type known to exist within antennal lobe glomeruli of the adult fly (Rybak et al., 2016). Beginning with ORN output synapses, we found that ORNs delivered about one-third of their synaptic output to PNs (Figure 1E). Most of the remainder was delivered to multiglomerular neurons (Figure 1E). Because most multiglomerular neurons are likely inhibitory local neurons, this pattern emphasizes the important role of feedforward inhibition in the antennal lobe circuit.

ORN axon terminals are not just presynaptic elements – they are also postsynaptic to other neurons (Berck et al., 2016; Rybak et al., 2016). We found that DM6 ORN axons received most of their synaptic input from multiglomerular neurons (Figure 1E). This is consistent with physiological studies showing that inhibitory local neurons exert potent control of neurotransmitter release from ORN axon terminals (Olsen and Wilson, 2008; Root et al., 2011; Root et al., 2008). About a third of synapses onto ORN axon terminals originated from PNs and ORNs. It is not known how PN and ORN inputs might affect ORN axon terminals; in principle, they might either facilitate or suppress neurotransmitter release.

Turning to the PN’s perspective, we found that the PNs received most of their input (~75%) from ORNs, as expected (Figure 1F). PNs also received a sizeable input (~20%) from multiglomerular neurons. This is also expected, as paired electrophysiological
recordings have demonstrated the existence of functional inhibitory synapses from local neurons onto PN dendrites (Liu and Wilson, 2013; Yaksi and Wilson, 2010).

PN dendrites are known to contain presynaptic elements as well as postsynaptic elements (Ng et al., 2002; Wilson et al., 2004). In this regard, PNs are analogous to olfactory bulb mitral/tufted cells, which also release neurotransmitter from their dendrites onto other cells in the same glomerulus (De Saint Jan et al., 2009; Pimentel and Margrie, 2008; Urban and Sakmann, 2002). Within the DM6 glomerulus, we observed that PNs devoted almost all of their output synapses (~90%) to multiglomerular neurons (Figure 1F). PNs devoted a small part of their output to ORN axon terminals. Finally, every PN also made connections with all the other PNs in the same glomerulus, consistent with electrophysiological evidence for reciprocal synaptic interactions between sister DM6 PNs (Kazama and Wilson, 2009).

2.2.3 The structure and strength of excitatory connections

We will use the term “unitary connection” to refer to all the synapses between one presynaptic cell and one postsynaptic cell. Most of the unitary connections we detected were composed of multiple synapses – i.e., multiple contacts at distinct locations, each with its own presynaptic specialization. This is illustrated by the typical ORN-PN pair shown in Figure 1D (Figure S1, shows all ORN-PN pairs).
On average, unitary ORN→PN connections were composed of about 23 synapses (Figure 1G). In principle, a connection composed of so many individual synapses should be both strong and reliable. Indeed, physiological studies have shown that each ORN axon makes a strong and reliable excitatory connection onto every PN in its target glomerulus (Gaudry et al., 2013; Kazama and Wilson, 2008; Kazama and Wilson, 2009). An isolated ORN spike typically depolarizes a PN by about 5 mV, and the size of this unitary excitatory postsynaptic potential (uEPSP) is highly reliable from trial to trial. The average number of synapses that we detected per unitary ORN→PN connection is similar to that predicted by quantal analysis in whole-cell recordings (Kazama and Wilson, 2008) and also by light microscopy methods (Mosca and Luo, 2014).

As compared to ORN→PN connections, the other connections involving ORNs and PNs were weaker, as judged by the number of synapses they contained. Unitary PN→PN connections were composed of about 11 synapses, on average (Figure 1G). ORN→ORN connections and PN→ORN connections typically consisted of just one or two synapses. However, the influence of ORN→ORN connections in particular is likely to be non-negligible, because there are so many ORNs in total, and so ORNs collectively provide a major input to other ORNs (Figure 1E).
2.2.4 Compensatory variations in dendrite size and synapse number

Usually, three PNs reside in glomerulus DM6, with no systematic left-right asymmetry in cell number (Figure S2). However, in the specimen we analyzed, there were only two DM6 PNs on the right side (Figure 2A). The right PNs also had larger dendritic arbors as compared to the left PNs (Figure 2A), possibly because right PNs had fewer sister cells, and so had more space to fill. Because it is atypical to find only two PNs in this glomerulus, we conclude that an error has occurred in its development. Related to this error, we found a number of differences between the left and right versions of DM6 that provide insight into the circuit’s developmental program.

First, we found that the number of ORN synapses received by an individual PN was 53% higher on the right than on the left (Figure 2B). Interestingly, the magnitude of this asymmetry produced a similar total number of ORN→PN synapses in the left and right glomerulus. The number of multiglomerular neuron synapses received by an individual PN was also higher on the right than on the left (Figure 2C). Finally, individual PNs on the right formed more presynaptic contacts than did individual PNs on the left (Figure 2D). The differences in ORN→PN synapse number and PN dendrite size resulted in a similar synaptic density in left and right PNs (left PNs had 0.61, 0.63 and 0.57 ORN→PN synapses/µm; right PNs had 0.59 and 0.60 ORN→PN synapses/µm).
Figure 2: Connectivity compensates for a missing cell.

(A) Skeletonized 3-D renderings of reconstructed PNs. Cells are viewed parasagittally from the left. For each cell, the total path length of all dendrite segments is indicated; note that PNs on the right side of the brain have longer path lengths. Axons are indicated with asterisks.

(B) Synapses received by each PN from ORNs.

(C) Synapses received by each PN from multi-glomerular (MG) neurons.

(D) Output synapses made by each PN within the DM6 glomerulus.
Figure 2 (Continued)

A

path length: 1720 µm 1769 µm 1619 µm 2553 µm 2702 µm

B  ORN → PN

C  MG → PN

D  PN outputs
What do these findings mean for PN function? In particular, what does the asymmetry in ORN synapse number mean for PNs, given that ORNs are the main drivers of PN activity? To address this question, we constructed a passive compartmental model of each PN’s dendritic tree. The length and diameter of each dendritic branch was taken directly from our reconstructions (Figure 3A). The locations of all ORN synapses were also taken from our reconstructions. The specific resistance and capacitance of the PN dendritic membrane were taken from a previous electrophysiological study which measured these values directly (Gouwens and Wilson, 2009). That same study also deduced the conductance produced by a single quantum of neurotransmitter released at ORN→PN synapses. This measurement was used to model the synaptic conductance, which had the same amplitude and time course at all synapses following at presynaptic spike. In short, all the model parameters were taken directly from data. The model therefore provides a highly-constrained analytical tool for exploring the functional implications of 3-D ultrastructure data.

We used the model to determine if right and left PNs will respond differently to ORN spikes. For each of the 260 ORN→PN connections in our reconstruction, we inferred the corresponding unitary excitatory postsynaptic potential (uEPSP) in the PN cell body (Figure 3B). Surprisingly, the simulated somatic uEPSP amplitudes were almost identical in right and left PNs (Figure 3C). In other words, the overall strength of unitary connections was the same on the right and left. This is notable because of the substantial difference in the number of synapses per ORN→PN connection on the right and the left (Figure 2B).
Figure 3: Dendritic arbor size equalizes average unitary responses.

(A) Volumetric 3-D rendering of an EM reconstructed PN dendrite. (The cell body is represented as a sphere for display purposes.) Compartmental models fit to ultrastructural and electrophysiological data were used to simulate the voltage responses of each PN to synaptic input from ORNs. Synaptic conductances were simulated in the PN dendrite, and voltage responses were recorded in either the cell body or in the dendritic compartment where a given synapse was located. Each of the 5 reconstructed PNs was modeled in this way.

(B) Example voltage responses recorded at the cell body of a model PN. A miniature EPSP (mEPSP) is the response to a quantum of neurotransmitter. A unitary EPSP (uEPSP) is the response to one spike in a single presynaptic axon, i.e. the combined effect of all the mEPSPs generated by that axon. Shown here are the largest and smallest mEPSPs and uEPSPs in this PN. In the model, a spike always produces the same conductance at all synapses, and so variations in mEPSP amplitude must be due to variations in the position of synapses on the dendrite.

(C) There is no left-right difference in the amplitude of uEPSPs, measured at the cell body of each PN. (mean ± SEM computed across unitary ORN→PN connections, $P > 0.7$, permutation test, $n = 156$ left and 104 right unitary connections). Here and elsewhere, box plots show median, 25th percentile and 75th percentile. Whiskers indicate 2.7 SDs (99.3% coverage of normally distributed data); for clarity, outliers beyond the whiskers are not displayed; notches indicate 95% confidence intervals.
Figure 3 (Continued)

(D) There is a significant left-right difference in the amplitude of mEPSPs, measured at the cell body of the PN (mean ± SEM computed across all ORN→PN synapses, \( P < 0.0001 \), permutation test, \( n = 3013 \) left and 3066 right synapses).

(E) There is a significant left-right difference in the amplitude of mEPSPs, measured at the site of each synapse in the dendrite (mean ± SEM computed across all ORN→PN synapses, \( P < 0.0001 \), permutation test).

(F) There is a significant left-right difference in dendritic input resistance, measured across all model compartments (mean ± SEM computed across all PN compartments, \( P < 0.0001 \), permutation test, \( n = 5520 \) left and 6048 right compartments).

(G) There is a significant left-right difference in the attenuation of mEPSPs as they travel from the site of the synapse to the soma (ratio of somatic to dendritic amplitude, mean ± SEM computed across all ORN→PN synapses, \( P < 0.0001 \), permutation test)
Figure 3 (Continued)
To better understand this result, we decomposed uEPSPs into their elemental components—i.e., miniature excitatory postsynaptic potentials (mEPSPs). When we measured mEPSPs at the soma, they were much smaller in right PNs than in left PNs (Figure 3D). The difference in mEPSP amplitude also appeared when we measured each mEPSP in the dendrite, at the site of the synapse itself (Figure 3E), reflecting a lower dendritic input resistance in right PNs (Figure 3F). Moreover, in right PNs, mEPSPs also decayed significantly more as they propagated from the dendrite to the cell body (Figure 3G), reflecting a longer average path length from synapse to cell body (Figure 2A). These differences highlight the important effect of the dendrite’s overall morphology.

In summary, we find that right and left PNs have uniform average voltage responses to ORN spikes, in spite of their marked differences in dendrite size and synapse number. In principle, synapse number might be altered to compensate for dendrite size, or vice versa. We think it likely that synapse number is altered to compensate for dendrite size (see Discussion). Notably, the functional effects of this compensation could not have been deduced from simply counting the number of increased synapses: they required us to examine the interactions between different anatomical changes, using the compartmental model.
2.2.5 A basis for odor lateralization in the structure of synaptic connections

*Drosophila* can lateralize odors by comparing ORN spike trains arising from the right and left antennae. In response to a laterally asymmetric odor stimulus, flies will tend to turn toward the antenna that is stimulated more strongly (Figure 4A; Borst, 1983; Duistermars et al., 2009; Flugge, 1934; Gaudry et al., 2013). Because fly ORNs project bilaterally (Figure 4B), odor lateralization would be impossible unless there were an asymmetry between ORN connections in the ipsi- and contralateral antennal lobes. Electrophysiological recordings have shown that unitary ORN→PN connections are 30–40% stronger on the side of the brain ipsilateral to the ORN’s cell body (Gaudry et al., 2013). We therefore asked if there is a structural basis for this ipso/contra difference.

Indeed, we found that PNs received more input synapses from ipsilateral ORNs than from contralateral ORNs (Figure 4C). Accordingly, our compartmental model predicted a systematic difference in the amplitude of ipsi- versus contralateral uEPSPs (Figure 4D). There was no systematic ipso-contra difference in the placement of synapses onto the PN’s dendritic tree, as judged by the mean mEPSP amplitude at the PN soma (Figure 4E). There was also no significant difference in the total path length of ipsi- and contralateral ORN axons within the boundaries of glomerulus DM6 (Figure S3).

In short, we find that the difference in the electrophysiological properties of ipsi- and contralateral connections is explained by a single structural difference: PNs receive more synapses from ipsilateral than from contralateral ORNs. This finding represents a case where a particular behavior (odor lateralization) can be traced to a systematic variation in
structure of connections. It also raises the interesting developmental problem of how ORN axons distinguish ipsilateral from contralateral glomeruli and adjust synapse number accordingly.
Figure 4: A basis for odor lateralization behavior in ORN wiring.

(A) Flies turn toward lateralized odor stimuli, a behavioral response termed osmotropotaxis.

(B) Schematic of an ORN axon projecting bilaterally. Note that ipsi and contra are defined relative to the location of the ORN cell body. Unitary EPSPs in PNs driven by ipsilateral ORNs are systematically larger than those driven by contralateral ORNs (Gaudry et al., 2013). Successful odor lateralization requires that ipsi- and contralateral synapses are systematically different.

(C) PNs receive significantly more synapses from ipsilateral ORNs than from contralateral ORNs. Each connected pair of points represents a PN ($P = 0.0032$, paired-sample t-test, $n = 5$ PNs). These 5 PNs collectively have 133 ipsi and 132 contra connections.

(D) There is a significant ipsi-contra difference in mean modeled uEPSP amplitudes. Each connected pair of points represents a PN, with values averaged across all the connections received by that PN ($P = 0.0059$, paired-sample t-test, $n = 5$ PNs).

(E) There is no ipsi-contra difference in modeled mEPSP amplitudes. Each connected pair of points represents a PN, with values averaged over all the synapses received by that PN ($P > 0.05$, paired-sample t-test, $n = 5$ PNs). These 5 PNs collectively have 3504 ipsi and 2575 contra synapses.)
Figure 4 (Continued)

A

odor

odor

B

ipsi PN
contra PN

ORN

C

ORN synapses on PN dendrites

D

somatic uEPSPs in model PNs

E

somatic mEPSPs in model PNs
2.2.6 Inequalities among olfactory receptor neurons

Neural noise represents a fundamental challenge to the computational capacity of the brain. Individual neurons can minimize the impact of electrical noise by pooling many inputs carrying a common signal, but with independent noise (Faisal et al., 2008). The olfactory system is often cited as one of the clearest examples of this strategy. By pooling across many ORNs that express the same odorant receptor, a postsynaptic neuron should be able to dramatically improve the trial-to-trial reliability of its odor responses. If we assume that all sister ORNs are equally reliable, then the optimal strategy is to weight them equally. Alternatively, if some sister ORNs are more reliable than others, then the optimal strategy is to weight these inputs more heavily. We therefore examined the structure of ORN→PN connections for clues as to how ORNs are weighted.

We focused first on connections made by ipsilateral ORN axons, so as to remove the factor of ipsi-contra differences (Figure 5A). Even among ipsilateral ORN axons, we found substantial structural variation among the connections that they formed with PN dendrites. The main source of variation was the number of synapses per connection. This number varied over a wide range: for example, a typical PN received only 10 synapses from one ipsilateral ORN, but 36 synapses from another ipsilateral ORN (left PN1, Figure 5B). The number of synapses per connection was correlated with the physical proximity of ORN axons and PN dendrites (Figure S4), suggesting the number of synapses connecting each ORN-PN pair simply scales with the amount of axonal and dendritic contact.
Figure 5: Wiring inequalities among sister ORNs.

(A) Schematic of ORNs connected to a PN with different numbers of synapses. Arrow size represents the number of synapses each ORN forms on an ipsilateral PN dendrite.

(B-G) Histograms showing variation among ipsilateral ORN→PN connections. The histograms are horizontally scaled so that the means of all distributions are aligned, in order to enable a visual comparison of CVs.

(B) Number of synapses that each ipsilateral ORN makes onto left PN1.

(C) Analogous to (B) but pooled across all PNs. To enable pooling, we first normalize the number of synapses made by each ipsilateral ORN to the total number of ipsilateral ORN input synapses a PN receives. This yields the percentage contribution of each ORN to the ipsilateral synapse pool. The mean of this value is relatively consistent across the five PNs (0.037, 0.037, 0.037, 0.039, and 0.039), but there is a large variation within each PN.

(D) Mean mEPSP amplitude for connections made by ipsilateral ORNs onto left PN1. At each unitary connection, the mean mEPSP amplitude is computed across all the synapses that contribute to that connection. This value is relatively consistent across unitary connections.

(E) Analogous to (D) but pooled across all PNs. Each mEPSP value is normalized to the grand average for that PN. This value is consistent across all unitary connections, both within and across PNs.

(F) Summation efficacy at connections made by ipsilateral ORNs onto left PN1. Summation efficacy is computed as the amplitude of the connection’s uEPSP, divided by the linearly summed amplitudes of all the mEPSPs that comprise the connection. Again, this value is relatively consistent across unitary connections.
Figure 5 (Continued)

(G) Same as (F) but pooled across all PNs.

(H) Correlation between synapse number per connection and uEPSP amplitude. Each data point is a unitary connection ($n = 260$), with ipsilateral (unfilled) and contralateral (filled) connections indicated. For each PN, there is a strong and significant correlation (Pearson’s $r$ ranges from 0.993 to 0.999; $P$ ranges from $9.78 \times 10^{-48}$ to $1.34 \times 10^{-65}$ after Bonferroni-Holm correction for multiple comparisons, $m = 5$ tests).
Figure 5 (Continued)

A

variability in ipsilateral ORN → PN connections

ipsi ORNs

PN

B

example PN (left PN1)

C

all PNs

# of connections

0 10 20 30 40

synapses per connection

contribution of connection to PN’s total ipsi synapse count (%)

0 6

D

CV: 0.32

E

CV: 0.31

F

CV: 0.020

G

CV: 0.014

H

left PN1
left PN2
left PN3
right PN2
right PN1

model PN uEPSP amplitude (mV)

0 5 10

number of synapses within connection

# of connections

0 10 20 30

mean mEPSP amplitude (mV)

(normalized to PN’s mean)

0 0.79 0.94 1.05

summation efficacy

(uEPSP = sum of mEPSPs)

0 30

(i) connections

(ii) contra connections

CV: 0.043

CV: 0.041

CV: 0.014

CV: 0.014

CV: 0.014
To normalize for the fact that different PNs receive different total numbers of synapses, we divided the number of synapses per connection by each PN’s total synapse count (Figure 5C). This value expresses the contribution of each ORN to a PN’s total synapse pool. Across all connections, the coefficient of variation (CV) in this value was 0.31, consistent with previous estimates based on optical methods (Mosca and Luo, 2014).

By comparison, there was little variability among connections in average synapse potency. Synapse potency is defined as the amplitude of a simulated mEPSP at the soma of the compartmental model. Average synapse potency is just the average of all the mEPSP values associated with that connection. We found that average synapse potency was quite uniform across connections (Figures 5D and 5E). This is because each connection comprised many synapses, and there was little systematic variation across connections in the placement of the synapses on the dendrite.

Summation efficacy was also relatively consistent across ORN→PN connections (Figures 5F and G). Summation efficacy is measured as the amplitude of the uEPSP, divided by the summed amplitudes of all the mEPSPs that contribute to that connection. Most connections had summation efficacies near 0.9, indicating weakly sublinear summation.

Why are average synapse potency and summation efficacy so consistent (Figures 5D-G)? We obtain a similar level of consistency if we randomly allocate synapses to ORN axons. Specifically, we allocate to each ORN axon the same number of synapses as before, but
we draw synapses randomly (without replacement) from the pool of ORN→PN synapse locations. After shuffling, average synapse potency is still consistent across connections ($CV_{\text{real}} = 0.014, CV_{\text{shuffled}} = 0.009$), as is summation efficacy ($CV_{\text{real}} = 0.041, CV_{\text{shuffled}} = 0.037$; 1000 shuffles). Because each ORN axon makes synapses at many locations on the dendritic tree, the differences among an ORN’s many synapses tend to average out. This makes the qualitative properties of each connection quite similar (i.e., the properties that do not depend on synapse number).

In short, the major source of variation among ORN→PN connections is simply the number of synapses per connection. Our model indicates that this source of variation should produce a relatively large range in uEPSP amplitudes (Figure 5H). Different ORNs in the same antenna should have quite different effects on the PN membrane potential, with the strongest ORNs outweighing the weakest ORNs by almost 10-fold. Thus, it seems that PNs do not assign equal weight to ORNs from the same antenna. Rather, the PN response is likely to be dominated by only a fraction of the ORN population.
2.2.7 Connection noise in olfactory receptor neuron projections

In principle, the variation in ORN→PN connections might be the result of developmental noise. Alternatively, it might represent a strategy to optimize PN signals by weighting the most reliable ORNs more heavily. We cannot know for certain because we cannot compare the spike trains of the ORNs in question. However, we can find a clue by comparing different connections made by the same ORN. Paired electrophysiological recordings from sister PNs show that ORN spikes virtually always produce synchronous synaptic events in all ipsi- and contralateral target PNs (Kazama and Wilson, 2009). In essence, all sister PNs experience the same ORN spike trains. Therefore, if PNs weight ORNs according to their reliability, then those weights should be correlated across all five PNs in our sample. Our analyses thus far have indicated that synapse number is the main correlate of connection strength variability (Figure 5H), so we will focus on synapse number here.

Correlations across PNs are easiest to assess if we first normalize each ORN’s contribution by the total contribution from the antenna in question. For example, there are 26 ORNs in the right antenna, which collectively make 893 synapses onto PN1 on the right side. A typical ORN from the right antenna contributes 34 synapses, or 3.81% (34/893) of the total contribution from that antenna. By focusing on these percentages, we can make a fair comparison between all connections, because this normalization procedure controls for systematic right-left differences as well as ipsi-contra differences.
Using this metric of connection strength, we found correlations between the three PNs on the left side (Figure 6B), and also correlations between the two PNs on the right side (Figure 6C). Specifically, 7 of the 8 ipsilateral comparisons produced a significant correlation (Pearson’s $r$ ranged from 0.44 to 0.78, $P < 0.05$; the exception is left PN2 and left PN3, where $r = 0.36$, $P = 0.07$). However, there was no correlation between right and left PNs (Figure 6B and 6C; for the 12 contralateral comparisons $r$ ranged from -0.21 to 0.34, $P > 0.09$).

The failure to find correlations among all PNs argues that ORN→PN connection strengths are not optimized to match some feature of each ORN’s spiking behavior. If they were optimized, they would be correlated among all five PNs, because all PNs witness identical ORN spike trains (Gaudry et al., 2013). In other words, if some ORNs are more reliable than other ORNs in the same antenna, then all five PNs should assign greater relative weight to these inputs. Because we do not observe this sort of correlation, then it seems likely that at least some of the variation in ORN→PN connection strengths is due to “connection noise”. This connection noise should limit the accuracy of a PNs estimate of the stimulus based on incoming ORN spike trains.
Figure 6: Correlated and independent variation in ORN wiring.

(A) Schematics illustrating alternative scenarios: ORN connection weights may be correlated across PNs or uncorrelated. Arrowhead size represents the strength of ORN→PN connections. ORN spikes faithfully invade both ipsi- and contralateral axonal arbors, and so if connection weights are optimized to reflect the spiking properties of each ORN, then connection weights should be correlated across all ipsi- and contralateral PNs.

(B) Contributions of individual ORNs to each PN’s pool of ORN synapses. Values are expressed as the percentage contribution of each ORN to the pool of synapses from that antenna. Within each of these 10 vectors, values sum to 100%. Within an antenna, ORNs are sorted according to the average strength of all the connections that they form onto left PNs. Note that left PNs are correlated with each other, but not with right PNs.
Figure 6 (Continued)

(C) Same data as in (B), but now sorted by average strength of connections onto right PNs rather than left PNs. Note that right PNs are correlated with each other, but not with left PNs. When we examined pairs of PNs in the same quadrant, we found that 7 of 8 PN pairs were significantly correlated with each other (Pearson’s $r$ ranges from 0.44 to 0.78, $P < 0.05$, $n = 27$ or 26 unitary connections for each PN for each test, $P$ values are corrected for multiple comparisons, $m = 8$ tests). The one exception was that left PN2 and left PN3 were not significantly correlated (Pearson’s $r = 0.36$, $P = 0.07$ after multiple comparisons correction). When we tested pairs PNs on opposite sides of the midline (again testing separately for correlations among right ORNs and left ORNs), we found that none of the 12 PN pairs were significantly correlated (Pearson’s $r$ ranges from -0.21 to 0.34, $P$ always $> 0.09$, $n = 27$ or 26 unitary connections for each PN for each test; tests were not corrected for multiple comparisons, as none were significant).

(D) Average contribution of each ORN to the PNs on the right side, plotted against the average contribution of the same ORN to the PNs on the left. Percentages are calculated as in (B) before averaging across all the PNs on the same side of the brain. There is no significant correlation (Pearson’s $r = 0.18$, $P = 0.20$, $n = 53$ unitary connections for each PN).
Figure 6 (Continued)

A

positively correlated weights

uncorrelated weights

ORNs

B

sorted by left PNs

sorted by right PNs

left ORNs

right ORNs

left PNs

right PNs

C

D

mean contribution to right PNs (%) vs. mean contribution to left PNs (%)
2.2.8 Functional implications of connection noise

Our results imply that at least some of the variation in ORN→PN connection strengths is unrelated to the content of ORN spike trains. Variation that is unrelated to ORN spiking is expected to degrade the performance of the organism on olfactory tasks. To estimate how large this effect could be, we performed an experiment using our compartmental models. Specifically, we asked how accurately an observer can judge the number of ORN spikes fired during a particular time window, based on a model PN’s time-averaged voltage response (Figure 7A). It is important to note that all ORNs fire spontaneously even in the absence of odor (de Bruyne et al., 1999; de Bruyne et al., 2001). Thus, at the perceptual threshold for odor detection, the olfactory system must be able to detect an odor based on an increase in ORN spikes above the expected number of spontaneous spikes.

The perceptual threshold for odor detection is known to be in the regime of low ORN spike numbers (Bell and Wilson, 2016; Gaudry et al., 2013). We therefore first focused on small odor-evoked increases in ORN spiking. We chose a 200-ms window for counting ORN spikes because it can take roughly this amount of time for a fly to show a behavioral response to an odor (Bhandawat et al., 2010; Budick and Dickinson, 2006; Gaudry et al., 2013; van Breugel and Dickinson, 2014). During this counting window, in one antenna, the entire DM6 ORN population fires an average of 12 spontaneous spikes in the absence of an odor (see Experimental Procedures). We want to estimate how connection noise can affect the ability to detect an increase in ORN spiking above this baseline.
Figure 7: Functional consequences of variability in ORN wiring.

(A) Schematic of total spike count discrimination task. We measured how accurately a binary linear classifier could detect a small increase in ORN spike number, based on the time-averaged voltage in model PNs. Simulated Poisson spike trains were assigned to reconstructed ORN axons and fed into our PN models. Only ORNs ipsilateral to the PN were simulated. Over a 200-ms period, ORNs fired either 12 spikes (the average number of spikes during this time period that DM6 ORNs fire in the absence of an odor), or 13 spikes (representing a minimal odor stimulus). Based on the distribution of the time-averaged PN voltage ($\mu$) in training trials, we classified each test trial as “non-odor” or “odor” (12 or 13 spikes). We repeated this many times for each of the 5 model PNs. The same procedure was used to measure discrimination accuracy when the “odor” elicited increasing numbers of spikes (14 to 20 spikes).

(B) Performance of the classifier as a function of the number of “odor-evoked” spikes, above the baseline level of 12 spikes. Each blue line represents a different model PN. As in all previous simulations, the PN dendrite morphology and the locations of all ORN synapses are taken directly from our reconstructions. Green lines show that performance increases after we equalize the number of synapses per connection (by randomly reassigning synapses to ORN axons, so that all axons now have essentially equal numbers of synapses).
Figure 7 (Continued)

(C) Schematic of left-right spike count discrimination task. Here we simulated “non-odor” activity (12 spikes) in one antenna and “odor” activity (13-20 spikes) in the other antenna. Classification was based on the difference between the average of the mean PN voltage values on the left, minus the average on the right (mean (µ_left) – mean (µ_right)).

(D) Performance of the classifier as a function of the number of “odor-evoked” spikes (the left-right asymmetry). The two blue lines represent an odor stimulus in either the right antenna or the left antenna. Green lines show that performance increases after we equalize the number of synapses per connection.
Figure 7 (Continued)

A. total spike count discrimination task

B. equalized ORN → PN connections

C. left-right spike count discrimination task

D. reconstructed ORN → PN connections

- Mean ($\mu$) and $\mu_{\text{no odor}}$, $\mu_{\text{odor}}$
- Correct classification as "no odor"
- Correct classification as left > right
- Correct classification as left < right
- Performance curve for evoked ORN spikes above "no-odor" level
- Performance curve for absolute left-right spike count difference
We simulated ORNs as independent Poisson spike generators, each with the same average spike rate. Each ensemble ORN spike pattern was fed into a model PN, and we measured the time-averaged voltage response of the PN (Figure 7A). Even when ORN spike numbers are held constant, the model PN voltage responses vary from trial to trial, because the timing of ORN spikes varies. We repeated this procedure many times, and then trained a classifier to use the PN response to discriminate “no odor” trials (12 ORN spikes per antenna) from “odor” trials (13 – 20 spikes per antenna). We repeated this for all five PNs and their associated ipsilateral ORNs. Average performance was poor when the number of “odor-evoked” spikes was small, and performance improved as the number of odor-evoked spikes was increased (Figure 7B, blue lines).

To estimate how much the natural variation in ORN→PN connection strengths degrades PN performance, we repeated this task, but now equalizing the number of synapses per ORN→PN connection. Specifically, we randomly reallocated ORN→PN synapses to presynaptic axons so that the number of synapses per axon was as equal as possible, but with each PN dendrite receiving synaptic input at all the same physical locations as before. Now performance was markedly improved (Figure 7B, green lines). This simulation shows that the normal variation in the structure of ORN→PN connections can impair the ability of PNs to transmit information about ORN spike counts.

We also considered an odor lateralization task (Figure 7C). This time, the ORN spike count in one antenna was held at the “no odor” level (12 spikes), and ORN spike counts in the other antenna were driven up by a lateralized “odor” (to 13 – 20 spikes). In this
simulation, each PN received input from all its presynaptic ORNs (both ipsi- and contralateral ORNs). Based on the difference between the mean voltage in right PNs versus left PNs, we trained a classifier to discriminate “right odor” from “left odor”. Performance in this task was especially poor (Figure 7D, blue lines) because the classifier operates on the difference between two variables (right and left) that are contaminated by independent connection noise. Averaging the activity of PNs on the same side of the brain is of limited benefit because wiring noise is correlated among these PNs. When we artificially equalized the number of synapses per connection by randomly reassigning synapses to ORNs so that the number of synapses per axon was as equal as possible, we found that performance increased dramatically, as expected (Figure 7D, green lines). This simulation shows that the normal variation in the structure of ORN→PN connections can impair the ability of PNs to transmit information about right-left differences in ORN spike counts, particularly because connection noise is correlated within each half of the brain, but uncorrelated across the midline.
2.3 Discussion

2.3.1 Strengths and limitations of our data

An olfactory glomerulus represents a discrete and spatially compact neural network. The spatial scale of this network allowed us to comprehensively reconstruct the connections between every excitatory principal cell (i.e., every ORN and PN). Another strength of this data set is the ability to integrate comprehensive structure with \textit{in vivo} electrophysiology. DM6 ORNs and PNs generally have similar physiological properties across different individuals. Therefore, existing electrophysiological measurements of these neurons (Gaudry et al., 2013; Hallem and Carlson, 2006; Kazama and Wilson, 2008; Kazama and Wilson, 2009; Kazama et al., 2011; Nagel et al., 2015) are directly relevant to the anatomical data we analyzed. In particular, because we know the specific resistance and capacitance of the PN membrane, as well as the typical quantal conductance at ORN→PN synapses (Gouwens and Wilson, 2009), we were able to construct highly-constrained compartmental models based on our EM reconstructions. The conclusions we drew from the model were robust to measured variations in the model parameters derived from electrophysiological experiments (Figure S5).

One limitation we faced was our lack of knowledge about the active properties of PN dendrites, if any. In principle, voltage-gated conductances in PN dendrites might alter the integrative properties of PNs. However, active properties are unlikely to play a large role in PN synaptic integration, because the current-voltage relationships in PNs are fairly linear (Gouwens and Wilson, 2009), whereas in other \textit{Drosophila} neurons these
relationships can be strongly nonlinear (A.W. Azevedo & R.I. Wilson, in preparation). Thus, our passive models are good first approximations in this case.

Another limitation is the inability to directly measure the synaptic conductance of different synapses. Our model assumes that conductance is identical at every ORN→PN synapse. This assumption is likely reasonable, because a previous quantal analysis predicated on this assumption predicted a number of release sites per unitary connection (12 – 50 sites/connection; Kazama and Wilson, 2008) which is consistent with our observation of about 3 – 52 synapses per connection. In principle, we might be able to examine heterogeneity in synaptic conductance by measuring variations in vesicle numbers at different synapses, or variations in the area of the postsynaptic density (PSD). However, our aldehyde-based fixation conditions were not optimized to preserve vesicles. Moreover, although indirect evidence exists for the idea that PSD size correlates with synaptic strength at mammalian synapses (Matsuzaki et al., 2001; Nusser et al., 1998; Takumi et al., 1999), it is unclear whether this applies to Drosophila synapses. In future, it would be valuable to develop methods to correlate the fine features of Drosophila central synapses with synaptic conductance.
2.3.2 Structural correlates of connection strength

We can think of connection strength as being determined by three major factors. The first is the number of synapses comprising that connection. The second is the conductance at each of those synapses. The third is the filtering of those conductances by the postsynaptic dendrite. We cannot measure the conductance at each synapse in our reconstruction, but our reconstruction informs us about the other two factors, and our results imply that the first of these factors is particularly important.

Notably, we found that the number of synapses per connection was strongly correlated with the strength of ORN→PN connections. The comparison between ipsi- and contralateral synapses represents the clearest example of this correlation, because we know from prior electrophysiology experiments that ipsilateral connections are 30 – 40% stronger (Gaudry et al., 2013). Here, we discovered that ipsilateral connections contain ~35% more synapses per connection (Figure 4C). This result argues that the difference in the number of synapses per connection is the main difference between ipsi and contra connections. By extension, we can infer that there is not a sizeable difference in the conductance at ipsi- and contralateral synapses, although we cannot measure the conductance at each synapse directly. We also found no difference in the way that ipsi-contra synapses are filtered by the PN dendritic tree, as evidenced by the fact that there is no ipsi-contra difference in simulated mEPSP amplitudes (Figure 4E). In short, the number of synapses per connection appears to be the dominant structural feature underlying the systematic difference between ipsi- and contralateral connections.
Interestingly, from the perspective of an individual PN, there was little variation across
ORN connections in the average strength of the synapses that comprised each connection
(Figure 5E). The efficacy of mEPSP summation at the level of uEPSPs was also notably
consistent across these connections (Figure 5G). Thus, insofar as our model accurately
represents the structure of each PN dendrite, it predicts that dendritic filtering has an
essentially uniform effect on all ORN→PN connections. This uniformity arises because
each connection is composed of many synapses, and synapses made by a given ORN
axon tend to be placed onto the dendrite in a relatively unbiased fashion. In essence, each
connection is composed of many quasi-random “samples” of dendritic filtering
properties, and so the average effect of dendritic filtering is similar across connections.

2.3.3 Co-variation in cell number, dendrite size, and synapse number

Although Drosophila neural networks are sometimes regarded as highly stereotyped, in
fact many networks exhibit slight variations in neuron number. In the optic lobe, a recent
EM study analyzed 7 repetitions of a modular neural network that normally contains 23
uniquely identifiable cells. In 3 of the 7 networks, one cell that ought to be present was in
fact missing (Takemura et al., 2015). If errors like this were unbiased, then this result
would imply that each neuron in the fly brain would be absent about 2% of the time, on
average (given 3 missing cells in 7×23 observations). Takemura et al. (2015) found that
in the case of one missing cell, a homologous cell in a neighboring column sent an extra
branch into the vacated space, where it received synapses from the normal presynaptic
partners of the missing cell. Thus, when a cell is missing, there can be compensatory
changes in wiring.
Small variations in antennal lobe PN numbers have been inferred previously based on Gal4 expression patterns, which show brain-to-brain variations in PN cell counts on the order of 5% (Tanaka et al., 2004). Indeed, based on Gal4 expression, we find that there are normally 3 PNs in each copy of glomerulus DM6, and only occasionally do we find 2 or 4 (Figure S2). The brain selected for large-scale serial section EM turned out to contain only two PNs on the right side. In this anomalous glomerulus, the dendrites of the remaining PNs were larger, presumably because they had more space to fill. Moreover, there was also a compensatory increase in synapse numbers per PN, so that the total number of synapses per glomerulus was similar on the left and right.

Our compartmental models allowed us to infer the functional consequences of these concerted changes in PN dendrite morphology and ORN→PN synapse numbers. Remarkably, taken together, these anatomical changes created completely normal PN responses to simulated ORN spikes: in the glomerulus where one PN was missing, the up-regulation in synapse number per ORN→PN connection was neatly balanced by the increased size of PN dendrites. As illustrated by classic work at the neuromuscular junction, increasing the size of a postsynaptic compartment produces a lower input resistance, and so each quantum of neurotransmitter produces a smaller depolarization (Katz and Thesleff, 1957). In each of the larger PNs, each presynaptic ORN spike should release more quanta than normal, but the postsynaptic voltage response to each quantum will be smaller. Thus, as a result of the counterbalanced changes in synapse number and dendrite size, the PN response to individual ORN spikes is essentially normal.
Counterbalanced effects like this can result from homeostatic mechanisms in the developing central nervous system. For example, in the larval ventral nerve cord, a decrease in presynaptic neurotransmitter release can elicit compensatory growth in postsynaptic dendrites (Tripodi et al., 2008). Moreover, there is direct evidence that the electrical properties of the dendrites of antennal lobe PNs can instruct changes in ORN→PN connections. One study used cell-specific K\(^+\) channel overexpression to decrease a PN’s input resistance, and found a compensatory increase in unitary excitatory synaptic currents at ORN connections onto that PN (Kazama and Wilson, 2008). That result argued that PN dendrites can up-regulate synaptic current to achieve sufficient levels of depolarization.

Together, these findings suggest the following scenario. When one PN failed to develop, the remaining PNs grew larger dendrites, and then synapse number increased to compensate for increased dendrite size. This scenario is consistent with the well-described instructive role of PN dendrites in ORN axon development: PN dendrites form a glomerular map prior to the arrival of migrating ORN axon terminals (Jefferis et al., 2004).

This scenario is reminiscent of the “size matching” principle that governs the development of vertebrate neuromuscular junctions, where the size of a muscle is matched to the size of the axon’s terminal arborization, thereby ensuring that large muscles (with low input resistance) receive a larger quantal content per presynaptic spike
(Kuno et al., 1971; Lichtman et al., 1987). Here too, the expansion of the postsynaptic cell seems to be primary, with the elaboration of the presynaptic arbor occurring in response (Balice-Gordon et al., 1990; Balice-Gordon and Lichtman, 1990).

2.3.4 Developmental noise in wiring

We found that the number of synapses per ORN→PN connection was quite variable. As a result, ORN→PN connections gave rise to simulated uEPSP amplitudes ranging from 1.6 to 10 mV (Figure 5H). If all ORNs were functionally identical, this sort of variation would be non-optimal, because each PN’s response would be dominated by a relatively small fraction of its presynaptic ORN axons. Indeed, our simulations showed that this sort of variation can substantially impair a PN’s ability to accurately transmit information about total ORN spike counts, as well as right-left differences in ORN spiking (Figure 7). Our simulations suggest that connection noise may be a factor limiting perceptual acuity.

The discovery of connection strength variability per se is not surprising: it was already clear that connection weights in the Drosophila brain can be variable. In the medulla of the optic lobe, Takemura et al. (2015) tabulated instances of connection motifs repeated across columns, and found that the CV of synapse number per connection ranged from 0.08 to 0.87, depending on connection type. In principle, this sort of variation may be either noise or evidence of adaptive plasticity. For example, systematic variations in upstream input (inherited from earlier layers of visual processing) might drive adaptive activity-dependent changes in the number of synapses per connection. Here, we focused on primary afferent synapses, so any systematic upstream variations are limited to
variations in ORN spike trains. Moreover, we know that all DM6 PNs witness identical ORN spike trains, because ORN spikes travel faithfully across the midline to invade both ipsi- and contralateral glomeruli (Kazama and Wilson, 2009). This fact allowed us to test the hypothesis of adaptive plasticity by reconstructing all the synapses that each ORN axon made onto all PNs. We found that the variation in synapse numbers was not faithfully correlated across all PNs (Figure 6), and so some of this variation is likely random – i.e., unrelated to ORN activity.

Intriguingly, we found that synapse number variations were correlated across sister PNs on the same side of the brain, even though they were uncorrelated on the opposite sides of the brain. In principle, this might be evidence of incomplete adaptive plasticity – plasticity that works at ipsilateral connections but somehow fails at contralateral connections. More likely is the scenario of correlated developmental noise – e.g., some ORN axons may simply arrive sooner at the ipsilateral glomerulus, and so may form more physical contact with ipsilateral PNs, and thus more synapses. This sort of correlated developmental noise may be one reason why sister PNs on the same side of the brain display such high levels of correlated electrical noise (Kazama and Wilson, 2009).

As we show here, sister PNs on the same side of the brain are dominated by the same pool of ORNs. These ipsilateral sister PNs converge onto higher-order neurons, which are especially sensitive to correlations in sister PN spike times. As a result, sister PN spike timing correlations represent a functionally-relevant constraint on circuit function which can affect both the speed and accuracy of odor stimulus responses (Jeanne and Wilson, 2015).
2.3.5 Comparison between adult and juvenile networks

In the larval antennal lobe, there are 21 glomeruli, as compared to ~50 in the adult. Each glomerulus in the larva is relatively simple: it contains just one ORN axon and one uniglomerular PN dendrite (Python and Stocker, 2002). The larval antennal lobe connectome has just been reconstructed (Berck et al., 2016), and it is instructive to compare our results with the results of that study. In both the larva and the adult, the pattern of binary connectivity between ORNs and PNs is highly precise: there are almost no “missed” ORN→PN connections. Also, ORNs distribute their synaptic output in a similar way in both the larva and the adult. In both cases, the majority of ORN synapses are formed onto multiglomerular neurons, with approximately a third of ORN output synapses devoted to PNs.

There are also distinct differences between the larva and the adult. In the larva, the average ORN→PN connection contains ~70 synapses, whereas in the adult, it contains 23 synapses. Thus, the increased number of ORNs in the adult is partly compensated by a decrease in the number of synapses per connection. Another distinctive difference is in the control of ORN output. In the larva, almost all synapses onto ORNs arise from multiglomerular neurons. In the adult, most synapses onto ORNs arise from multiglomerular neurons, but a substantial minority arise from PNs and ORNs. This suggests that the adult network may exert more complicated control of ORN neurotransmitter release. In future, it will be interesting to extend these comparisons to
the domain of multiglomerular neuron networks, which are complex and intriguing in the larva (Berck et al., 2016).

### 2.3.6 Variations in the connectome: signal and noise

The brain’s computational power would be substantially reduced if all synaptic connections were identical. From this perspective, systematic variations in connection strength are evidence of the brain’s functional capacity – the capacity to match a connection’s strength to its required function. Our results show how systematic variations in connection strength can arise as a result of systematic differences in the number of synapses per connection.

On the other hand, unsystematic wiring variations (“connection noise”) must limit the capacity of every neural system. Some of these noisy variations can be balanced by homeostatic changes to other parameters, including synaptic parameters (Prinz et al., 2004; Roffman et al., 2012). Our findings provide insight into the mechanisms underlying such compensatory changes, but our results also argue for the existence of residual non-optimal wiring variations that can demonstrably impair neural computations.

Large-scale EM offers an unprecedented opportunity to study all these variations – and co-variations – in brain neural network wiring. *Drosophila melanogaster* is likely to be the next organism whose brain is fully mapped at the connectomic level. As such, it provides an opportunity to gain insight into the causes and consequences of systematic and noisy variations in network architecture.
2.4 Experimental Procedures

2.4.1 EM material preparation

The brain of an adult *Drosophila melanogaster* female (aged 8-10 days post-eclosion, genotype GH146-GAL4/+; UAS-CD2::HRP+/+) was immobilized by cooling on ice, and then submerged in a drop of fixative (2% paraformaldehyde/2.5% glutaraldehyde in 0.1 M cacodylate buffer with 0.04% CaCl$_2$ for membrane stabilization). The head capsule was opened to allow fixative to access the brain before dissection (Meinertzhagen, 1996). Following dissection, the brain was processed for serial-section transmission EM. The dissected brain was post-fixed and stained with 1% osmium tetroxide/1.5% potassium ferrocyanide, followed by 1% uranyl acetate, then lead aspartate (Walton, 1979), then dehydrated with a graded ethanol series, and embedded in resin (TAAB 812 Epon, Canemco). Approximately 1900 serial thin (<50 nm) sections were cut on an ultramicrotome (Leica UC7) using a 35 degree diamond knife (EMS-Diatome) and manually collected on 1×2 mm dot-notch slot grids (Synaptek) that were coated with a pale gold Pioloform support film (Ted Pella), then carbon coated and glow-discharged. Grids were subsequently post-stained with uranyl acetate (saturated) in 50% methanol and 0.2% lead citrate.
2.4.2 Large-scale TEM imaging and alignment

We imaged the ~1900 sections using a custom-built Transmission Electron Microscope Camera Array (TEMCA) (Bock et al., 2011; Lee et al., 2016). Acquired at 4 nm/pixel in plane, this amounted to ~50 terabytes of raw data comprising ~250 million cubic microns of brain and > 4 million (4000×2672 pixel) camera images. Magnification at the scope was 2000×, accelerating potential was 120 kV, and beam current was ~90 microamperes through a tungsten filament. Images suitable for circuit reconstruction were acquired at a net rate of 5-8 MPix/s. The series was aligned using open source software developed at Pittsburgh Supercomputing Center (AlignTK) (Bock et al., 2011; Lee et al., 2016). The aligned series was then imported into CATMAID (Saalfeld et al., 2009) for distributed online visualization and segmentation. Within the portion of the volume spanned by the DM6 glomeruli, there were 9 single-section losses, 2 instances of 2-section losses, 1 instance of 3-section losses, and 2 instances of 4-section losses (losses refer to consecutive sections). Across the entire series of ~1900 sections there were 50 single-section losses, 16 instances 2-section losses, 10 instances of 3-section losses, 3 instances of 4-section losses, 3 instances of 5-section losses, and one instance of a 6-section loss. Folds, staining artifacts, and cracks occasionally occurred during section processing, but were typically isolated to edges of our large sections and therefore did not usually interfere with manual segmentation.
2.4.3 Reconstruction and verification

We reconstructed the arbors of ORNs and PNs in the EM dataset by using CATMAID to manually place a series of marker points down the midline of each process to generate a wire-frame model of the axonal and dendritic arbors (Lee et al., 2016; Saalfeld et al., 2009). We identified synapses using a combination of ultrastructural criteria – namely, the existence of a presynaptic T-bar, presynaptic vesicles, a synaptic cleft, and postsynaptic densities. The presence of most, though not necessarily all, of these features over multiple sections was required for a synapse to be annotated. PNs were easily identifiable based on having dendrites restricted to DM6 and axons projecting into the inner antennocerebral tract. Annotators began by identifying putative PNs within the DM6 volume (based on their large gauge processes), and then traced the wire-frame structure of each PN dendrite while also comprehensively annotating each PN input synapse and output synapse. This procedure follows a previously described and validated protocol for manual tracing in serial section TEM data sets such as ours (Schneider-Mizell et al., 2016). Subsequently, all profiles presynaptic to each PN were annotated in the same manner. Profiles were categorized as ORNs if they arrived in the antennal lobe from the antennal nerve bundle; all such profiles innervated a single glomerulus either bilaterally (in the case of 51 ORNs) or unilaterally (in the case of 2 ORN). Because ORN axons travel from the antennal nerve to DM6 in a distinctive trajectory, it was clear even before an ORN exited DM6 that it was indeed an ORN. Profiles not annotated as either PNs or ORNs were categorized as multiglomerular neurons; all such profiles presynaptic to PNs were traced until they reached the border of DM6 before their tracing was
suspended. The multiglomerular neurons in DM6 likely include local neurons, multiglomerular PNs, and neurons innervating the antennal lobe from other brain regions (extrinsic neurons). For all reconstructed neurons included in our analysis, at least one additional independent annotator(s) verified the tracing by working backward from the most distal end of every process. Due to the oblique orientation and fine calibre of axons traveling through the anterior commissure, it is formally possible that ORN axon profiles might be mis-traced in this region, and so to verify our reconstructions of ORN axons in the region of the commissure, we re-imaged sections containing DM6 ORN axons in the commissure at higher magnification (20,000×). We then aligned the higher-resolution data set to the lower-resolution data set, and an additional independent annotator (who was blind to the original reconstructions) was assigned to trace all the DM6 axons through the commissure.

2.4.4 Labeling DM6 PNs for cell counting

To count the number of PNs that are normally present in a DM6 glomerulus, we labeled and counted these cells in five additional flies. We used NP3481-Gal4 to drive expression of photoactivatable GFP (PA-GFP) (Datta et al., 2008; Patterson and Lippincott-Schwartz, 2002) in DM6 PNs, along with several other PN types (Tanaka et al., 2012). By selectively photoactivating within the neuropil of DM6, we could photolabel the DM6 PNs alone, and then count the number of PNs innervating that glomerulus. Photoactivation was performed using a custom built two-photon laser-scanning microscope. We first imaged the antennal lobe at 925 nm and low laser power to identify DM6. After defining volumes of interest restricted to the core of the glomerular neuropil
based on these images, PA-GFP was photoconverted by imaging through the volume with 710-nm light. In each photoactivation block, we moved through the z depth of the volume of interest with 0.25-µm steps. Each glomerulus was subject to three photoactivation blocks at intervals of five to ten minutes. After PA-GFP is photoactivated in the glomerular neuropil (i.e., axons and dendrites), it diffuses into the somata of cells. We then imaged each brain using an Andor XD spinning disk confocal microscope equipped with a Yokogawa CSU-X1 spinning disk unit and a Zyla 4.2 CMOS camera. For this imaging we used laser illumination at 488 nm. We found 3.1 ± 0.57 (mean ± SD) photoactivated DM6 PN somata on each side of the brain in 5 flies (10 glomeruli total).

2.4.5 Compartmental models

To generate compartmental models, we first inflated our wire-frame reconstructions of PNs to create a representation of the entire volume of each dendritic segment. We did this in the CATMAID environment by measuring the average neurite caliber between each pair of skeleton branch points. We then used this value as the radius of the distal branch point (relative to the soma) and all nodes leading up to the proximal branch point. This process was repeated until the entire skeleton was inflated.

Next, we exported PN morphologies along with ORN input synapse locations as neuroML 1.8.1 models (Gleeson et al., 2010). Using the software tool neuroConstruct (Gleeson et al., 2007), we defined PN membrane properties and synaptic conductances, and subsequently exported these models to the NEURON simulation environment (Hines and Carnevale, 1997). Additionally, we used neuroConstruct to remesh the PN models to
ensure each segment had an electrotonic length between 0.1 and 0.0001. We gave PN membranes uniform, passive properties. A previous experimental study (Gouwens and Wilson, 2009) used electrophysiological recordings from PNs to derive values for their specific membrane resistance (20.8 kΩ cm²), specific membrane capacitance (0.8 µf/cm²), and specific axial resistivity (266.1 Ω cm). The measurements of that study were taken from DM1 PNs, so in order to use these measurements in our study, we assume that the intensive (size-independent) properties of DM6 PNs are similar to those of DM1 PNs. The ORN to PN synaptic conductance waveform we used was also adapted from this study. This was modeled as the sum of two exponentials, with a rising time constant of 0.2 ms and a decay time constant of 1.1 ms. Gouwens and Wilson (2009) modeled the maximum synaptic conductance as having a value of 0.27 nS (it was incorrectly reported in that paper as $2.7 \times 10^{-4}$ nS, but the value used was actually 0.27 nS); we used a slightly different value here (0.1 nS) because this produced more realistic uEPSP amplitudes (on average roughly 5 mV).

To measure the amplitude of individual mEPSPs, we sequentially activated individual synapses in the modeled PN dendrite, allowing enough time (200 ms) between events for the PN membrane potential to decay to baseline. We recorded PN voltage responses either at the cell body (somatic mEPSPs) or within the compartment where the synaptic conductance was activated (dendritic mEPSPs). To simulate unitary EPSPs, we synchronously activated all synapses from an individual ORN. In this case we always measured the PN voltage response at the cell body (somatic uEPSPs).
2.4.6 Spike Count Discrimination Classifier

We modeled the ORNs ipsilateral to each PN as independent Poisson spike generators. Spike trains in which two spikes in the same neuron occurred at an interval < 4 ms were rejected, in order to create a refractory period. Each modeled ORN spike train was randomly assigned to an ORN axon. The mean spontaneous firing rate of the DM6 ORNs cannot easily be measured from single-sensillum recordings on the antenna because the sensillum which houses DM6 ORNs is the ab10 sensillum (Couto et al., 2005), which is small and has remained undetected in surveys of single-sensillum physiology (de Bruyne et al., 2001; Hallem and Carlson, 2004). We therefore measured the mean spontaneous firing rate of DM6 ORNs by measuring the rate of large spontaneous EPSCs in voltage-clamp recordings from DM6 PNs in a re-analysis of data collected from DM6 PNs for a previously published study (Gaudry et al., 2013). In all recordings we analyzed, the contralateral antenna had been removed just before the recording, so PNs were receiving spiking input from ipsilateral ORNs only. The rate of these events was 58 Hz, and so dividing by 26.5 ORNs, we obtain 2.2 spikes/s/ORN. This method (using spontaneous EPSC rates) has been shown to provide a good agreement with single-sensillum recordings of ORN spike rates in the case of a different glomerulus, glomerulus DM4 (Kazama and Wilson, 2008). Multiplying the estimated spontaneous ORN spike rate of 2.2 spikes/s by a window of 200 ms and rounding to the nearest integer yields a basal “no odor” value of 12 spikes.

In each trial, the ipsilateral population of 26 or 27 ORNs fired a specified number of spikes within the first 200 ms, ranging from 12 to 20, and no spikes in the second 200 ms.
This allowed the PN membrane potential returned to baseline by the end of each trial. We then used the time-averaged PN membrane potential, recorded at the soma, to train and test a linear classifier to discriminate incoming spike counts. For each of the 5 model PNs, we ran 2500 trials for training and 2500 independent trials for testing. We initially performed this exercise using model PNs based directly on our reconstructions, where each ORN spike activated all synapses attributed to that ORN in our reconstruction. Subsequently, we artificially equalized the number of synapses per ORN axon in the following manner. We defined a pool of synapse locations on the PN dendrite corresponding to all the synapses made by ipsilateral ORNs onto that PN. We then allocated synapses arbitrarily and evenly to ORNs by drawing from this pool (without replacement) until synapses were re-allocated. When the total number of ipsilateral ORN synapses was not evenly divisible by the number of ipsilateral ORNs, the remainders were randomly assigned to simulated ORNs. When synapse numbers are artificially equalized in this manner, summation efficacy increases, and so uEPSP amplitudes increase. In order to keep average uEPSP amplitudes the same as before, the maximum conductance of our synapse model was reduced to 0.0958 nS. Thus, our synapse equalization procedure made uEPSP amplitudes more uniform across connections without changing the mean uEPSP amplitude. As before, for each of the 5 model PNs, we ran 2500 trials for training and 2500 independent trials for testing. Synapses were independently re-allocated in each trial.
2.4.7 Lateralization Classifier

The procedure here was the same as for the spike count classifier, except in every trial we modeled ORNs in the right antenna as well as ORNs in the left antenna, and all PNs received both right and left ORN input. On any given trial, the ORNs in one antenna fired 12 spikes, and the ORNs in the other antenna fired 13 to 20 spikes. In every trial, both right and left ORN spike trains were fed into the dendrites of all 5 PN models. We then used the means of the resulting PN responses to train and test a linear classifier to discriminate trials in which right or left ORNs fired more spikes. In the equalized case, we equalized synapse numbers independently for each PN-antenna combination. For example, we forced all ORNs in the right antenna to have equal contributions to right PN1, and we also forced all ORNs in the left antenna to have equal contributions to right PN1, but the average asymmetry between ipsi- and contralateral connections was preserved. In the equalized case, the maximum conductance of our synapse model was reduced to 0.0958 nS, as before.
2.4.8 Statistics

The number of observations of any given variable was dictated by the number of cells and synapses in glomerulus DM6, and so was not predetermined using statistical methods. Statistical comparisons between sample distributions were done with Permutation tests (i.e. Monte Carlo-based Randomization tests) unless otherwise noted. Permutation tests were used because they do not assume the underlying distributions are normal, and because observations do not need to be independent. For Permutation tests, we computed the incidence of differences between means or Pearson's linear correlation coefficient of randomly drawn samples from combined sample distributions exceeding the empirical difference.

2.4.9 Code and Data Availability

Custom code is available upon request. The aligned EM dataset will be made a freely accessible resource at http://neurodata.io/projects/XXX/.
Chapter 3

Conclusion

In the course of this project we have documented several forms of structural variability that exist among cells and connections in the glomerular network. Additionally, we have tried to predict functional implications of our findings. The EM strategy we took in pursuing these goals allowed us an unprecedented view of the detailed anatomy of this system. We integrated this anatomy with known electrophysiological parameters to model the behavior of reconstructed cells. These models revealed plausible functional consequences of structural variability that were not obvious given the anatomy alone. The combination of comprehensive detailed anatomy and data-constrained modeling make the study unique in this particular system. However, the limitations of our approach also leave many intriguing questions unanswered.

One particularly fascinating topic we could not address is that of the mechanisms underlying the generation of structural variability among cells of the same type. Hints may be provided by a clearer understanding of the development of the glomerulus at single cell resolution. For instance, it could be that individual ORN axons arrive at the developing glomerulus in a staggered fashion. Perhaps this contributes to the inequalities between cells that we observed. Early arriving ORNs may initially be able to form synapses on PNs without competition from other ORNs for space or growth factors. By capturing more resources early these cells may connect to PNs with more synapses in the adult. To test the hypothesis of staggered arrival, one could label different individuals of the same ORN type with differently colored flurophores (Hadjieconomou et al., 2011; Hampel et al., 2011). Imaging these brains around the time of ORN axon arrival in the
glomerulus would show whether some ORNs are further along then others in their invasion. Another idea is that differences between ORNs and PNs of the same type are a result of differences in gene expression. Single cell RNA sequencing techniques might be used to test this hypothesis. It would also be interesting to know how early in development appreciable differences between cells are evident. In one extreme, staggered cell birth may establish differences that persist into the adult brain. Alternatively, competition within the glomerulus could drive differences between cells. This could cause cells to differ in size, synapse number and position or connectivity pattern independent of any differences that existed before innervation began. Finally, the role of neural activity in establishing diversity is unknown. We have argued that activity is unlikely to contribute to the differences between ORNs from the same antenna we describe. On the other hand, it seems plausible that activity is involved in matching PN dendrite size and ORN input synapse number. Addressing these ideas will likely require correlating the activity of specific neurons and their anatomy, ideally at multiple points during development. While this is a tall order, it promises rich rewards.

Another outstanding question is how PN dendrite size and ORN input synapse number are matched. In principle, synapse number might increase to compensate for increased dendrite size. Alternatively, the dendrite might grow larger to correct for the increase in synapse number, or else these two effects might be independent. We think the increase in dendrite size comes first, and then synapse number increases to compensate for increased dendrite size. Developmental studies have shown that PN dendrites form a glomerular map and undergo substantial growth and branching prior to the arrival of migrating ORN axon terminals (Jefferis et al., 2004). Indeed, PN dendrites help guide
ORN axons to their correct terminal position (Hong et al., 2009). Moreover, there is direct evidence that the electrical properties of the PN dendrite can instruct changes in ORN→PN connections. One study used cell-specific K⁺ channel overexpression to decrease a PN’s input resistance, and found a compensatory increase in unitary excitatory synaptic currents at ORN connections onto that PN (Kazama and Wilson, 2008). That result argued that PN dendrites can upregulate synaptic current to achieve sufficient levels of depolarization. However, based on the experiments in that study, it was unclear if upregulation was pre- or postsynaptic. Here, we showed that individual ORN axons form more synapses onto larger PN dendrites. As our compartmental model illustrated, larger PN dendrites are also less excitable. If the same homeostatic process were at work here and in the previous study (Kazama and Wilson, 2008), then it would mean that a postsynaptic voltage sensor (in PNs) is inducing ORNs to devote more presynaptic sites to the connections that they form with large PN dendrites, so that synaptic currents are increased, and voltage responses are equalized.

If this model is correct, then it has implications not only for the way the circuit responds to developmental errors, but also for the normal development of the circuit. Some glomeruli are characteristically larger than other glomeruli. PNs in the larger glomeruli also have larger dendrites, meaning they should have a lower input resistance. In PNs having larger dendrites, unitary excitatory postsynaptic currents are also systematically larger, and thus despite the lower input resistance in these PNs, mean uEPSP amplitude is relatively uniform across glomeruli (Kazama and Wilson, 2008). Our results here suggest a structural mechanism for matching dendrite size with synapse
number per connection, and thus ensuring that all PNs respond similarly to a presynaptic ORN spike, regardless of the PN’s size.

Conceptually, this phenomenon is similar to “size matching” at the developing neuromuscular junction (NMJ). At the NMJ, the size of a muscle is matched to the size of the axon’s terminal arborization, ensuring that large muscles (with low input resistance) receive a larger quantal content per presynaptic spike (Kuno et al., 1971; Lichtman et al., 1987). Here too, the expansion of the postsynaptic cell seems to be primary, with the elaboration of the presynaptic arbor occurring in response (Balice-Gordon et al., 1990; Balice-Gordon and Lichtman, 1990).

It may be possible to use the ORN→PN circuit to study the mechanisms of size matching, given that ORN release sites can be counted using light microscopy methods. Mosca and Luo (2014) used a genetic method to fluorescently label the release sites in single ORN axons. Interestingly, the number of fluorescent puncta was lower in a smaller glomerulus, as we might predict from size matching. Thus, light microscopy techniques evidently have the resolution to measure systematic variations in synapse number across glomeruli, and may also be able to track variations in synapse structure triggered by perturbations in electrical activity (Acebes et al., 2012; Das et al., 2011; Kazama and Wilson, 2008; Kazama et al., 2011; Sachse et al., 2007; Yu et al., 2004).

Another mystery we are left with is the mechanism that ensures PNs receive stronger input from ipsilateral than from contralateral ORNs. The asymmetry in PN number in our dataset provided some observations that rule out a class of mechanism. Specifically, we can rule out any mechanism that would ensure that ipsilateral ORN-to-PN pairs are connected by more synapses than contralateral pairs. Consider the ORNs in
our data set that arise from the left-hand antenna. These cells distribute their synapses across three postsynaptic PNs ipsilaterally and only two PNs contralaterally. While they tend to form more synapses in the ipsilateral glomerulus than in the contralateral glomerulus, these synapses are distributed across more postsynaptic cells. This results in ORN→PN connections that are comprised of a similar number of synapses in the two brain hemispheres. It seems, therefore, that the underlying mechanism does not enforce an asymmetry in the number of synapses that make up ipsi and contra pairwise connections. Rather, it seems to ensure that ORNs form more synapses in ipsilateral than contralateral glomeruli. This makes it unlikely that ORNs identify individual postsynaptic PNs as being ipsilateral or contralateral and adjust the number of synapses they form on them accordingly. A more plausible mechanism might be a proximal-to-distal gradient of resources (ribosomes, mitochondria, etc.) relative to ORN cell bodies. For example, if there are more mitochondria or synaptic proteins in the proximal (ipsilateral) axon tuft, this could allow the cell to construct more synapses here. Alternatively, a staggered invasion of the glomerulus during development could be responsible for the synapse number difference. If ipsilateral axons arrive before contralateral axons they may experience less competition for space and growth factors allowing them to form more synapses. Finally, there may be molecular cues that identify glomeruli as being ipsilateral or contralateral to an ORN and instruct it to develop more or less synapses accordingly.

This mechanism is an attractive study subject because it could provide insight into how cells achieve functionally relevant, non-uniform synaptic distributions.

An interesting extension to our modeling work would be to explore a larger parameter space than we have explored here. In general, we restricted ourselves to the
dendrite morphologies provided by the anatomy. Furthermore, although in some cases we shuffled synapses among ORNs, we only ever used the true synapse positions revealed by the reconstructions. One could relax these restrictions and measure model behavior for a wider range of dendrite morphologies and synapse positions. It would be interesting to see if, like models of central pattern generating neurons and networks, the behavior of a model PN is more sensitive to movements along some axes in parameter space than others, and if so what the “sensitive” axes correspond to.

I am particularly pleased to be able to make the data we collected public. It may never receive more than a passing glance from the odd internet cruiser. Yet the possibility that someone else may make use of it, perhaps better use than I, is of some consolation at the end of this long road.
Appendix 1

Supplementary Figures
Figure S1: Variations in the number of PNs in glomerulus DM6.

By counting Gal4-expressing PNs in a glomerulus, we can obtain a lower bound on the number of PNs that reside in that glomerulus. No Gal4 line has been identified which drives expression exclusively in DM6 PNs. However, the NP3481-Gal4 line drives expression in DM6 PNs along with PNs in several other glomeruli (total count is 9.5 PNs on average, according to Tanaka et al., 2012). In order to limit a fluorescent marker to DM6 PNs alone, we used NP3481-Gal4 to drive expression of photoactivatable GFP (UAS-SPA; Datta et al., 2008), and we used 2-photon excitation to specifically photoactivate GFP within the DM6 glomerulus. Because the dendritic arbor of each PN typically ramifies throughout the entire glomerulus, photoactivating within a large fraction of the glomerulus should label each Gal4+ PN. In five experiments, we photoactivated both the right and left copies of DM6. Images shown here are maximum-intensity projections of confocal stacks imaged in a coronal plane (dorsal is up; red asterisks denote dim somata that were not photoactivated and that are not associated with DM6, based on inspection of the 3D stack). Most frequently we found three PNs per glomerulus, but we also occasionally found four or two PNs. The number of PNs was often different on the two sides of the same brain, but there was no systematic difference between right and left. This result implies that the number of Gal4+ DM6 PNs can vary, consistent with variable counts in other glomeruli in the number of Gal4+ PNs (Tanaka et al., 2004). Our EM reconstruction implies that at least some of this variability is due to true variation in PN counts, and is not merely due to variations in Gal4 expression patterns.
Figure S1 (Continued)
Table S1

<table>
<thead>
<tr>
<th>brain</th>
<th>genotype</th>
<th>left PNs</th>
<th>right PNs</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>NP3481-Gal4/Y; UAS-SPA-GFP/+; UAS-SPA-GFP/+</td>
<td>4</td>
<td>3</td>
</tr>
<tr>
<td>2</td>
<td>NP3481-Gal4/++; UAS-SPA-GFP/+; UAS-SPA-GFP/+</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>3</td>
<td>NP3481-Gal4/Y; UAS-SPA-GFP/+; UAS-SPA-GFP/+</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>4</td>
<td>NP3481-Gal4/++; UAS-SPA-GFP/+; UAS-SPA-GFP/+</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>5</td>
<td>NP3481-Gal4/++; UAS-SPA-GFP/+; UAS-SPA-GFP/+</td>
<td>2</td>
<td>3</td>
</tr>
</tbody>
</table>
Figure S2: Comparing anatomical features of ipsi- and contralateral ORN axons in glomerulus DM6.

(A) Total path length of each ORN axon within DM6 (P > 0.11, permutation test, n = 106, because the 52 bilateral axons were each counted 2 times, and the two unilateral 2 axons were each counted 1 time). For each axon, we identified the first node upstream (proximal) to all synapses within the glomerulus, and then we computed the sum of the Euclidean distance between all connected nodes downstream from that node.

(B) Total number of presynaptic specializations (T-bars) for each ORN axon within DM6 (P < 0.0001, permutation test).

(C) Density of presynaptic specializations (T-bars) for each ORN axon within DM6 (P < 0.0001, permutation test). For each axon, the total number of T-bars was divided by the total cable length.

(D) Postsynaptic profile density (P < 0.025, permutation test). We counted the number of cellular profiles postsynaptic to each axon (the number of outgoing edges) within DM6, and then divided this by the total path length of the axon in that glomerulus.

(E) Synaptic divergence (polyady) (P < 0.0001, permutation test). We counted the number of profiles postsynaptic to each axon in DM6 and divided this by the number of presynaptic specializations (T-bars) in that axon in that glomerulus.

(F) Fraction of output to PNs (P < 0.0001, permutation test). This is the fraction of the profiles postsynaptic to each axon in DM6 that are PN profiles.

(G) Total number of postsynaptic profiles (P < 0.002, permutation test). This is the number of profiles postsynaptic to each axon.
Figure S2 (Continued)

A  intraglomerular axon length (μm)  B  # of presynaptic specializations  C  density of presynaptic specializations (per μm)  D  density of postsynaptic profiles (per μm)

A: 200  B: 90  C: 0.6  D: 2

ipsi ORNs contra ORNs  ipsi ORNs contra ORNs  ipsi ORNs contra ORNs  ipsi ORNs contra ORNs

E  synaptic divergence  F  fractional output to PNs  G  total postsynaptic profiles

E: 5  F: 0.6  G: 300

ipsi ORNs contra ORNs  ipsi ORNs contra ORNs  ipsi ORNs contra ORNs
Figure S3: Axon-dendrite proximity correlates with the number of synapses per ORN-PN connection.

For each ORN-PN connection (n = 260), we measured the “potential connection length” (Ld) as the total path length of the PN dendrite within 500 nm of the ORN axon (Lee et al., 2016). For every PN, this estimate of proximity was strongly correlated with the number of synapses per connection (Pearson’s r ranges from 0.67 to 0.74; P-values range from $4.95 \times 10^{-8}$ to $2.46 \times 10^{-9}$ after Bonferroni-Holm correction for multiple comparisons, m = 5 tests).
Figure S3 (Continued)

The scatter plot illustrates the relationship between the number of synapses within a connection and the potential connection length $L_d$ (μm). The data points are color-coded by the location of the synapses:
- **Ipsi connections** are represented by circles and indicate a connection within the same hemisphere.
- **Contra connections** are represented by filled circles and indicate a connection between hemispheres.

The plot shows a trend where the number of synapses increases with the potential connection length, particularly visible for the right PN1 and right PN2 connections. The left PN1, left PN2, and left PN3 connections also show a similar trend, albeit with less data points.

The y-axis represents the potential connection length $L_d$ (μm), ranging from 0 to 200 μm. The x-axis represents the number of synapses within a connection, ranging from 0 to 60. The data points are distributed across the plot, indicating a correlation between the two variables.
Figure S4: Comparing model output sensitivity to parameter value changes.

Here we explored three sets of models (5 model PNs per set), with each set using specific intracellular resistivity, membrane resistance, and membrane capacitance values obtained from different electrophysiological experiments (Cell 1, Cell 2, and Cell 3 of Gouwens & Wilson, 2009). Cell 3 was intermediate between Cell 1 and Cell 2, so it was used throughout the main figures of our study.

(A) Left-right comparison of uEPSP amplitudes measured at the cell body of modeled PNs. Cell 3 (bottom panel) is reproduced from Figure 3C. Using parameters fit to Cell 1 and Cell 2, we obtain overall similar results, except with Cell 2 parameters we find a very small but statistically significant left-right difference (PCell 1 > 0.07, PCell 2 > 0.02, PCell 3 > 0.7, permutation test, n = 156 left and 104 right unitary connections).

(B) Ipsi-contra comparison of uEPSP amplitudes measured at the cell body of modeled PNs. Cell 3 (bottom panel) is reproduced from Figure 4D. The ipsi-contra difference is similar in all three cases (PCell 1 = 0.007, PCell 2 = 0.006, PCell 3 = 0.0059, paired-sample t-test, n = 5 PNs).

(C) Correlations between synapse number and mean uEPSP amplitudes are consistently strong. Cell 3 (bottom panel) is reproduced from Figure 5H. Pearson’s r ranges from 0.984 to 0.997 (Cell 1), 0.998 to 0.999 (Cell 2), 0.993 to 0.999 (Cell 3). P-values range from 1.59 ×10-39 to 2.94 ×10-56 (Cell 1), 3.85 ×10-60 to 1.22 ×10-72 (Cell 2), 9.78 ×10-48 to 1.34 ×10-65 (Cell 3) after Bonferroni-Holm correction for multiple comparisons, m = 5 tests).
Figure S4 (Continued)

(A) somatic uEPSPs in model PNs

(B) mean uEPSPs in model PNs

(C) somatic uEPSPs in model PNs versus synapse number

Cell 1

Cell 2

Cell 3

amplitude (mV)

0 10

left PNs right PNs

ipsi ORNs contra ORNs

number of synapses within connection

0 60
Bibliography


